Soybean DP-1 prote DP-1 transcription DP-1 transcription

Human brain expres Plant dimerisation

Pyruvate oxidase

Staphylococcus epi Staphylococcus epi E2F activity inhib

Fragment from a wh Human polypeptide Propionibacterium Human novel foetal Human orky protein Human nervous syst Human polypeptide Human protein frag Peptide #12567 enc

Human liver peptid Human peptide #482 Peptide #508 encod Protein #474 encod Human brain expres Human bone marrow

Fragment of human

Peptide #491 encod Peptide #500 encod Peptide #479 encod Human peptide enco Human novel protei

Polypeptide fragments of the DP-1 transcription factor - used for

NPI; 1998-377596/32.

Score

Result Š. 2 2 4 5 9 7 8 9

Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

Database

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DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
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                                         AAM3 0511

AAM53 051

AAM725 78

AAB73 8852

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AAB73 8852

AAB77 655

AAM6 111

AAM10 1790

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 (PROL-) PROLIFIX LTD.

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 AAW30502;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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This peptide comprises amino acid residues 175-183 in the DEF box region (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30502-07) containing this and/or another motif (see AAW30503) of the DEF box, are antagonists of the heterodimeriaation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially contraining substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and membrane translocation sequence (see AAW30508), expression vectors encoding (I)-(III) and host cells. (I)-(III) are used therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in viro, e.g. for purging bone marrow. Surgical stens comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNN-binding activity of DP/E2F heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-I/E2F dimerisation and as immunoassay nucleic acids encoding (I)-(III) to control by laced simunoassay nucleic acids encoding (I)-(III) to control by levels in cells, particularly by gone therapy. When formulated with cytotoxic or cytostatic agents, (I)-(III) enhance cell killing.
 inducing apoptosis, specifically in tumour and cardiovascular cells,
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                   e.g. for preventing restenosis
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Gaps

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                                                                                                                         Peptide H5 comprises amino acid residues 168-183 in the DBF box (I) (see AAM30501) of transcription factor DP1. Claimed peptides (II) (see AAM30504-07) containing one or both of 2 morifs (see AAM30502-03) of the DBF box are capable of antagonising the heterodimerisation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and a membrane translocation sequence (see AAM30508), expression vectors cardiovascular cells, either in vivo or in vitro, e.g. for purging therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging treat or prevent restenosis in patients who have undergone angioplasty. (I) (III) function by inactivating the DNA-binding activity of DP/E2F heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunosasay agents. Also described is the use of sequences antisense to nucleic acids encoding (I) (III) enhance cell killing.
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                             Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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tive 0; Mismatches 0; Indels
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                                                                                                 Claim 4; Page 44; 55pp; English.
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WPI; 1998-377596/32
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(i) (see AAW30501) of transcription factor DP1. Claimed poptides (II) (see AAW30501) of transcription factor DP1. Claimed poptides (II) (see AAW30501-07) containing one or both of 2 motifs (see AAW30502-03) of the DEF box are capable of antagonising the heterodimerisation of a DP protein with an BZP protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (III) and membrane translocation sequence (see AAW30508), expression vectors encoding (I)-(III) and host cells, specifically in tumour or therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding activity of DP/BZP heterodimers. They are also used as research reagents as positive controls in assays for identifying antagonists of DP-1/BZP dimerisation and as immunoassay agents.

Also described is the use of sequences antisense to nucleic acids cencoding (I)-(III) becauted by levels in cells, particularly by control of the property of the prevent or prevent care or preventiated with cytotoxic or cytostatic agents,
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/note= "Claim 3"
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AAW30505
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                                                                                                                                                                                Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                         Peptide H2mt2 is based on peptide H2 (see AAW30504) from the DEF box
                                                                                                                                                                                                                                                                                                                                                                                                                    (see AAW30501) of transcription factor DP1. In HZmt2, amino acid aresidues of HZ that correspond to DP1 residues Arg167 and Asp171 are substituted by Ala residues. HZ is an antagonist of the heterodimerisation of DP1 with EZF. HZmt2 retains some, but not heterodimerisation of activity. HZ and other claimed peptides (see AAW30504-07) from the DEF box region of DP1 can be used to induce apoptosis, specifically in tumour and cardiovascular cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription factor; antagonist; E2F protein; apoptosis; proliferation; cardiovascular cell; restenosis; tumour;
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/note= "Claim 3"
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                                                                Bandara LR, La Thangue NB;
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(PROL-) PROLIFIX LTD.
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                                        Peptide H3 comprises amino acid residues 174-193 in the DEF box (C [1] (see AAW30501) of transcription factor DP1. Claimed peptides (C [1]) (see AAW30504-07) containing one or both of 2 motifes (see (II) (see AAW30504-07) containing one or both of 2 motifes (see (II) (see AAW30504-07) containing one or both of 2 motifes (see (II) capture) to the containing the residued are variants of these peptides, especially containing claimed are variants of these peptides, especially containing claimed are variants of these peptides, especially containing containing and 175 of DP-1, fusion proteins (II) comprising (I) of (II) and a containing containing (I) of (III) are used to cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging creat or prevent restenosis in patients who have undergone treat or prevent restenosis in patients who have undergone antioplasty. (I)-(III) function by inactivating the DNA-binding angioplasty. (I)-(III) function in assays for identifying cardiovascular is a positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunosasky agents.

Also described is the use of sequences antisense to nucleic acids encoding (I)-(III) to control DP levels in cells, particularly by control of the particularly by control of the prevent capture of the particularly by control of the control of t
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                           Claim 4; Page 44; 55pp; English.
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This represents a compound that can inhibit E2F activity. The compound is of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acide. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
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                                                                 This represents a compound that can inhibit E2F activity. The compound also of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy hetero, and A1 is an B2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
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iive 0; Mismatches 0;
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                                        Example 3; Page 27; 52pp; Japanese.
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                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
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                                                                      Length 28;
                                                                                                                                     0; Indels
                                                        100.0%; Score 42; DB 19;
Similarity 100.0%; Pred. No. 0.016;
9; Conservative 0; Mismatches 0:
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/note= "Claim 3"
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                                                                                                                                                                                                                                                      19 NVLMAMNII 27
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                                                            Query Match
Best Local Similarity
28 AA;
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      Sequence
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encoding (I)-(III) to control DP levels in cells, particularly by gene therapy. When formulated with cytotoxic or cytostatic agents, (I)-(III) enhance cell killing.
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                                                                                                                                                                              Score 42; DB 19; Length 30;
Pred. No. 0.017;
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                     Gaps
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100.0%; Score 42; DB 19; Length 37; 100.0%; Pred. No. 0.022; ive 0; Mismatches 0; Indels
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             Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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This sequence represents 42% of the middle region of soybean cell cycle regulatory protein DP-1, as deduced from an isolated cDNA clone (see AAZ34579). The invention relates to nucleic acid fragments (see AAZ34575-83) encoding plant CDC-16, DP-1, DP-2 and E2F cell cycle regulatory proteins (see AAY32159-67). It also relates to the construction of a chimeric gene encoding all or a portion of the cell cycle regulatory protein, in sense or antisense orientation, where expression of the chimeric gene results in producton of altered levels of the cell cycle regulatory protein in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein TM, Morakinyo LO, Odell JT, Sakai H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant-derived cell cycle regulatory proteins
                                                                                                DP-1, soybean, cell cycle regulatory protein, transcription factor, herbicide.
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                                                                                                                                                                                                                                                                                                                                                                                               'note= "encoded by NAT"
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     AAY32163 standard; Protein; 83 AA.
                                                                                                                                                                                                                                  note= "encoded
                                                                            Soybean DP-1 protein fragment.
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                                                      (first entry)
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Query Match Matches

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Peptide H6 comprises amino acid residues 167-180 in the DEF box region (see AAW30501) of transcription factor DP1. Unlike claimed peptides (see AAW30504-07) that contain one or both of 2 motifs (see AAW30502-03) of the DP1 DEF box, peptide H6 is not capable of antagonishing the heterodimerisation of a DP protein with an E2F protein. The claimed peptides, their variants and fusion proteins can be used to induce apoptosis, specifically in tumour and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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                      Score 36; DB 19; Length 19;
Pred. No. 0.22;
0; Mismatches 1; Indels
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                      85.7%;
88.9%;
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                       AAW30511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM58362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
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                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM58362
                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SXXX
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                                                                                                                                         셤
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                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide HZmt3 is based on peptide H2 (see AAW30504) from the DEF box (see AAW30501) of transcription factor DP1. In H2mt3, amino acid residues of H2 that correspond to DP1 residues Leu173 and Leu176 are substituted by Arg residues. H2 is an antagonist of the heterodimerisation of DP1 with E2F. H2mt3 has none of the antagonistic activity of H2. H2 and other claimed peptides (see AAW30504-07) from the DEF box region of DP1 can be used to induce apoptosis, specifically in tunmour and cardiovascular cells, e.g. for the prevention of restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
a transformed host cell. The nucleic acids and proteins may be used to facilitate studies of cell cycle regulation in plants, provide genetic tools to enhance cell growth in tissue culture, increase gene transfer efficiency and provide more stable transformations. The proteins may also provide targets to facilitate design and/or identification of cell cycle regulatory proteins that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                       88.1%; Score 37; DB 20; Length 83; 88.9%; Pred. No. 0.8;
                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DP-1 transcription factor peptide H2mt3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "L176R mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "L173R mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example D; Page 26; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW30517 standard; Peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-GB03506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96GB-0026589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell proliferation; card surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                          15 NVLMAMDII 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROL-) PROLIFIX LTD.
                                                                                                                                                                                                                                                                                       1 NVLMAMNII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-377596/32.
                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                83 AA;
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Misc-difference Misc-difference

22-DEC-1997; 20-DEC-1996;

Bandara LR,

WO9828334-A1

02-JUL-1998

Homo sapiens

Synthetic

26-OCT-1998

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Gaps

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19 AA;

Sequence

Magyar Z;

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The invention relates to a novel cell cycle protein (CCP) and the polymucleotides encoding them. CCP is useful for identifying a compound polymucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the coll cycle or growth of a plant such as Arabidopsis thalians, rice, wheat, cycle or growth of a plant such as Arabidopsis thalians, rice, wheat, cycle or growth of a plant such as Arabidopsis thalians, rice, wheat, cycle or growth of a plant such as Arabidopsis thalians, rice, wheat, cycle or growth of a plant such as Arabidopsis collars, encourage collars, oilseed rape, soybean, sunflower and canola. CC maize, tomato, affalia, oilseed rape, soybean, sunflower and canola. CC maize, tomato, affalia, oilseed rape, soybean, sunflower geneting collars of cc protein or production of CCP protein for modulate the activity aberrant activity. Compounds that bind to or modulate the activity of polympoptide are useful for modifying cell fate, plant development, collars or plant morphology, blochemistry and/or physiology, the length of the Gl, stimulation or enhancement of cell cycle of a plant, initiation, geed set, of GT pand for manched formation, shoot and root initiation and/or development, tuber, fruit, leaf formation, seed set, conditions or resistence to stress copy the polymcleotide conditions, including abiotic stress such as pathogen attack, to modulate e.g. enhance crop yields, conditions and setenuate plant architecture, plant quality traits, plant, conditions and attenuate plant architecture, plant quality traits, plant, conditions and attenuate plant architecture, plant quality traits, plant, ells, processed to an attenuate plant architecture, plant quality traits, plant is parter. CCP is a plant of the plant of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     storage tissues and/or storage organs of plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to screen for naturally occurring CCP substrates. The polymucleotide is useful for expressing CCP protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to endulate CCP activity. The present sequence represents a motif which may be found in a CCP protein of the invention.
                                                                                                                                                                                                                                                                                                       New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29; DB 23; Length 8;
Pred. No. 9.3e+05;
1; Mismatches 0; Indel8
                                                                                                                                                                                                               Acosta JAT,
                                                                                                                                                                                                                    De Veylder L,
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; Page 93; 316pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW77753 standard; Protein; 88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.0%;
85.7%;
                                                                  14-MAY-2001; 2001WO-IB01307.
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                                                                                                                                                                    (CROP-) CROPDESIGN NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NVLMAMN 7
                                                                                                                                                                                                                    Boudolf V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AA;
                                                                                                                  12-MAY-2000;
                     15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrania, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                  Human brain expressed single exon probe encoded protein SEQ ID NO: 30467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid
                                                                                                  Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant dimerisation protein (DP) E2F heterodimerisation domain #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               א Match 13.8%; Score 31; DB 22; Length 67; Local Similarity 55.6%; Pred. No. 14; הרארז הפה 5; Conservative 4; Mismatches הי דרארז
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-MG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0236359.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00667
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             05-NOV-2001 (first entry)
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43 NIIIAINII 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483446/52
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Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 AA;
                                                                                                                                                                  epilepsy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200185946-A2.
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                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                       09-AUG-2001.
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Query Match Best Loc Matches

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Gaps

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Length 8;

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This sequence represents a Staphylococcus aureus protein, that based on homology with a Lactobacillus plantarum protein, is a pyruvateoxidase (EC 1.2.3.3) mutant (ith P1785, S188M, and A458V mutations) A chain, and is encoded by a DNA sequence of the invention.

The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides.

Conditions which may be treated include bacterial infections, especially centiarty, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection.
              Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid sequences from Staphylococcus aureus WCHU29 -
useful in vaccines and for treatment of bacterial infections of e.g.
respiratory tract and central nervous system
                                                                                                                                                                                                             /note= "residues designated X are unspecified, at
    represented as Xaa in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knowles DJC;
Reichard RW, Rosenberg M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Black MT, Burnham MKR, Hodgson JE,
Lonetto MA, Nicholas RO, Pratt JM,
Ward JM;
                                                                                                                                                                             Location/Qualifiers 1..88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 372; 390pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                            96US-0027032.
                                                                                                                                                                                                                                                                                                                                      97EP-0307485.
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nes 6; Conservative
                                                                                                                                          Staphylococcus aureus
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N-PSDB; AAV53541.
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NVLVPINII
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                                                                                                                                                                             Key
Misc-difference
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                                                                                                                                                                                                                                                                                                       13-MAY-1998
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ABP38852
ID ABP3
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AC ABP3
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                                    epidermidis; open reading frame; ORF; bacterial infection; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                       ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35134 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
             Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3434.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB
Pred. No. 54;
1; Mismatches
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                                                                                                                                                                                                                                     (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.0%;
                                                                                                                                                                                                         97US-064964P.
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antibacterial; gene therapy
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                                                                                 Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                            WPI; 2002-381255/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLMALNI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VLMAMNI 8
                                                                                                                                                                                                                                                                 Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 AA;
                                                                                                                                                                                                                                                                                                         N-PSDB; ABN91397
                                       Staphylococcus
antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1998;
                                                                                                            US6380370-B1
                                                                                                                                                                  13-AUG-1998;
                                                                                                                                                                                            14-AUG-1997;
                                                                                                                                                                                                           08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-APR-2002
                                                                                                                                      30-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP38589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP38589
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99ES-0002127
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                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gutierrez-Armenta C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-257972/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum monococcum
                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                           10 NVLMAM 15
                                                                                                                                                                                                                                                 1 NVLMAM 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF80148
                                                                                                                                                                         15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200121644-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-11999;
                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-2001.
                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                  AAB67766;
                                                                                                                                                                           Sequence
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                   RESULT 20
                                                                                                                                                                                                                                                                                                                                AAB67766
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                                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                     ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to compounds able to interfere with the S. epidermidis lifection. N.B. The sequence data for inhibit S. epidermidis infection.
N.B. The sequence data for this patent did not form part of the printed separation, but was obtained in electronic format directly from the sequence.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                          Novel isolated nucleic acid encoding a Staphylococcus epidermidis
polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E2F activity; inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 23; Length 100;
Pred. No. 63;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yoshida T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
/note= "C-terminal amide"
                                                                                                                                                                  Disclosure; SEQ ID 3434; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E2F activity inhibiting compound Ib-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamasaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW57052 standard; peptide; 15 AA
                                         (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                           69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-JP03442
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    97US-055779P
97US-064964P
                                                                  Doucette-Stamm LA, Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mizukami T, Shibata K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-240020/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 VLMALNI 55
                                                                                          WPI; 2002-381255/41.
N-PSDB; ABN91134.
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            2 VLMAMNI 8
                                                                                                                                                                                                                                                                                                                                                   100 AA;
                                                                                                                                                                                                                                                                                                                            USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-1997;
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      14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW57052;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 19
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This represents a compound that can inhibit E2F activity. The compound is of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or anino, and A is an E2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated, enriched, cell free and/or recombinant nucleic acid
useful for e.g. altering cell proliferation characteristic such as to
alter plant cell, organ or tissue size -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB67764-68 represent fragments of a wheat E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
E2F activity inhibitors - for treatment and prevention of tumours and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fragment from a wheat E2F-dimerisation partner (DP) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ramirez-Parra E;
                                                                                                                                                 Example 4; Page 28; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB67766 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 50; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                              Gaps
particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue size.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 14386; 1399pp + Sequence Listing; English.
                                                                              22; Length 56;
                                                                                                            1; Indels
                                                                              Score 28; DB
Pred. No. 52;
                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 14386.
                                                                                                                                                                                                                                                         AAO00494 standard; Protein; 91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT, Liu C, Drmanac RT;
                                                                              66.7%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001; 2001WO-US04927,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                            5; Conservative
                                                                                                                                                             1 NVLMAMNII 9
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N-PSDB; AAI80425.
                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                              56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                       06-NOV-2001
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                                                                                                                                                                                                                                                                                         AAO00494;
                                                                                                                                                                            22
                                              Sequence
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                                                                                                              Matches
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention of and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to commend activity of P. acnes polypeptides and activity of P. acnes polypeptides and activity of P. acnes propedies may also be used as clasmostic agents for determining P. acnes presence, by account of immunosorbent assay (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                              SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.3%; Score 27; DB 22; Length 83 ilarity 62.5%; Pred. No. 1.4e+02; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                             Propionibacterium acnes immunogenic protein #5395.
                                                                                                                                                                                                                                                                                                                                                                  dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID No 5694; 1069pp; English.
                                                                                                                                        AAU44499 standard; Protein; 83 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                       27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes.
                                     30 NILKSINII 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
1 NVLMAMNII
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                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200181581-A2
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                                                                                                                                                                               AAU44499;
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                                                                                                RESULT 22
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66.7%; Score 28; DB 22; Length 91; 55.6%; Pred. No. 94; ive 3; Mismatches 1; Indels

Query Match
Best Local Similarity 55.6
Matches 5; Conservative

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2000US-0241786.
2000US-0241787.
2000US-0241809.
2000US-0241809.
2000US-0241826.
2000US-024617.
2000US-0246475.
2000US-0246477.
2000US-0246477.
2000US-0246477.
05-SEP-2000; 2000US-0229509.
05-SEP-2000; 2000US-0229513.
06-SEP-2000; 2000US-0230437.
08-SEP-2000; 2000US-0231242.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231413.
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2000US-0249215
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000US-0236802
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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20-OCT-2000;
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14-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
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1-SEP-2000;
1-SEP-2000;
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25-SEP-2000;
26-SEP-2000;
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27-SEP-2000;
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                                                                                                                                                                                   Human; foetal tissue antigen; antiinflammatory; neuroprotective; immunomodulator; cardiovascular; cytostatic; nephrothropic; cardiovascular; autoimmune disease; rheumatoid arthritis; cardiovascular disorder; breast neoplasm; cancer; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cardiac arrest; cerebrovascular disorder; cardiac arrest; cerebrovascular disorder; cardiovascular disorder; cerebral isorder; disease; infection; coular disorder; corneal infection; wound healing; epithelial cell proliferation; food additive.
                                                                                                                                                                  Human novel foetal antigen, SEQ ID NO 1555.
                                                                                                AAU21311 standard; Protein; 48 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0224519.
2000US-0225213.
2000US-0225214.
2000US-0225266.
2000US-0225266.
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2000US-0217487.
2000US-0217496.
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2000US-0216647
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2000US-0220963
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17-WAR-2000; 2000US-0190076
18-APR-2000; 2000US-0198123
19-WAY-2000; 2000US-0205515
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                                                                                                                                              (first entry)
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NVLVNMAN 16
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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14-AUG-2000;
14-AUG-2000;
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                                                                                                                                            18-DEC-2001
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                       02-AUG-2001.
                                                                                                                      AAU21311;
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                                                                            RESULT 23
                                                                                        AAU21311
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Human; colon cancer; colon cancer antigen; diagnosis; detection;

colorectal carcinoma; chromosome 1.

Human colon cancer antigen protein SEQ ID NO:6056.

03-SEP-2001 (first entry)

AAG75292;

AAG75292 standard; Protein; 55 AA

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New polynucleotides and polypeptides for diagnosing, treating, preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and respiratory systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.9%; Score 26; DB 22; Length 48; 62.5%; Pred. No. 1.2e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID No 1555; 642pp; English.
                                                                                                                                                                                                                             Barash SC, Ruben SM;
                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                           01-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0251980.
05-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0251989.
                                        17-NOV-2000; 2000US-0249264.
                                                         17-NOV-2000; 2000US-0249297
17-NOV-2000; 2000US-0249299
17-NOV-2000; 2000US-0249300
01-DEC-2000; 2000US-0250160.
                                                                                                                                        2000US-0251856
                                                                                                                                                                                          05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                              WPI; 2001-488782/53.
                                                                                                                                                                                                                                                      N-PSDB; AAS34131
                                                                                                                                      08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                        17-NOV-2000;
                                                                                                                                                                         08-DEC-2000
                                                                                                                                                                                                                            Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -

Claim 11; Page 7535-7536; 9803pp; English.

Birse CE, Rosen CA;

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Barash SC, WPI; 2001-235357/24.

N-PSDB; AAH34697

99US-0157137. 99US-0163280.

29-SEP-1999;

03-NOV-1999;

28-SEP-2000; 2000WO-US26524.

WO200122920-A2.

05-APR-2001

Homo sapiens.

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The invention relates to novel nucleic acids encoding novel human foetal antigens. The nucleic acids and proteins are used to prevent, treat (e.g. by gene therapy) or ameliotzate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition. The antibodies to the antigens can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunoassays (BLISA). Disorders which are diagnosed or treated immunoassays (BLISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, viruses and fungi and ocular disorders e.g. cardiac arrest, by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be accepted all wound healing and epithelial ecll proliferation, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevent skin aging due to sunburn, to maintain organs before transplantarion, for supporting cell culture of primary issues, to regenerate tissues and in chemotaxis. The polypeptides can also be use a food additive or preservative to increase or decrease storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. Numerous examples of diseases and disorders treated by the nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins are given in the specification. The present sequence
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and cancer antigens. The colon cancer antigens have cytostatic activity and cancer antigens. The colon cancer antigens are collectively may be used in gene therapy and vaccine production. N and P may be used in the prevention, caypression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing to expressing the nucleic acids into a host cell and culturing the cell color cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell concertal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.9%; Score 26; DB 22; Length 55; 62.5%; Pred. No. 1.4e+02; ive 2; Mismatches 1; Indels
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SEQ ID NO:1027 to 1052, 7921 and 7922.
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Matches 5; Conservative
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Best Local Similarity 62.5 Matches 5; Conservative

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX in the specification). ABN15762 to ABN27252 encode the human ORFX creating given in ABB0010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a graduence can be used in the manufacture of a medicament for treating a sequence can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, treatment of cancer, hyperproliferative disorders, introbes of liver, transplantation, cardiovascular diseases, disbetes mellitus, systemic clupus errythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious disease autoimmune inflammentory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, correction or regenerative disorders, or periodomtal disease, and for gut correction or regenerative disorders, or periodomtal disease, and for gut correction or regeneration and treatment of lung or liver fibrosis, men who servence das experience or sequence or have a maintiple scleroid gut second correction or regeneration and treatment of lung or liver fibrosis, mented and experience or systemic cytchine damage.
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                                         Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.9%; Score 26; DB 23; Length 58; Best Local Similarity 55.6%; Pred. No. 1.5e+02; Matches 5; Conservative 2; Mismatches 2; Indels
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         Human ORFX protein sequence SEQ ID NO:7428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, SEQ ID 7428; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-106308/14.
                                                                                                                                                                                                                            myasthenia gravis
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                                                                                                                                                                                                                                                                                                                       WO200192523-A2
                                                                                                                                                                                                                                                                           Homo sapiens.
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparastitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                           Human nervous system related polypeptide SEQ ID NO 6147.
               ABB17490 standard; Protein; 62 AA.
                                                                                                                                                                                                                                                                                                                                                                                    2000US-0225213.
2000US-0225214.
2000US-0225266.
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                                                                                                                                                                                                  17-JAN-2001; 2001WO-US01334
                                                                                                                                                                                                                                                   2000US-0189874
                                                (first entry)
                                                                                                                                                                 WO200159063-A2.
                                                                                                                                                 Homo sapiens.
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                                                23-JAN-2002
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                                ABB17490;
RESULT 26
         ABB17490
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2000US-0231244

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58 AA;

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20-OCT-2000; 2000US-0241785.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241868.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-0244674.
08-NOV-2000; 2000US-0246474.
08-NOV-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246524.
08-NOV-2000; 2000US-0246524.
08-NOV-2000; 2000US-0246524.
08-NOV-2000; 2000US-0246527.
08-SEP-2000; 2000US-0231413.
08-SEP-2000; 2000US-0231414.
08-SEP-2000; 2000US-0232080.
08-SEP-2000; 2000US-0232081.
12-SEP-2000; 2000US-0232981.
14-SEP-2000; 2000US-0232397.
14-SEP-2000; 2000US-0232398.
14-SEP-2000; 2000US-023398.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0234274.
25-SEP-2000; 2000US-0234274.
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17-NOV-2000; 2000US-0249210.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249212.
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17-NOV-2000; 2000US-0249265
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
13-OCT-2000;
13-OCT-2000;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are solutions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergias, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections.

(Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
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50.0%; Pred. No. 1.7e+02;
tive 3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                   Ruben SM;
                                                             2000US-0251160.
2000US-0251030.
2000US-0251988.
                                                                                                            2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0251869.
2000US-0251989.
                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
               2000US-0249299
2000US-0249300
                                             2000US-0250391
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                                                                                                                                                                                                                                                                                                                                                                                                                    useful for preventing, dicancers and metastases -
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                                                                                                                                                                                                                                                                                                                 Rosen CA, Barash SC,
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Best Local Similarity
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44 NILLILNI
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                                         01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
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WO200192523-A2.

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27525 encode the human ORFX in the specification). ABN15762 to ABN27525 encode the human ORFX coproteins given in ABB0010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a squence can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, treatment of cancer, hyperproliferative disorders, introsis of liver, consolvantials, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders infectious consensative disorders such as multiple sclerosis, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid disease and autoimmune inflammators of organization gravis, graft-versus-host consensative disorders incisions, ulcers, for treating osteoporosis, or periodomical disease, and for gut correction or regeneration and treatment of lung or liver fibrosis, repertusion injury in various tissues and conditions resulting from the manager.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                      Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 23; Length 72;
Pred. No. 2e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. pylori cytoplasmic protein, 22542803.aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID 6832; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW20232 standard; Protein; 79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.9%;
71.4%;
                                                                                                                                      30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                        29-MAY-2001; 2001WO-US10836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                           Shimkets RA, Leach MD;
                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                              2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||:|:|
24 LMAVNLI 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 AA;
                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABN19177
                                             06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW20232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polympetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, mematopoissis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and activity and activity and activity and activity activity and activity and activity and activity of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; dyperprofiferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 25682; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.9%; Score 26; DB 22; Length 71;
44.4%; Pred. No. 2e+02;
ive 3; Mismatches 2; Indels
     nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ORFX protein sequence SEQ ID NO:6832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP03425 standard; Protein; 72 AA
                                                                                                                                                                                                                                                                                                                                                                        rang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                   28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                      26-FEB-2001; 2001WO-US04927
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Best Local Similarity 44...
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:| ||::
63 NLLQLMNLV 71
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                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-514838/56.
N-PSDB; AAI91721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 AA;
                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                          WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation.
                                                               Homo gapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-2002
                                                                                                                                                        07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders
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Gaps

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RESULT 28
ABP03425
ID ABP03425
XX
AC ABP03
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DT 24-JU
DE HUMAN
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KW GEGEN
KW APPER
KW IMMUN
KW IMMU

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Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORPs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of fellocobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated human polynucleotides containing single nucleotide polymorphisms, useful for the treatment and diagnosis of e.g. cancer, infection and diabetes -
                                                                                                                                                                                    Helicobacter pylori nucleic acids and proteins - used to develop products for the detection, prevention and treatment of H. pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, single nucleotide polymorphism, SNP, paternity test,
forensic test, aberrant protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26; DB 19;
Pred. No. 2.8e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                Claims 27, 31; Page 176; 279pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein fragment SEQ ID NO: 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM00188 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.9%;
ilarity 62.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JAN-2001; 2001WO-US00322.
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             96US-0759739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-451871/48.
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                                                                                                                               WPI; 1998-271811/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NVLMAMNI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                         Smith D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 AA;
                                                   (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH89297
                                                                                                                                               N-PSDB; AAX30439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200151670-A2.
28-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
             06-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2001
                                                                                                                                                                                                                            infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                       Alm RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a H. pylori cytoplasmic protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from everlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORP of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.9%; Score 26; DB 18; Length 79; 62.5%; Pred. No. 2.2e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein; cellular protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. pylori ORF 03ee11215_22542803_f1_7 secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 61; Page 440-41; 1481pp; English.
                                                                                                                                                                                                                                                                Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY10972 standard; Protein; 96 AA.
                                                                                                                               96WO-US09122.
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                                                                                                                                                                 96US-0630405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 62.
                                                                                                                                                                                                                                                                Berglindh OT, Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||| ::
NVLMATDV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NVLMAMNI 8
                                                                                                                                                                                                                                                                                                    WPI; 1997-052306/05.
               Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 AA;
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                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT67454
                                                                                                                                                                                                                        (ASTR ) ASTRA
                                                   WO9640893-A1
                                                                                                                             06-JUN-1996;
                                                                                                                                                                   01-APR-1996;
                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1997;
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                                                                                       19-DEC-1996
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Sequence

Query Match Best Loc Matches AAY10972;

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Gaps

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22; Length 25;

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Query Match
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                      The present invention relates to human nucleic acids containing single nucleotide polymorphisms (SNPs). These can be used in forensic and paternity tests, and to aid in the treatment of diseases associated with aberrant protein expression, including cancer, amyloidosis, diabetes, Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis, glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis, meningitis, muscular disorders, dementia, neurological diseases, tuberous soclerosis, male infertility, hypercalcaemia, blood pressure disorders, osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or autoimmunity. The present sequence is a peptide encoded by a polymorphism-containing oligonucleotide fragment of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #12567 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for
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                                                                                                                                                                                                                                                   Score 25; DB 22; Length 14;
Pred. No. 45;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID No 38799; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
Disclosure; Page 314; 475pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM38530 standard; Protein; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-053366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                             59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                         Local Similarity 62.5
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                                                                                                                                                                                                                                                                                                                                                        7 NYLOALNI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                             1 NVLMAMNI 8
                                                                                                                                                                                                                                14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM38530;
                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                              Matches
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25 AA;

Sequence

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As series of synthesised peptides (AAR63492-9) based on the amino acid sequence of the novel rat serotonin receptor REC20. The peptides were used either in the generation of antibodies for the diagnosis of the cued either in the generation of antibodies for the diagnosis of the receptors in the detection of materials binding to the receptors.

Serotonin receptors belong to at least two protein superfamilies:
Serotonin receptors containing 7 TMDs (including of FPM2) and ligand-gated ion channel receptors with 4 protectives that fall into three new serotonin subfamily classifications:
TMDs (5-HT13). The serotonin receptors presented in the pattent represent protectypes that fall into three new serotonin subfamily classifications:
TMDs (6-HT3). The serotonin receptors presented in the pattent represent claudivided into 5-HT5alpha, rat REC17 - AAQ72259 and 5-HT5a

Sequences found in the TMDs. Degenerate primers were conserved amino acid sequences found in the TMDs. Degenerate primers were constructed to sequences and used in two rounds of nested PCR amplification of a mplification, degenerate primers corresponding to conserved residues camplification, degenerate primers corresponding to conserved residues those receptors. The resultant fragments were cloned into pBluescript those receptors.
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serotonin; receptor; transmembrane; domain; kinase; phosphorylation; sensory; motor; behaviour; central nervous system; CNS; superfamily; G-protein; ligand-gated; ion channel; subsfamily; human; rat; amplify; primer; PCR; amplification; brain; hypothalamus; indolamine; drug; hypothalamus; therapeutic; neurological; pathology; dementia; insomnia; Parkinson's disease, eating disorder; anxiety; migraine; headache.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat REC20 serotonin receptor extracellular loop 1 antigenic peptide.
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in diagnosis and treatment of neurological processes and
                                                              1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "undetermined amino acid"
Score 25; DB 2
Pred. No. 91;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sutcliffe JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 45; Page 174; 198pp; English.
                                                                                                                                                                                                                                                                                                                                                                   AAR63496 standard; Peptide; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erlander MG, Lovenberg TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US02839
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      59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
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                                         Best Local Similarity 33.3
Matches 3; Conservative
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                                                                                                                                           σ
                                                                                                                                              1 NVLMAMNII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathologies.
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25-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR63496;
                                                                                                                                                                                                                                                                                                               RESULT 33
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       cDNA library to obtain full length clones. The nucleic acids molecules and their corresponding proteins may be used in methods for determining ligand binding activity, detecting and altering expression of serotonin receptors, drug screening and therapeutic treatments involving human serotonin receptors. Serotonin receptors are also known to participate in neurological processes. Pathologies including dementia, Parkinson's disease, eating disorders, pathological anxiety, migraine, headaches, insommia and other conditions.

(Updated on 25-MAR-2003 to correct PN field.)
 The plasmid fragments were used to screen a rat hypothalamus
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA, Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;
                                                                                                                                                                ö
                                                                                                                                         59.5%; Score 25; DB 15; Length 32; 44.4%; Pred. No. 1.2e+02;
                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                 Fragment of human secreted protein encoded by gene 2.
                                                                                                                                                               4; Mismatches
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Endress GA, Ebner R;
                                                                                                                                                                                                                                                                AAY76229 standard; Protein; 35 AA.
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98US-0085105.
98US-0085180.
98US-0085906.
98US-0085920.
98US-0085921.
98US-0085922.
98US-0085923.
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                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                    Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                 22 NVFIAMDVM 30
                                                                                                                                                                                   1 NVLMAMNII 9
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                                                                                                                     32 AA;
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18 - MAX - 1998
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                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                     AAY76229;
                                                                                                                                          Query Match
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AAZ65250 to AAZ65150 represent 97 isolated human secreted protein genes.

AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human genes. This sequence represents a fragment of one of the human secreted proteins. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foctal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, achizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, diseases, inflammation, allergies, Alzheimer's and cognitive disorders, diseases, infections and AIDS. The polypeptides are also useful for identifying their binding partners.

The sequences shown in AAY76224 to AAY76424 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 21; Length 35;
Pred. No. 1.4e+02;
1; Mismatches 0; Indels
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Disclosure; Page 417; 475pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.5%;
83.3%;
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2000US-0207456.
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2000US-0234687.
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||MALNII 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MAMNII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 AA;
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27-SEP-2000;
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     The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human peptide #482 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label
                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID NO 10799; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; microarray; single exon probe; gene expression; breast
                                                                                                                                                                                                                                                                                                         59.5%; Score 25; DB 22; Length 51; 71.4%; Pred. No. 2.2e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                       from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB27831 standard; Peptide; 51 AA.
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2000US-0234687.
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04-OCT-2000; 2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                  Conservative
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ses 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     3 LMAMNII 9
                                                                                                                                                                                                                                                                              51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease; cancer.
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21-SEP-2000; 2
27-SEP-2000; 2
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                                                                                                                                                                                                                                                                                Sequence
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bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysts is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human feetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                    probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #508 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 25637; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                         Score 25; DB 22; Length 51;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB33002 standard; Peptide; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
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26-MAY-2000; 2000US-0207456.
30-UTM-2000; 2000US-0608408.
03-MUG-2000; 2000US-063336.
21-SEP-2000; 2000US-023689.
                                                                                                                                                                                                                                                                                                            59.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                         Local Similarity 71.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                       17 LMAMNTL 23
                                                                                                                                                                                                                                                                                                                                                                                 3 LMAMNII 9
                                                                                                                                                                                                                                                                             51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157277-A2.
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                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 37
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LMAMNTL 23
   3 LMAMNII 9
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                                                                                                                                                                                                                                                                                                        WO200157275-A2
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30-JUN-2000;
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27-SEP-2000;
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                                                                                                                               AAM53800;
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Matches
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                                                                                       AAM53800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM66186
                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                       Protein #474 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                                     Gaps
                                                                                     ö
                                                                                                                                                                                                                                                                                                                                  Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                         Length 51;
                                                                                     1; Indels
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                         Score 25; DB 22;
Pred. No. 2.2e+02;
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                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; SEQ ID No 20245; 530pp; English.
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                                                                                                                                                                                                                  ABB18475 standard; Protein; 51 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
                                                         59.5%;
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2000US-0608408.
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                                        Query Match
Query Match
Beet Local Similarity 71.4%,
Beilhea 5; Conservative
                                                                                                                                                                                                                                                                          23-JAN-2002 (first entry)
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Best Local Similarity 71.4°
                                                                                                                                                                                                                                                                                                                                                                congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG, Hanzel DK,
                                                                                                                                            17 LMAMNTL 23
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                                                                                                                LMAMNII 9
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                            51 AA;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                            Sequence
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                                                                                                                                                                                       RESULT 38
ABB18475
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Gaps ö

59.5%; Score 25; DB 22; Length 51; 71.4%; Pred. No. 2.2e+02; ive 1; Mismatches 1; Indels

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                                                                                                                                                           Human brain expressed single exon probe encoded protein SEQ ID NO: 25905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human brains - \,
                                                                                                                                                                                                             Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO: 25905; 650pp + Sequence Listing; English.
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AAM53800 standard; Protein; 51 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0207456.
2000US-0608408.
2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0234687
2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LMAMNII 9
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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                                                                            Penn SG, Hanzel DK,
                                                                                               WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                         3 LMAMNII 9
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17 LMAMNTL
                                                                                                                                                                                                                                                                                  51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                              AAM26463;
                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                         RESULT 42
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                                                                                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #491 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; human; microarray; gene expression; cervical epithelial cell;
                      Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
   Human bone marrow expressed probe encoded protein SEQ ID NO: 26492.
                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 26492; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                   59.5%; Score 25; DB 22; Length 51; 71.4%; Pred. No. 2.2e+02; rive 1; Mismatches 1; Indels
                                                                                                                                                                                                                             Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM14057 standard; Protein; 51 AA.
                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                             Chen W,
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26-MAY-2000; 2000US-0207456
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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Best Local Similarity 71...
5; Conservative
                                                                                                                                                                                                                              Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 LMAMNTL 23
                                                                                                                                                                                                                                                 WPI; 2001-488900/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cervical cancer
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                                                                         WO200157276-A2
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                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #500 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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Pred. No. 2.2e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID No 18883; 487pp; English
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                                                                                                                       Chen W, Rank DR;
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                                                         (MOLE-) MOLECULAR DYNAMICS INC
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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04-OCT-2000; 2000GB-0024263
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ABG35836;
                                                                 Sequence
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                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development,
                                                                                                                                                                                                                                                                                                                                                           encoded by probe for measuring human breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                     encoded by one
                                                                      The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                             Probe; human; breast disease; breast cancer; development disorder;
                    genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                             ö
                                                                                                                                                                      Score 25; DB 22; Length 51;
Pred. No. 2.2e+02;
1; Mismatches 1; Indels
                                analyzing gene expression in human placenta
                                                   Claim 27; SEQ ID No 26732; 654pp; English
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                                                                                                                                                                                                                                                                                          AAM01797 standard; Protein; 51 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                   59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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2000US-0608408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                             Conservative
                                                                                                                            human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-476286/51
 WPI; 2001-488897/53
                                                                                                                                                                                                                                       LMAMNTL 23
                                                                                                                                                                                 Local Similarity
nes 5, Conserv
                                                                                                                                                                                                                  3 LMAMNII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in a human breast
                                                                                                                                                   51 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                           Peptide #479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                     09-0CT-2001
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                                                                                                                                                                                                                                                                                                                 AAM01797;
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                                                                                                                                                   Sequence
                                                                                                                                                                       Query Match
                      Human
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inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human peptide encoded by genome-derived single exon probe SEQ ID 25501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicoyrosis; lymphangiolelenomyoncosis; Karagener syndrome; pulmonary alveolar proteinnosis; fibrocyetic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic Obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
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                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                             Score 25; DB 22;
Pred. No. 2.2e+02;
1; Mismatches 1;
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                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences
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Similarity 71.4%;
5; Conservative
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2000US-0608408.
2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyaline membrane disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                       17 LMAMNTL 23
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          3 LMAMNII 9
                                                                                                                                                                                          51 AA;
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30-JUN-2000;
03-AUG-2000;
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mRNA, and (b) measuring the label detectably bound to each probe of mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising

(a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting at seat one exon from genomic sequences of the eukaryote; and (b) detecting appecific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of acroarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes of 12011 sequences, mentioned in the specification, or encoded by the probes are used for gene of 12011 sequences, mentioned in the specification, or encoded by the probes are used for gene of 12011 sequences, mentioned in the study of lung diseases using human lung derived mRNA and for the study of lung diseases (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, hermonally and proverse (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary content disease, Hermann-Pick disease, Hermannsky-Pudlas syndrome, saccidesis, pulmonary becames at the exons the exons in the probes of Hermannsky-Pudlas syndrome, saccidesis, pulmonary becames and the probes of Hermannsky-Pudlas syndrome, saccidesis, pulmonary and proventing and p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiaviral; antibacterial; antialierglic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haemosiderosis, pulmonary histiocytosis, lymphangioleiomyontosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
collection of detectably labeled nucleic acids derived from human lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.5%; Score 25; DB 23; Length 51; 71.4%; Pred. No. 2.2e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 71.7
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AA;
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The invention relates to polymucleotides encoding novel human correcting or their active domains. The polymeptides, polymucleotides and antibodies raised against the polymeptides are used in a method of contraction of antibodies caused by the aberrant correction activity. The polymeptides caused by the aberrant corresponds which bind to the protein expression or activity. The polymeptides can be used as complements, and in antibody production. The polymeptides are used to identify compounds which bind to the polymeptides. Polymucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the polymeptides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the corresponds of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to target drugs to a tumour, in assays to determine biological activity, to target drugs to a tumour, in assays to determine biological activity, to cases antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Copypeptides of the invention may also be useful in treating platelet copypeptides of the invention may also be useful in treating platelet contraceptive, treating observations, and diseases, amylotrophic lateral ing antibodies and osteoarthritis, anaemia, allered information or from autoinmunity, cancer, allered, anaemia, contraceptive, treating one copyment of stems and huntington's allsease, amylotrophic lateral contraceptive, immune deficiencies resulting from bacterial, viral or copyment in a fine and any anaemia, allered and all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                   Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders, and infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-inflammatory diseases, nervous system disorders, and i
The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             grařt-versus-host disease, eczema, haemophilia,
anti-inflammatory diseases, nervous system disor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 22;
Pred. No. 2.2e+02;
1; Mismatches 0;
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                                                                                                                                                                                                                            Example 4; Page 581; 894pp; English
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Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                          WPI; 2001-451939/48.
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Best Local Similarity
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1 MALNII 6
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                                                                                     N-PSDB; AAS22537
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   Tang YT,
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February 17, 2004, 10:53:48; Search time 13.1881 Seconds (without alignments) 142.889 Million cell updates/sec
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1: 'cgn2_6'ptodata_1/pubpaa/PCT_NEW_PUB.pep:*
2: 'cgn2_6'ptodata_1/pubpaa/NSO7_NEW_PUB.pep:*
4: 'cgn2_6'ptodata_1/pubpaa/USO6_NEW_PUB.pep:*
4: 'cgn2_6'ptodata_1/pubpaa/USO6_NEW_PUB.pep:*
5: 'cgn2_6'ptodata_1/pubpaa/USO8_NEW_PUB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO8_NEW_PUB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO8_PUBCOMB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO8_PUBCOMB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO8_PUBCOMB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO8_PUBCOMB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO9_NEW_PUB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO9_NEW_PUB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO9_NEW_PUB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO9_NEW_PUB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO9_NEW_PUB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO08_PUBCOMB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO08_NEW_PUB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO08_NEW_PUB.pep:*
7: 'cgn2_6'ptodata_1/pubpaa/USO08_NEW_PUB.pep:*
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GenCore version 5.1.6
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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seq length: 100
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	2, Appli 5, Appli	3, Appli	4, Appli	9	1, Appli	10, Appl	15,	17,		3263, A	13, App	6066, Ap	8875, A
Description	Sequence 2,	Sequence 3,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 11	Sequence 43263,	Sequence 513, App	Sequence 6066,	Sequence 48875
SUMMARIES	US-09-900-147-5 US-09-900-147-5	US-09-900-147-3	US-09-900-147-4	9-900-147-6	9-900-147-1	US-10-214-188-10	US-09-900-147-15	US-09-900-147-17	US-09-900-147-11	US-09-864-761-43263	JS-09-939-980-513	US-10-106-698-6066	JS-09-864-761-48875
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RESULT 2 US-09-900-147-5 ; Sequence 5, Application US/09900147 ; Patent No. US20020103121A1

1 NVLMAMNII 9 |||||||| 1 NVLMAMNII 9

8 8

Sequence 228, App	Sequence 230, App	Sequence 31645, A	Sequence 33773, A	Sequence 339, App	Sequence 811, App	Sequence 8, Appli	Sequence 47543, A		1030,	Sequence 5276, Ap	3623,	Sequence 1032, Ap	Sequence 1032, Ap	Sequence 33793, A	Sequence 44843, A	Sequence 66, Appl	Sequence 46815, A	Sequence 112, App	Sequence 40663, A	Sequence 27, Appl	Sequence 6, Appli	Sequence 40202, A	Sequence 54, Appl		Sequence 202, App	4,	Sequence 2, Appli		Sequence 72, Appl
US-09-892-877-228	US-09-948-783-230	US-10-029-386-31645	US-09-864-761-33773	US-10-291-265-339	US-10-291-265-811	US-10-044-359-8	US-09-864-761-47543	US-09-933-767-1030	US-10-023-282-1030	US-09-864-408A-5276	US-09-864-761-33623	US-09-933-767-1032	US-10-023-282-1032	US-10-029-386-33793	US-09-864-761-44843	US-10-376-121A-66	US-09-864-761-46815	US-10-120-604-112	US-09-864-761-40663	US-10-387-977-27	US-10-224-260-6	US-09-864-761-40202	US-10-321-857-54	US-10-318-675-54	US-10-231-417-202	US-09-864-761-36764	US-10-044-359-2	US-10-044-359-10	US-09-864-408A-72
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 2, Application US/09900147

Sequence 2, Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935

PRIOR PELING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

LENGTH: 9

TYPE: PR

CORANIES: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-900-147-2

Query Match

Best Local Similarity 100.0%; Pred. No. 70+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
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RESULT 6
US-09-900-147-6
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US-09-900-147-3

US-09-900-147-3

Sequence 3, Application US/09900147

Sequence 3, Application US/09900147

Sequence 3, Application US/09900147

Sequence 3, Application US/0900147

Sequence 3, Application US/0900147

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

CURRENT FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: US/09/900,147

PRIOR PLING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATCHILN VOY: 2.1
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09;
PRIOR APPLICATION NUMBER: RARLIER APPLICATION NUMBER: 09/308,935
PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR PELING DATE: EARLIER FILING DATE: 1996-012-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
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Patent No. US20020103121A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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LENGTH: 19
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APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPERENCE: 620-67
CURRENT PELING DATE: 2001-07-09
PRIOR PILING DATE: BALLIER PILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: GB 9626589.7
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 20
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GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Lasantha R
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Esptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935

PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR PILING DATE: EARLIER PILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENT Ver. 2.1

SEQ ID NO 16

LENGTH: 19
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100.0%; Score 42; DB 10;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0;
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; Patent No. US20020103121A1
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US-09-900-147-4
Sequence 4, Application US/09900147
Patent No. US20020103121A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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COMPUTER: IBM PC compatible
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Best Local Similarity 88.5
Matches 8; Conservative
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APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67-69
CURRENT PILING DATE: 2001-07-69
FRIOR PELING DATE: EARLIER PILING DATE: 1999-05-27
PRIOR PELING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 1
: LENGTH: 37
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                                                                                                                                        FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-900-147-6
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Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels
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HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 6 LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/10214188
Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence i, Application US/09900147
Patent No. US20020103121A1
GENERAL INFORMATION:
                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
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US-10-214-188-10
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US-09-900-147-1
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APPLICANT: La Thangue, Nicholas B
TITLE OF INVENTION: Peptide autagonists of DP transcription factors
TITLE OF INVENTION: Peptide autagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
PRIOR PILING DATE: ERRLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 0.42;
0; Mismatches 1
                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                       NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEBHOND: (703) 816-4000
TELEBAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/09900147 Patent No. US20020103121A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 74 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.5%;
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; Sequence 513, Application US/09939980
; Patent No. US20020082234A1
; GENERAL INFORMATION:
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Nicholas, Richard
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Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.8
Best Local Similarity 55.6
Matches 5; Conservative
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43 NIIIAINII 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NVLMAMNII 9
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US-09-939-980-513
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Sequence 11, Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, LaBantha R

APPLICANT: Bandara, LaBantha R

APPLICANT: Bandara, LaBantha R

APPLICANT: Bandara, LaBantha R

APPLICANT: BANDARA: LABANTHA NUMBER: 0500-07-09

FILE REFERENCE: 620-67

CURRENT FILING DATE: 2001-07-09

PRIOR FILING DATE: BARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: BARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PALENTER FILING DATE: 1996-12-20

SOFTWARE: PALENTER FILING DATE: 1996-12-20
                         PAPPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Lasantha R
APPLICANT: La Thangue, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR PILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
LENTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Description of Artificial Sequence: Synthetic.
US-09-900-147-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.9%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 81.0
Best Local Similarity 100.
Matches 7; Conservative
US20020103121A1
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|NVLMAMN 14
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US-09-900-147-11
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HOWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPERSESTON ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPERSESTON ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILLE DATE: 2001-05-23
PRIOR PLILOR DATE: 2000-05-26
PRIOR PLILOR DATE: 2000-05-26
PRIOR PLILOR DATE: 2000-06-26
PRIOR PLILOR DATE: 3000-06-26
PRIOR PLILOR DATE: 3000-06-26
PRIOR PLILOR DATE: 3000-06-26
PRIOR PLILOR DATE: 3000-06-26
PRIOR PLILOR DATE: 3000-06-27
PRIOR PLILOR DATE: 3000-06-20
PRI
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                             ö
                     ORGANISM: Homo sapiens
FRATURE:
INAMES/KEX: MISC_FEATURE
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6066
                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                          Length 55;
                                                                                                                                                                                                                                                             1; Indels
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 48875
LENGTH: 25
                                                                                                                                                                                                    Score 26; DB 15;
Pred. No. 3.1e+02;
2; Mismatches 1.
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PRIOR FILING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: US 09/632,366
PRIOR PLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PLICATION NUMBER: US 60/236,359
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48875, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                       Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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ORGANISM: Homo sapiens
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Sequence 6066, Application US/1030069041
SEQUENCE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide TITLE REFERENCE: PAGOSP1
CURRENT APPLICATION NUMBER: US/10/106,698
SETOR FILING DATE: 2002-09-28
SETOR FILING DATE: 2000-09-28
SETOR FILING DATE: 1999-09-29
SETOR FILING DATE: 1999-11-03
SETOR FILING DATE: 1999-11-03
                                                                                            TITLE OF INVENTION: U. US20020082234Alel Prokaryotic Polynucleotides, Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
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                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 19406-0339
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.0%; Score 29; DB 9; 1
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 513:
US-09-939-980-513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P50549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/936,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                        Reichard, Richard
Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 88 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 513:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
Pratt, Julie
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SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 6066
LENGTH: 55
                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||::|||
55 NVLVPINII 63
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TYPE: PRT
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US-09-892-877-228
; Sequence 228, Application US/09892877
; Publication No. US20030077809A1
; GENERAL INFORMATION:
; APPLICANT: RUDEN et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; TILE REFERENCE: PZ028P1
; CURRENT PELLING DATE: 2001-66-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
; PRIOR FILING DATE: EARLIER FILING DATE:-1999-11-10
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: PAECHLIN Ver. 2.0
; SEQ ID NO 228
                                                                                                                                                                                                                  Gaps
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                    OTHER INFORMATION: MAP TO AC019181.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
OTHER INFORMATION: EST_HUMAN HIT: BF677515.1, EVALUE 4.00e-07
US-09-864-761-48875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 11; Length 35;
Pred. No. 3e+02;
1; Mismatches 0; Indels
                                                                                                                                                     Query Match 59.5%; Score 25; DB 9; Length 25; Best Local Similarity 33.3%; Pred. No. 2.16+02; Matches 3; Conservative 5; Mismatches 1; Indels
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US-09-94B-743-230

FUBLICATION NO. US20030100051A1

GENERAL INFORMATION:

APPLICANT: Ruben etc. al.

TITLE REFERENCE: PZ028P2

CURRENT APPLICATION NUMBER: US/09/948,783

CURRENT FILING DATE: 2001-09-10

FRIOR PRIOR APPLICATION NUMBER: 09/892,877

PRIOR FILING DATE: 2000-09-11

PRIOR PRIOR APPLICATION NUMBER: 09/892,877

PRIOR FILING DATE: 2001-06-28

FRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-05-06

PRIOR FILING DATE: 1999-05-06

PRIOR FILING DATE: 1999-05-06

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13
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Matches 5, Conservative
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ORGANISM: Homo sapiens
US-09-892-877-228
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15 NILMSLOLL 23
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FEATURE:
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US-10-029-386-31645
US-10-029-386-31645, Application US/10029386
Sequence 31645, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
SOFTWARE ANDOMAS SEQUENCE Listing Engine vers. 1.1
SEQ ID NO 31645
LENGTH: 50
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Pred. No. 4.4e+02;
4; Mismatches 1; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 35;
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OTHER INFORMATION: EXPRESEED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESEED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESEED IN HART, SIGNAL = 2.3

OTHER INFORMATION: EXPRESEED IN ADULT LIVER, SIGNAL = 1.5

OTHER INFORMATION: SMISSPROT HIT: P52746, EVALUE 6.300+00
US-10-029-386-31645
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Pred. No. 3e+02;
1; Mismatches
PRIOR APPLICATION NUMBER: 60/085,924
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,922
PRIOR APPLICATION NUMBER: 60/085,921
PRIOR APPLICATION NUMBER: 60/085,923
PRIOR FILING DATE: 1998-05-18
PRIOR PILING DATE: 1998-05-18
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; Sequence 33773, Application US/09864761
; Patent No. US20020048763A1
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83.3%;
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Best Local Similarity 44.4%;
Matches 4; Conservative
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21 NLLMSLGIL 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-09-948-783-230
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Best Local Similarity
Matches 5; Conserv
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US-10-291-265-811

i Sequence 811, Application US/10291265

i Publication No. US20030232054A1

i GENERAL INFORMATION:

i APPLICANT: Hyeeq, Inc.

APPLICANT: Tang et al

i TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-017 (785)

CURRENT APPLICATION NUMBER: 09/491,404

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR APPLICATION NUMBER: 09/611,746

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-17

PRIOR FILING DATE: 2000-09-15

PRIOR FILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 944

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 52

TENGTH: 52

TENGTH: 52

TENGTH: 52

TENGTH: 52

TENGTH: 52

TENGTH: 52
                                                                                                                                        GENERAL INFUGANT:

JERNEKAL INFUGANT:

APPLICANT: Hyseq, Inc.

APPLICANT: Tang et al.

TITIE OF INVENTION: No. US20030232054Alel Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-017 (785)

CURRENT APPLICATION NUMBER: US/10/291,265

CURRENT APPLICATION NUMBER: US/491,404

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR APPLICATION NUMBER: 09/491,406

PRIOR APPLICATION NUMBER: 09/617,746

PRIOR APPLICATION NUMBER: 09/611,451

PRIOR APPLICATION NUMBER: 09/631,451

PRIOR FILING DATE: 2000-09-15

PRIOR PRILING DATE: 2000-09-15

PRIOR PRILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 944

SOFTWARE: FastSEQ for Windows Version 3.0

LEGID NO 339

LEGID NO 339
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Pred. No. 4.6e+02;
1; Mismatches 0;
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Pred. No. 4.6e+02;
1; Mismatches 0;
                                                                        US-10-291-265-339
. Sequence 339, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
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Similarity 83.3%;
5; Conservative
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US-10-291-265-811
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17 LMAMNTL 23
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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  OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HETAL LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HEALTH 2.10
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33773
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO AL034406.1
OTHER INFORMATION: EXPRESSED IN BT474
OTHER INFORMATION: EXPRESSED IN BONE
OTHER INFORMATION: EXPRESSED IN PETAL
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ORGANISM: Homo sapiens
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3 LMAMNII 9

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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.61

OTHER INFORMATION: SKPRESSED IN BONE MARROW, SIGNAL = 0.98

OTHER INFORMATION: SWISSPROT HIT: 014867, EVALUE 1.00e-32

OTHER INFORMATION: EST_HUMAN HIT: BF512320.1, EVALUE 2.00e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.5%; Score 25; DB 9; Length 66; 57.1%; Pred. No. 5.9e+02; tive 3; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 47543
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JS-09-933-767-1030

JSEQUENCE 1030, Application US/09933767

PUBLIcation No. US20030181692A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFRENCE: PZ007P2

CURRENT APPLICATION NUMBER: US/09/933,767

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/184,836

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/193,170

PRIOR APPLICATION NUMBER: 60/193,170

PRIOR FILING DATE: 1998-12-04

PRIOR FILING DATE: 1998-12-04

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-06

PRIOR APPLICATION NUMBER: 60/049,375

PRIOR APPLICATION NUMBER: 60/049,375

PRIOR APPLICATION NUMBER: 60/049,375

PRIOR APPLICATION NUMBER: 60/049,880

PRIOR FILING DATE: 1997-06-06

PRIOR APPLICATION NUMBER: 60/049,880

PRIOR FILING DATE: 1997-06-06

PRIOR APPLICATION NUMBER: 60/049,880

PRIOR FILING DATE: 1997-06-06

PRIOR PILING DATE: 1997-06-06

PRIOR PILING DATE: 1997-06-06

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PRIOR PILING DATE: 1997-06-06
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PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,876
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APPLICATION NUMBER: 60/048,895
FILING DATE: 1997-06-06
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PRIOR APPLICATION NUMBER: 60/048,896
PRIOR FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Matches 4; Conserv
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Sequence 47543, Application US/09864761
Sequence 47543, Application US/09864761
Sequence 47543, Application US/09864761
SEQUENCE 47543, Application US/09864761
SEQUENCE 1 NEOWENTION: Application G. Sequence 47547 Sequence 4754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 14;
Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                     APPLICANT: Herrman, Rafael
APPLICANT: Wong, James F.
APPLICANT: Wong, James F.
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: 09/599,416
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR PILING DATE: 2002-01-11
PRIOR PILING DATE: 2000-06-22
PRIOR PILING DATE: 1999-06-22
PRIOR PILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                                                   ; Sequence 8, Application US/10044359; Publication No. US20020160454A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.5%;
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US-10-044-359-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 37.5
Warches 3; Conservative
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R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/049,374

R FLING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,917

R FLING DATE: 1997-06-06

R RPLING DATE: 1997-06-06

R RILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,974

OR RILING DATE: 1997-06-06

OR APPLICATION NUMBER: 60/048,974

OR PILING DATE: 1997-06-06
               R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,894
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,971
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,964
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,882
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,899
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,899
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RR APPLICATION NUMBER: 60/048,878

RR FILING DATE: 1997-06-06

RR APPLICATION NUMBER: 60/068,054

RR FILING DATE: 1997-12-18

RAPLICATION NUMBER: 60/068,064

RR APPLICATION NUMBER: 60/068,064

RR APPLICATION NUMBER: 60/068,064
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APPLICATION NUMBER: 60/073,159
FILING DATE: 1998-01-30
APPLICATION NUMBER: 60/073,165
FILING DATE: 1998-01-30
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APPLICATION NUMBER: 60/048,900
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,901
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,970
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,897
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,963
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APPLICATION NUMBER: 60/070,923
FILING DATE: 1997-12-18
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FILING DATE: 1998-01-30
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,875
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APPLICATION NUMBER: 60/048,962
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APPLICATION NUMBER: 60/048,877
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 APPLICATION NUMBER: 60/048,884
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PRIOR
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US-10-023-282-1030

Sequence 1030, Application US/10023282

Publication No. US20030092893A1

GENERAL INFORMATION:

TITLE OF INVENTION 207 Human Secreted Proteins

TITLE OF INVENTION 1207 Human Secreted Proteins

TITLE OF INVENTION 1207 Human Secreted Proteins

CURRENT APPLICATION NUMBER: US/10/023,282

CURRENT PILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: PCT/US98/11422

EARLIER PILING DATE: 1998-06-06

EARLIER APPLICATION NUMBER: 60/048,885

EARLIER APPLICATION NUMBER: 60/048,885

EARLIER APPLICATION NUMBER: 60/048,881

EARLIER PILING DATE: 1997-06-06

EARLIER
                                                                                                                                PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,922
PRIOR APPLICATION NUMBER: 60/095,921
PRIOR PILING DATE: 1998-05-18
PRIOR PILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1245
SOFTWARE: Patentin Ver. 2.0
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EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
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APPLICATION NUMBER: 60/048,899
FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
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FILING DATE: 1997-06-06
                           APPLICATION NUMBER: 60/085,921
FILING DATE: 1998-05-18
                                                                                                     APPLICATION NUMBER: 60/085,923
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Similarity 44.4%;
4; Conservative
FILING DATE: 1998-05-18
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CRGANISM: Homo sapiens
US-09-933-767-1030
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58 NILKALGIV 66
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Best Local Similarity
Matches 4; Conserv
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LENGTH: 66
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US-09-664-761-33623 Application US/09864761
Sequence 31621, Application US/09864761
Sequence 31621, Application US/09864761
Sequence 31621, Application US/09864761
Sequence 31621, Application US/09864761
APPLICANT BRAK David K.
APPLICANT Chan Wensheng
TITLE OF INVENTION: CENE EXPRESSION ARALYSIS BY MICROARRAY
TITLE OF INVENTION: US/09/64-761
CURRENT APPLICATION NUMBER: US/09-864-761
CURRENT APPLICATION NUMBER: US/09-864-761
PRIOR APPLICATION NUMBER: PCT/USO1/0666
PRIOR PLIING DATE: 2001-01-01
PRIOR PLIING
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CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 5276
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 59.5
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-09-864-408A-5276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 NVKMSMN 28
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US-09-864-761-33623
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Sequence 5276, Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets Richard A.
APPLICANT: Shimkets Richard A.
TITLE OF INVENTION: No. US20040009474A1e1 Human Polynucleotides and Polypeptides Enco
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44.4%; Pred. No. 5.9e+02;
tive 3; Mismatches 2; Indels
                         EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 66/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 19
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Best Local Similarity 44.4.
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58 NILKALGIV 66
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US-09-864-408A-5276
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R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,949

R FILING DATE: 1997-06-06

R PILING DATE: 1997-06-06

R PILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,883

R FILING DATE: 1997-06-06

R FILING DATE: 1997-06-06

R FILING DATE: 1997-06-06

R PILING DATE: 1997-06-06

R PILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,897
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APPLICATION NUMBER: 60/048,916
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-06-06
APPLICATION WUMBER: 60/049,019
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,970
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FILING DATE: 1998-01-30
APPLICATION NUMBER: 60/073,165
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APPLICATION NUMBER: 60/085,922
FILING DATE: 1998-05-18
                                                                                                                                                                                 APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,900
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APPLICATION NUMBER: 60/048,901
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/070,923
FILING DATE: 1997-12-18
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FILING DATE: 1998-01-30
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APPLICATION NUMBER: 60/073,164
FILING DATE: 1998-01-30
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FILING DATE: 1998-05-18
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APPLICATION NUMBER: 60/048,915
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APPLICATION NUMBER: 60/048,972
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APPLICATION NUMBER: 60/048,917
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/068,054
FILING DATE: 1997-12-18
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FILING DATE: 1997-12-18
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APPLICATION NUMBER: 60/048,877
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APPLICATION NUMBER: 60/092,921
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                                                                                                                                        FILING DATE: 1997-06-06
                                                                        ORGANISM: Homo sapiens

ORGANISM: Homo sapiens

ORGANISM: Homo sapiens

FATURE:
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BLACENTA, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN HELA', SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN HELA', SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN HEART SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN HEART SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN HEART SIGNAL = 1.0

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TITLE OF INVENTION:

TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REPRENCE: P2007P2

CURRENT APPLICATION NUMBER: US/09/933,767

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/184,836

PRIOR FILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1990-12-04

PRIOR FILING DATE: 1990-12-04

PRIOR PILING DATE: 1999-06-06

PRIOR PILING DATE: 1997-06-06

PRIOR PILING DATE: 1997-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 59.5
Best Local Similarity 57.1
Matches 4; Conservative
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NVLLSLN 25
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SEQ ID NO 33623
LENGTH: 78
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EARLIER I
EARLIER
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Pred. No. 7.7e+02;
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TITLE OF INVENTION: 207 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE KEFKENCY PAIR
CURRENT PELICATION NUMBER: US/10/023,282
CURRENT FILING DATE: 2001-12-20
CURRENT FILING DATE: 2001-12-20
EARLIER APPLICATION NUMBER: 09/205,258
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-0
                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
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APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
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; Sequence 1032, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION WUMBER: 60/094,657
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1245
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1332
LENGTH: 84
                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.5%;
Best Local Similarity 44.4%;
Matches 4; Conservative
                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-09-933-767-1032
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71 NILKALGIV 79
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Sequence 33793, Application US/10029386

Sequence 33793, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn. Sharron G.
APPLICANT: Penn. Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: APPLICANTON: HUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34289
CURRENT FILING DATE: ANDOMAX Sequence Listing Engine vers. 1.1
SEQ ID NO 33793
LENGTH: 88
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Pred. No. 7.7e+02;
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EARLIER APPLICATION NUMBER: 60/048,877
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER APPLICATION NUMBER: 60/049,923
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/094,657
                                                                                                        R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,875
R FILING DATE: 1997-06-06
R PILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,374
R APPLICATION NUMBER: 60/049,917
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/048,883
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,897
                 APPLICATION NUMBER: 60/048,916
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
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APPLICATION NUMBER: 60/048,974
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APPLICATION NUMBER: 60/048,963
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FILING DATE: 1997-06-06
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1032
LENGTH: 84
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; ORGANISM: Homo sapiens
US-10-023-282-1032
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71 NILKALGIV 79
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Best Local Similarity
Matches 4; Conserv
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Gaps
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Publication No. US20030216544A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTOANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
                                                                                                       EXPRESSED IN BONE MARROW, SIGNAL = 0.7
EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
EXPRESSED IN BRAIN, SIGNAL = 1.3
EXT HUMAN HIT: A1650936, 1, EVALUE 6.00e-29
SWISSPROT HIT: P49454, EVALUE 5.90e+00
                                                                                                                                                                                                                                                                                                                                                                     Score 24.5; DB 9; Length 64;
Pred. No. 7.2e+02;
1; Mismatches 1; Indels
                   )10430:...
IN PLACENTA, SIGNAL = 0.76
IN FETAL LIVER, SIGNAL = 0.76
IN BONE MARROW, SIGNAL = 0.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
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FILING DATE: APPLI 13, 1992
APPLICATION NUMBER: 07/648_205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..8
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                58.3%;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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CTHER INFORMATION: M. OTHER INFORMATION: ES OTHER INFORMATION: STORMER INFORMER INFORMER INFORMATION: STORMER INFORMER INFORMER INFORMER INFORMER INFORMATION: STORMER INFORMER INFORMER
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                                                                                                                                                                                                                                                         Score 25; DB 12; Length 88; Pred. No. 8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Aeonivaler: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                        OTHER INFORMATION: MAP TO AC010522.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.8
CHER INFORMATION: SMISSPROT HIT: 043296, EVALUE 9.90e-02
US-10-029-386-33790
                                                                                                                                                                                                                                                                                                                                          1; Indels
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SEQ ID NO 44843
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00667
PRIOR PPLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-30
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R APPLICATION NUMBER: PCT/US01/00661

R PILING DATE: 2001-01-30

R APPLICATION NUMBER: PCT/US01/00670

R FILING DATE: 2001-01-30

R APPLICATION NUMBER: US 60/234,687

R FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-01-30
PELLIANION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44843, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0
   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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                                      FEATURE
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요 8

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## PRICE APPLICATION | POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTG.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTG.

TITLE OF INVENTION: HGPREMY28 AND HGPREMY29, AND SPLICE VARIANTS THEREOF

TITLE OF INVENTION: HGPREMY28 AND HGPREMY29, AND SPLICE VARIANTS THEREOF

TITLE OF INVENTION: HGPREMY28 AND HGPREMY29, AND SPLICE TOWNER: US /10/120,604

CURRENT APPLICATION NUMBER: US 60/283,145

PRIOR FILING DATE: 2001-04-11

PRIOR PAPLICATION NUMBER: US 60/283,161

PRIOR PAPLICATION NUMBER: US 60/283,619

PRIOR PAPLICATION NUMBER: US 60/280,619

PRIOR PAPLICATION NUMBER: US 60/300,619

PRIOR PAPLICATION NUMBER: US 60/300,619

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 226

SEQ ID NO 112

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERRACE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-06-26

PRIOR PILING DATE: 2000-06-36

PRIOR PILING DATE: 2000-09-36

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-07

PRIOR PILING DATE: 2000-09-07

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-09-27

PRIOR FILING DATE: 2001-01-30
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                            Length 25;
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3.3e+02;
                            57.1%; Score 24; DB 9; 144.4%; Pred. No. 3.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 40663, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                          Sequence 112, Application US/10120604
Publication No. US20030096347A1
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50.0%;
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Best Local Similarity 50.0
Matches 4; Conservative
                                 Query Match 57.1
Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-10-120-604-112
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7 NMLLAISMI 15
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11 VIVAVNLI 18
                                                                                                      1 NVLMAMNII 9
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US-09-864-761-40663
US-09-864-761-46815
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US-10-120-604-112
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EXPRESSED IN LUNG, SIGNAL = 0.8
EXPRESSED IN FETAL LIVER, SIGNAL = 0.59
EXPRESSED IN HELA, SIGNAL = 0.59
EXPRESSED IN ADULT LIVER, SIGNAL = 0.89
EXPRESSED IN ADULT LIVER, SIGNAL = 0.84
EXT. HUMAN HIT: BF340337.1, EVALUE 3.00e-06
SWISSPROT HIT: P29266, EVALUE 5.00e-07
                          Indels
       Pred. No. 7e+C
1; Mismatches
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OTHER INFORMATION: EXPRESSED IN BT474,
OTHER INFORMATION: EXPRESSED IN LUNG, S
OTHER INFORMATION: EXPRESSED IN PETAL I
OTHER INFORMATION: EXPRESSED IN HELA, S
OTHER INFORMATION: EXPRESSED IN ADULT I
OTHER INFORMATION: STATEMEN HIT: BF34
OTHER INFORMATION: SMISSPROT HIT: P2926
             75.0%;
           Best Local Similarity 75.0
Matches 6; Conservative
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Gaps

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Score 24; DB 12; Length 29;
Pred. No. 3.9e+02;
3; Mismatches 1; Indels
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
     ; SEQ ID NO 27
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino aci
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4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                           Best Local Similarity 50.0 Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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US-10-224-260-6
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                                                                                                                                                                                      Query Match
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US-10-387-977-27
i Sequence 27, Application US/10387977
j Publication No. US20040005276A1
j GENERAL INFORMATION:
APPLICANT: O'Brien-Simpson, Neil Martin
j APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
J TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
FILE REFERENCE: 529282000301
CURRENT APPLICATION NUMBER: US/09/423,056
PRIOR PLING DATE: 2003-07-18
PRIOR PLING DATE: 1998-04-30
PRIOR PLING DATE: 1998-04-30
PRIOR PLING DATE: 1998-04-30
PRIOR PLING DATE: 1999-04-30
PRIOR PLING DATE: 1999-04-30
PRIOR PLING DATE: 1999-04-30
PRIOR PLING DATE: 1999-04-30
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.1%; Score 24; DB 9; Length 28; 55.6%; Pred. No. 3.8e+02; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                             NE TILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00664

OR PILING DATE: 2001-01-30

OR PILING DATE: 2001-01-30

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00669

OR APPLICATION NUMBER: PCT/US01/00669

OR APPLICATION NUMBER: PCT/US01/00669

OR PILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00663

OR PILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00662

OR PILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00662

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00661

OR PILING DATE: 2001-01-30

OR PILING DATE: 2001-01-30

OR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-1
PRIOR PLING DATE: 2000-09-1
PRIOR PLING DATE: 2000-09-1
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-30
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SILKDMNII 13
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Matches 5; Conserv
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LENGTH: 28
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Sequence 6, Application US/10224260
Publication No. US20030059845A1
GENERAL INFORMATION:
APPLICATI: Van Tol, Hubert H.M.
TILE OF INVENTION: A No. US20030059845A1e1 Human Dopamine Receptor and Uses NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                     COMPUBLIES Allogretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION UNDERS: US/10/224,260
FILING DATE: 20-Aug-2002
CLASSIFICATION UNDERS: US/10/224,260
FILING DATE: <UNKNOWN>
PRIOR APPLICATION UNDERS: 07/928,611
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: NO. US200330059845Alnan, Kevin E
REGISTRATION UNDERS: 35,303
REPERRENCE/DOCKET VNDERSER: 36,1092-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%; Score 24; DB 15; Length 37;
44.4%; Pred. No. 5e+02;
tive 4; Mismatches 1; Indels
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US-09-864-761-40202
Sequence 40202, Application US/09864761
Perent No. US20020048763A1
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US-10-321-857-54

US-10-321-857-54

Sequence 54, Application US/10321857

Publication No. US20030180816A1

GENERAL INFORMATION:
APPLICANT: Applied NanoSystems B.V.
TILE OF INVENTION: A method to provide bacterial ghosts with antigens
FILE REFERENCE: 2183-5547US

CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/10/321,857

CURRENT FILING DATE: 2002-06-11

PRIOR PILING DATE: 2002-06-11

PRIOR FILING DATE: 2001-06-11

PRIOR FILING DATE: 2001-06-11

SROW FILING DATE: 2001-06-11
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APPLICANT: Applied NanoSystems B.V.

TITLE OF INVENTION: Bacterial ghosts provided with antigens
FILE REFERENCE: 2183-5546US

CURRENT APPLICATION NUMBER: US/10/318,675

CURRENT FILING DATE: 2002-12-13

PRIOR APPLICATION NUMBER: PCT/NL02/00383

PRIOR FILING DATE: 2002-06-11

PRIOR FILING DATE: 2001-06-11

PRIOR FILING DATE: 2001-06-11

PRIOR FILING DATE: 2001-06-11

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 54

LENTH: 44
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FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(44)
CHER INFORMATION: AcmA cell wall binding domain homologue
US-10-318-675-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(44)
COTHER INFORMATION: AcmA cell wall binding domain homologue
US-10-321-857-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indela
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Similarity 42.9%; Pred. No. 6.1e+02;
3; Conservative 4; Mismatches 0;
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US-10-318-675-54
; Sequence 54, Application US/10318675
; Publication No. US20030186851A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 3; Conserv
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21 NILLSIN 27
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CENERAL INPORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hannel, David R.
APPLICANT: Chen, Weneheng
TITLE OF INVERTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FROBES USEFUL FOR TITLE OF INVERTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FROBES USEFUL FOR TITLE OF INVERTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FROBES USEFUL FOR TITLE OF INVERTION WINBER: 1001-05-23
FRIOR PLINE DAVID SINGLE ACID SINGLE SINGLE EXON MICHAEL SOLID SINGLE SINGLE ACID SINGLE SINGLE ACID SINGLE SOLID SINGLE SINGLE ACID SINGLE SINGLE ACID SINGLE SOLID SO
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8

OTHER INFORMATION: SYNISSPROT HIT: P54938, EVALUE 7.00e-18

US-09-864-761-40202
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Pred. No. 5.6e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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Gaps ö RESULT 41

29 NVKMALDI 36

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1 NVLMAMN 7

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                                                                                                                                                                                                                                                                         TYPE: PRT
OCAGANISM: Homo sapiens
PERTURE:
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.0.5
OTHER INFORMATION: EXPRESSED IN PLACEWIA, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN LIVE, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN MUG, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84
SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 9; Length 57;
Pred. No. 8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
      PRIOR APPLICATION NUMBER: PCJ/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 36764
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wong, James F.
APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR FILING DATE: 2000-06-22
PRIOR PILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: MICROSOFT OF SEQ ID NOS: 28
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10044359; Publication No. US20020160454A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Hottentotta judaica
US-10-044-359-2
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0
Matches 4; Conservative
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      Sequence 202, Application US/10231417
Publication No. US20030176681A1
GENERAL INFORMATION:
APPLICANT: Feng et al.
TITLE OF INVENTION: 148 Human Secreted Proteins
FILE REFRENCE: PZ01391
CURRENT APPLICATION NUMBER: US/10/231,417
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US/09/296,622
PRIOR PILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 619
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 202
ILBNGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.1%; Score 24; DB 12; Best Local Similarity 33.3%; Pred. No. 7.3e+02; Matches 3; Conservative 6; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa equals stop translation US-10-231-417-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36764, Application US/09864761; Patent No. US20020048763A1; GENERAL INFORMATION:
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8 SLLVALNVL 16
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ORGANISM: Homo sapiens
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US-10-231-417-202
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US-09-864-408A-72
US-09-864-408A-72
US-09-864-408A-72
US-09-864-408A-72
Sequence 72, Application US/09864408A

| Publication No. US20040009474A1
| GENERAL INFORNATION:
| APPLICANT: Leach, Martin D.
| APPLICANT: Esch, Martin D.
| PILE REFERENCE: 21402-012
| CURRENT APPLICATION NUMBER: US/09/864,408A
| CURRENT FILING DATE: 2001-05-24
| VINER OF FILING DATE: 2000-05-24
| NUMBER OF SEQ ID NOS: 9068
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 72
| LENGTH: 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 57.1%; Score 24; DB 14; Length 59; Best Local Similarity 37.5%; Pred. No. 8.3e+02; Matches 3; Conservative 4; Mismatches 1; Indels
Sequence 10, Application US/10044359
Publication No. US200201604541
GENERAL INFORMATION:
APPLICANT: Herrman, Rafael
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2000-06-22
FRIOR FILING DATE: 2000-06-22
FRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 59
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
SOGNANISM: Hottentotta judaica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: February 17, 2004, 11:02:20 Job time : 14.1881 secs
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Best Local Similarity 62.5
Matches 5; Conservative
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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 17, 2004, 10:50:13 ; Search time 5.43564 Seconds (without alignments) 159.230 Million cell updates/sec Run on:

US-09-900-147-2 42

1 NVLMAMNII 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 100 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TodR protein - Pse hypothetical prote alpha-internexin -hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable membrane NADH2 dehydrogenas NADH2 dehydrogenas NADH2 dehydrogenas NADH2 dehydrogenas NADH2 dehydrogenas probable membrane probable membrane hypothetical prote hypothetical prote hypothetical prote cytochrome c553 pr hypothetical prote conserved domain p ywcE protein - Bac NADH2 dehydrogenas truncated transpos NADH2 dehydrogenas probable membrane Description SUMMARIES G91230 F86077 F90284 D91064 AH0720 T111163 F90842 C85700 B64867 F71843 AG3416 E84008 E64024 D89831 T17162 541828 F89891 Query Match Length 66.7 66.7 66.7 66.7 64.3 64.3 Result

hypothetical prote hypothetical prote protein-tyrosine k	hypothetical prote acyl carrier prote hypothetical 9.4K	hypothetical prote hypothetical prote chloride conductan	hypothetical prote hypothetical prote exo-alpha-sialidas	hypothetical prote hypothetical prote NADH2 dehydrogenas NADH2 dehydrogenas
E82163 AF2809 I83374	A12538 G82881 S40833	A69985 B84222 A55571	T17418 G69034 B39378	G84065 S00119 S47878 S24920
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67 68 70	70 77 81	85 86 87	8 8 8 9 6 6	9 9 9 9 9 8 8 8
57.1	57.1 57.1 57.1	57.1 57.1 57.1	57.1 57.1 57.1	57.1 57.1 57.1 57.1
2 2 2 4 4 4	4 4 4	2 7 4 2 4 4	5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	4444
30 31	1 W W W	36 37 38	39 41 41	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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truncated transposase [imported] - Staphylococcus aureus (strain N315)
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C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

CjAccession: F98991
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Tinoue, R.; Katto, C.; Sekimizu, K.; F.; Sawano, T.; Inoue, R.; Katto, C.; Sekimizu, K.; F.; Sabiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: F89891
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 «KUR»
A;Cross-references: GB:BA000018; PID:g13700994; PIDN:BAB42290.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:

A;Gene: truncated(tnp)

Gaps ö Query Match 69.0%; Score 29; DB 2; Length 70; Best Local Similarity 85.7%; Pred. No. 22; Matches 6; Conservative 1; Mismatches 0; Indels

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||||:|| VLMALNI 28 2 VLMAMNI 8 ð g

truncated transposase [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: lo-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F89915
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
R;Kuroda, M.; Ohta, T.; Wobayashi, N.; Sawano, T.; Inoue, R.; Katto, C.; Sekimizu, K.; F.
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Fitles Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; WUID:21311952; PMID:11418146

A,Status: preliminary A,Molecule type: DNA A,Residues: 1-96 «KUX» A,Cross-references: GB:BA000018; PID:g13701187; PIDN:BAB42482.1; GSPDB:GN00149 A,Experimental source: strain N315

C;Genetics:

A, Gene: truncated-SA

69.0%; Score 29; DB 2; Length 98; Query Match

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NADIZ dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L [similarity] - Pygathrix roxellans (Species: mitochondrion Pygathrix roxellana (Species: mitochondrion Pygathrix roxellana (Species: mitochondrion Pygathrix roxellana (Species: mitochondrion Pygathrix roxellana (Species: mitochondrion 19.May-2000 #sequence_revision 19-May-2000 #text_change 03-Jun-2002 (Species: T1777 * May W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.Q.; Hu, H.G.; Xif Int. J. Primatol. 18, 305-320, 1997 * Mither * Phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences. A; Reference number: Z18709 * Molecule type: DNA * Molecule type: Molecule type: Molecule type: DNA * Molecule type: Mole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: EMBL:U92956; NID:92290437; PID:92290439; PIDN:AAD08822.1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
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Pred. No. 52;
2; Mismatches 1; Indels
     Length 98;
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62.5%; Pred. No. 52;
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Score 28; DB 2;
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2; Mismatches
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Best Local Similarity 62.5%;
Matches 5; Conservative 2
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Best Local Similarity 62.5
Matches 5, Conservative
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NTLMALNM 51
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44 NTLMALNM 51
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A; Status: preliminary
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A;Experimental source: isolate CJ3
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - Pygathrix bieti mitochondrion C;Species: Pygathrix bieti mitochondrion C;Species: Pygathrix bieti mitochondrion C;Species: Pygathrix bieti mitochondrion C;Date: 04-Mar-2000 #sequence revision 04-Mar-2000 #text_change 03-Jun-2002 C;Date: 04-Mar-2000 #sequence revision 04-Mar-2000 #text_change 03-Jun-2002 R;Wang, W: Forstner: T17165; T17168 T17
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A; Experimental source: isolate DJ4
A; Accession: T17168
A; Accession: T17168
A; Accession: T17168
A; Cross-references: EMBL: U92958; NID: g2290445; PID: g2290447; PIDN: AAD08828.1
A; Cross-references: EMBL: U92958; NID: g2290447; PIDN: AAD08828.1
A; Experimental source: isolate DJ5
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A;Reaidues: 1-98 <WAN>
A;Cross_references: EMBL:U92961; NID:g2290457; PID:g2290459; PIDN:AAD04660.1
A;Experimental source: isolate CJ1
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Experimental source: isolate DJ1
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1; Mismatches
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6, Conservative
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44 NTLMALNM 51
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59 VLMALNI 65
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A; Residues: 1-98 < WA2>
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A; Status: preliminary
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Residues: 1-98 <WAN>
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A;Residues: 1-98 <WA2>
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Mypotherical protein EC83484 [imported] - Escherichia coli (strain O157:H7, substrain RIN C'Species: Escherichia coli (c'Species: Escherichia coli (strain 18-Jul-2001 #sequence_revision 18-Jul-2001 #s.) A.; Han, C.G.; gasawara, N.; Yashunga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: D91064 A;Status: preliminary
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Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Faterence number: ABO502; MUID:21534947; PMID:11677608
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R;Black IV, W.C.; Roehrdanz, R.L.
Mol. Biol. Evol. 15, 1772-1785, 1998
A;Title: Mitochondrial gene order is not conserved in arthropods: prostriate and metastr)
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A,Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0720
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C,Species: mitochondrion Rhipicephalus sanguineus
C,Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
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Pred. No. 73;
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Pred. No. 1e+02;
3; Mismatches
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A; Residues: 1-53 <HAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bscherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: F86-2001
R;Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A8B480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SS01296 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: F90284
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: GB:AE005174; NID:g12518781; PIDN:AAG59082.1; GSPDB:GN00145; UWGP:Z54
A,Experimental source: strain O157:H7, substrain EDL933
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A;Residues: 1-99 «KUR»
A;Cross-references: GB:AE006641; NID:g13814497; PIDN:AAK41533.1; GSPDB:GN00155
C;Genetics:
A;Gene: SS01296
                                                                                                                                          A;Cross-references: GB:BA000007; PIDN:BAB38238.1; PID:g13364291; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC94815
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44.4%; Pred. No. 88;
iive 4; Mismatches 1; Indels
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A; Reference number: A99629; MUID: 21156231; PMID: 11258796
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Pred. No. 70;
2; Mismatches
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Pred. No. 70;
2; Mismatches
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Best Local Similarity 44.4
Matches 4; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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                                                                                    A; Molecule type: DNA A; Residues: 1-81 < HAY>
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A;Residues: 1-81 <STO>
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                                                            A;Status: preliminary
                           A; Accession: G91230
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C;Genetics: A;Gene: yiiE

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cytochrome c553 precursor - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Mar-2000
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Mar-2000
C;Accession, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A):Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathol. A):Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-96 <ARN>
A;Cross-references: GB:AE001542; GB:AE001439; NID:g4155739; PIDN:AAD06721.1; PID:g415574;
A;Experimental source: strain J99
                                                                                                                                                    A;Cross-references: GB:AE000219; GB:U00096; NID:g1787453; PIDN:AAC74289.1; PID:g1787456; A;Experimental source: strain K-12; substrain MG1655
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Pred. No. 1.4e+02;
2; Mismatches 1; Indels
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C;Keywords: transmembrane protein
F;9-25/Domain: transmembrane #status predicted <TMl>
F;45-61/Domain: transmembrane #status predicted <TM2>
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61.9%; Score 26; DB 2; 1
Best Local Similarity 44.4%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 2
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Best Local Similarity 62.5
Matches 5, Conservative
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15 NVLMATDV 22
                                  11 NVLMGLGLV 19
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1 NVLMAMNII 9
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
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A;Experimental source: strain O157:H7, substrain EDL933
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001
C;Accession: F99842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cjaccesion: F90842
Klaysahi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A; Afterence number: A99629; MUID:21156231; PMID:11258796
A; Accession: F90842
A; Ascession: Prollaminary
A; Residues: 1-92 CHAY.
A; Residues: 1-92 CHAY.
A; Residues: 1-92 CHAY.
                                                                                                   A,Molecule type: DNA
A;Residues: 1-91 <BLA>
A;Residues: 1-91 <BLA>
A;Conserreferences: EMBL:AF081829; NID:g4164556; PID:g4164567; PIDN:AAD05527.1
C;Genetics: mitochondrion
A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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Pred. No. 1.3e+02;
3; Mismatches 2; Indels
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Pred. No. 1.3e+02;
4; Mismatches 0; Indels
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           A;Reference number: Z17252; MUID:99083443; PMID:9866211
A;Accession: T11163
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 1.3e+02;
3; Mismatches 2;
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44.4%;
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Best Local Similarity 50.0%;
Matches 4; Conservative
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Best Local Similarity 44.4
Matches 4; Conservative
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Matches 4; Conservative
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11 NVLMGLGLV 19
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LMMSMNLI 89
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C; Species: Staphylococcus aureus
C; Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C; Accession: D89831
R; Wucda, M: Ohta, T: Uchiyama, I:; Baba, T:; Yuzawa, H:; Kobayashi, I:; Cui, L:; Oguch ma, A:; Mizutani-Ui, Y:; Kobayashi, N:; Sawano, T:; Inoue, R:; Kaito, C:; Sekimizu, K:; Inoue, R:; Kaito, C:; Sekimizu, K:; Inocet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; WUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riffertelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I snon, T.; Hickey, E.K.; Holt, I.E.
Science 233, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
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A;Experimental source: strain TIGR4
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-63.<TIGR>
A;Cross-references: GB:U32807; GB:L42023; NID:g1574725; PID:g1574726; TIGR:HI1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:BA000018; PID:g13700510; PIDN:BAB41807.1; GSPDB:GN00149
A;Experimental source: strain N315
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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: F95210
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    Staphylococcus aureus (strain N315)

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                                                                                                                            Length 63;
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Pred. No. 1.7e+02;
2; Mismatches 2; Indels
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                                                                                                                         Score 25; DB 2; Le:
Pred. No. 1.5e+02;
5; Mismatches 0;
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Pred. No. 1.9e+02;
2; Mismatches 1;
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                                                                                                                            Query Match
Best Local Similarity 37.5%;
Matches 3; Conservative
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Similarity 62.5%;
5; Conservative
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38 NALVDLNII 46
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25 SILLALNV 32
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Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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A; Residues: 1-79 < KUR>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-74 < KUR>
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                                                                                         C'Species: Brucella melitensis
C'Date: Ol-Feb-2002 #sequence_revision Ol-Feb-2002 #text_change Ol-Feb-2002
C'Accession. AGG446
R'DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein BH2869 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: E84008
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Mucleic Asids Res. 28, 4317-4317, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID: 20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: E84008
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-59 <STO>
A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06588.1; GSPDB:GN0C
C;Genetics:
A;Gene: BH2869
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E64024

E64024

E64024

Cypothetical protein HI1270 - Haemophilus influenzae (strain Rd KW20)

Cypothetical protein HI1270 - Haemophilus influenzae

Cybate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 10-Oct-1997

CyAccession: E64024

RyFleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.P.; Kerlavage, P. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; A.; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Rittle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
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A,Residues: 1-98 «KUR»
A,Cross-references: GB:AE008917; PIDN:AAL52498.1; PID:g17983307; GSPDB:GN00190
A,Experimental source: strain 16M
RESULT 17
AG3416
hypothetical protein BME11317 [imported] - Brucella melitensis (strain 16M)
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Conservative

Local Similarity

Query Match Best Local S: Matches

:|:|:|: ILVALNLV 42 2 VLMAMNII 9

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A; Accession: E64024

Query Match
Best Local Similarity 55.00,

C,Genetics: A,Gene: BMEI1317 A,Map position: I

A;Accession: AG3416 A;Status: preliminary

| |:|:||: 25 NRLVAINIV 33 1 NVLMAMNII 9

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TodR protein - Pseudomonas putida
TodR protein - Pseudomonas putida
C;Species: Pseudomonas putida
C;Species: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
C;Accession: S53994
G;Accession: S53994
Mol. Gen. Genet. 246, 570-579, 1995
A;Title: Identification of a membrane protein and a truncated LysR-type regulator associal A;Reference number: S53994
A;Accession: S53994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - nine-banded armadillo mitochondi (5,5cise: mitochondrion Dasypus novemcinctus (nine-banded armadillo) (5,5cise: mitochondrion Dasypus novemcinctus (nine-banded armadillo) (5,5cise: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002 (5,Accession: T11449 M). Januara, U.; Gullberg, A.; Janke, A. Mol. Biol. Evol. 14, 762-768, 1997 M,7title: Phylogenetic analysis of mitochondrial DNA suggest a sister group relationship & A;Title: Phylogenetic analysis of mitochondrial DNA suggest a sister group relationship & A;Accession: T11449 M,5catesion: T11449 M,5catesion: T1449 M,5catesion: T1849 M,5catesion: T18
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A;Note: the authors translated the codon GAG for residue 71 as Asp and CGC for residue 8"
        C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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hypothetical protein VCA0844 [imported] - Vibrio cholerae (strain N16961 serogroup Ol)
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                                                                                                                       Score 25; DB 2; Length 98;
Pred. No. 2.4e+02;
2; Mismatches 1; Indels
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Pred. No. 2.4e+02;
3; Mismatches 1; Indels
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62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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7 NIIMAFSI 14
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7 NVLMAFSM 14
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nes 4; Conserv
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Matches 4; Conserv
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A,Molecule type: DNA
A,Residues: 1-100 <WAN>
                                                                                                                                                                                                                                                                                                         1 NVLMAMNI 8
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A; Genetic code: SGC1
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A;Start codon: GTG
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C;Superfamil...
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A, Racterance number: Si9bbb; MULD: 50x0231; FILL: 50x026
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
A, Machedle Cype: DNA
A, Residues: 1-87 cGLAA
A, Residues: 1-87 cGLAA
A, COSS = references: EMBL: X3124; NID: 9413923; FIDN: CAA51597.1; PID: 9413965
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
A, Rivolace: S. D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. A, Authors: Foulger, D.; Pritz, C.; Fujita, M.; Fujita, Y.; Puna, S.; Galler, A; Anthors: Lee's M.; Liu, H.; Masuel, S.; Hager, M.; Rivolace, A.; Handar, M.; Manuel, S.; Kundors: Schlach, S.; Schlach, S.; Kundors, S. H.; Parro, V.; Pohl, T. M.; Serolan, A, Authors: Schlach, S.; Schlach, S.; Schlach, S.; Schlach, S.; Schlach, S.; Schlach, S.; Schlach, R.; Scoffone, P.; Schlach, A.; Yamanoto, M.; Yamanoto, M.; Yata, K.; Yata, K.; Yashida, M.; Handrer, P.; Wipher, A.; Yamanoto, H.; Yamanoto, M.; Yamanoto, M.; Yata, K.; Yashida, M.; A, Athorse Yoshikawa, H.F.; Zunstein, B.; Yoshikawa, H.; Danchin, A.; Arcession: H70052
A, Accession: H70052
A, Accession: H70052
A, Residues: Learning source: Schlach Rain Residues: Learness GB299123; GB:AL009126; NID:g2636240; PIDN:CABIS839.1; PID:ell86312; A; Experimental source: Strain 168
C, Generices CB2929123; GB:AL009126; NID:g2636240; PIDN:CABIS839.1; PID:ell86312; A; Generices
A, Gene: Veryonche: Train Residues: Lance Residue Residues: Lance Residue Residues: Lance Residue Residues: Lance Residue Residue Residue Residue Residue Residue Residue Residue Residue Resi
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R;Arnason, U.; Gullberg, A.
D; Mol. Bvol. 37, 312-322, 1993
A;Title: Comparison between the complete mtDNA sequences of the blue and the fin whale, A;Title: Comparison between the complete mtDNA sequences of the blue and the fin whale, A;Recession: $41820; MUD:94141932; PMID:8308901
A;Accession: $41828
A;Molecule type: DNA
A;Residues: 1-98 cARN>
A;Cross-references: EMBL:X72204; NID:g414126; PIDN:CAA51003.1; PID:g575317
                                                                                                                                        NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - blue whale mitochondrion N;Alternate names: NADH-ubiquinone oxidoreductase chain 4L C;Species: mitochondrion Balaenoptera musculus (blue whale) C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002 C;Accession: S44828
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50.0%; Pred. No. 2.1e+02;
tive 3; Mismatches 1;
                                                                                                                                    - Bacillus subtilis
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Best Local Similarity 50.0
Matches 4; Conservative
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59 ILFAVNVI 66
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as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E.
A,Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunnes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak,
A,Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveire
A,Feference number: A59328
A,Contents: annotation
C;Genetics:
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:U39646; NID:g1049351; PID:g1049358; PIDN:AAA80373.1; CESP:F47B7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F47B7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16386
R;Leimbach, D.
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A;Description: The sequence of C. elegans cosmid F47B7.
A;Reference number: Z18504
A;Accession: T16386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 2; I Pred. No. 2.3e+02;
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Pred. No. 2.2e+02;
5; Mismatches 1;
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A,Molecule type: DNA
A,Residues: 1-59 <LEI>
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Best Local Similarity 33.30,
Best Local Similarity 33.30,
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Best Local Similarity 55.00,
100 5; Conservative
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37 NLIAAINVL 45
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A; Introns: 18/3
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A,Gene: VC1733
A,Map position: 1
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C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C; Accession: B8267
Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717; PMID:10910347
A; Recession: B82667
A; Accession: B82667
A; Accession: B82667
A; Setus: preliminary
A; Sesidues: 1-57 <SIM>A; Residues: Caractor Substantial Source: Strain 9a5c
B; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-18; 19-28; 29-45; 46-57 <TAN>
C; Comment: This intermediate filament protein polymerizes to form filament itself, in vi
C; Superfamily: cytoskeletal keratin
C; Superfamily: cytoskeletal keratin
C; Keywords: brain; intermediate filament
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: 'GB:AE004412; GB:AE003853; NID:g9658269; PIDN:AAF96742.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: O.5-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999
C;Accession: PN0624
R;Tanaka, J.; Ogawara, M.; Ando, S.; Shibata, M.; Yatani, R.; Kusagawa, M.; Inagaki, M. Biochem: Biophys. Res. Commun. 196, 115-123, 1993
A;Title: Phosphorylation of a 62kD porcine alpha-internexin, a newly identified intermed A;Reference number: PN0624; MUID:94029981; PMID:8216281
   C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: H82409
C;Accession: H82409
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardelberg, J.F.; Eisen, J.A.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Axture 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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E82667
hypothetical protein XF1541 [imported] - Xylella fastidiosa (strain 9a5c)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.1%; Score 24; DB 2; Length 48; 50.0%; Pred. No. 1.8e+02; ive 3; Mismatches 1; Indels
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-48 <HEI>
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Query Match 57.1%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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LSAMNLI 43
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Best Local Similarity
Matches 4; Conserv
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A;Genetic code: SGC3
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R;Hebert, B.; Bergeron, J.; Tijssen, P.; Potworowski, E.F.

R;Hebert, B.; Bergeron, J.; Tijssen, P.; Potworowski, E.F.

R;Hebert, B.; Bergeron, J.; Tijssen, P.; Potworowski, E.F.

A;Title: Protein tyrosine kinases transcribed in a murine thymic medullary epithelial ce
A;Reference number: 160294; MUID:94266162; PMID:8206383

A;Reference number: 160294; MUID:94266162; PMID:BDJ
                                                                                                                                                                                                                                                                                                                                                                            Appointed and protein Atu1896 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) Appointed and Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens) (Argoraterium tumefaciens) (Argorate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Atritle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-68 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42892.1; PID:g17740345; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
A;Genetics:
A;Genetics: Atu1896
A;Map position: circular chromosome
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C;Species: Mus musculus (house mouse)
C;Daté: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
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   Length 67;
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Similarity 66.7%; Pred. No. 2.6e+02;
4; Conservative 2; Mismatches 0; Indels
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A;Gene: PTK
A;Gene: PTK
C;Superfamily: protein kinase homology
F;1-70/Domain: protein kinase homology (fragment) <KIN>
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57.1%; Score 24; DB 2; L
Best Local Similarity 44.4%; Pred. No. 2.6e+02;
Matches 4; Conservative 4; Mismatches 1;
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A;Molecule type: mRNA
A;Residues: 1-70 <RES>
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11 NILVGENLI 19
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27 NVLISFDVI 35
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       Query Match
Best Local Similarity
Matches 4; Conserv
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36 ILLAMN 41
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RESULT 33

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injunctiventical process against as 17596 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120bc. Cippociston Nostoco sp. PCC 7120 is a synonym of anabeas sp. strain PCC 7120 co. Cippociston Nostoco sp. PCC 7120 is a synonym of anabeas sp. strain PCC 7120 co. Cippociston Nostoco sp. Strain PCC 7120 is a synonym of anabeas sp. strain PCC 7120 is specially the PCC 7120 is sequenced. Straints PCC 7120 is sequenced. Straints No. Straints No. PCC 7120 is specially No.
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57.1%; 50.0%;

Query Match Best Local Similarity 50.0°

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2 VLMAMNII 9

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Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A,Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lic A,Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: B84222
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R;Morrison, B.W.; Moorman, J.R.; Kowdley, G.C.; Kobayashi, Y.M.; Jones, L.R.; Leder, P. Biol. Chem. 270, 2176-2182, 1995
A;Title: Mat-8, a novel phospholemman-like protein expressed in human breast tumors, indt A;Reference number: A55571; MUID:95138184; PMID:7836447
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R;Nowak-Thompson, B.; Chaney, N.; Wing, J.S.; Gould, S.J.; Loper, J.E.
J. Bacteriol. 181, 2166-2174, 1999
A;Title: Characterization of the pyoluteorin biosynthetic gene cluster of Pseudomonas flua;Reference number: Z18776; MUID:99194726; PMID:10094695
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
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A,MoLecule type: DNA
A,Residues: 1-88 <NOW>
A,Cross-references: EMBL:AF081920; NID:g4582974; FID:g4582982; PIDN:AAD24885.1
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C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 28-May-1999
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C;Species: Pseudomonas fluorescens
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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Pred. No. 3.5e+02;
0; Mismatches 2;
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Pred. No. 3.4e+02;
1; Mismatches 1;
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Best Local Similarity 75.0
Matches 6; Conservative
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Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-86 <STO>
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A;Molecule type: mRNA
A;Residues: 1-87 <MOR>
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: A69985
R;Kunst, F: Ogasawara, N: Moszer, I: Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Broom, S: Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sado, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama,
T.; Winters, Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Atterence number: A69988
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                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-81 <BLAT>
A;Cross-references: GB:AE000464; GB:U00096; NID:g2367324; PIDN:AAD13451.1; PID:g1790322;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yilE
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A;Bxperimental source: strain 168
C;Genetics:
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C;Species: Halobacterium sp. NRC-1
C;Date-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84222
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
                          Accession: Date of Brown Reference of Receiver of Reference of Referen
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Pred. No. 3.2e+02;
3; Mismatches 1;
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57.1%; 50.0%;

Query Match
Best Local Similarity
4; Conserv

C,Genetics: A,Gene: yshA

Conservative

57 VLTAVNVV 64

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RESULT 37

VLMAMNII 9

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Query Match 57.1
Best Local Similarity 62.5
Matches 5; Conservative
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11 VMALNIL 17
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2 VLIKLNII
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                                                                                                                     A; Gene: BH3327
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R; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUD:20512582; PMID:11058132
A; Accession: G84065
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                 Wypothetical protein MTH1255 - Methanobacterium thermoautotrophicum (strain Delta H) hypothetical protein MTH1255 - Methanobacterium thermoautotrophicum C; Bate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 (C; Accession: G69034 R; Mills (C; Accession: G69
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A;Experimental Bource: strain Delta H
C;Genetics:
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C;Species: Trypanosoma cruzi
C;Date: 20-Nar-1992 #sequence_revision 20-Mar-1992 #text_change 11-Jan-2000
C;Accession: B39378
R;Kahn, S.; Colbert, T.G.; Wallace, J.C.; Hoagland, N.A.; Eisen, H.
Proc. Natl. Acad. Sci. US.A. 88, 4481.4485, 1991
A;Title: The major 85-kDa surface antigen of the mammalian-stage forms of Trypanosoma A;Refearence number: A39378; MUID:91239592; PMID:2034687
A;Accession: B39378
A;Accession: B39378
A;Accession: B39378
A;Accession: B19978
A;Crosa-references: GB:M62736
C;Superfamily: trypomastigote-specific surface antigen
C;Keywords: glycosidase; hydrolase
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Best Local Similarity 50.0
Matches 4; Conservative
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47 LLLAVNIL 54
39 ILNSMNIV 46
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - North American opossum mitochond in mitochondrion Didelphis virginiana, Didelphis marsupialis virginiana (North An C;Species: mitochondrion Didelphis virginiana, Didelphis marsupialis virginiana (North An C;Date: 19-Mar-1997 #text_change 03-Jun-2002 C;Accession: 847878; $42818 R;Janke, A.; Feldmaier-Fuchs, G.; Thomas, W.K.; von Haeseler, A.; Paeaebo, S. Genetics 137, 243-256, 1994 Mitochondrial genome and the evolution of placental mammals. A;Title: The marsupial mitochondrial genome and the evolution of placental mammals. A;Accession: 847870; MUID:94333786; PMID:8056314
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A;Genome: code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C - Proteus vulgaris
C;Species: Proteus vulgaris
C;Species: Proteus vulgaris
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 14-Apr-2003
C;Date: 30-00119
R;Cole, S.T.
Eur. J. Biochem. 167, 481-488, 1987
A;Title: Nucleotide sequence and comparative analysis of the frd operon encoding the fume d-linked ampC cephalosporinase gene.
A;Reference number: S00107; MUID:88004470; PMID:3308458
A;Accession: S00119
A;Cross-references: GB.Ap001518; GB:BA000004; NID:g10175792; PIDN:BAB07046.1; GSPDB:GN001
A;Experimental source: strain C-125
C;Genetics:
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A,Residues: 1-98 «JAN»
A,Cross-references: EMBL:Z29573; NID:g452251; PIDN:CAA82685.1; PID:g555588
A,Experimental source: liver
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A;Reaidues: 1-96 <COL>
A;Cross-references: EMBL:X06151; NID:g45907; PIDN:CAA29511.1; PID:g45910
C;Superfamily: [NiFe]-hydrogenase maturation chaperone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3%; Pred. No. 3.88+02;
Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                            Length 93;
                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                Query Match
57.1%; Score 24; DB 2; 1
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 0
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - finback whale mitochondrion C;Species: mitochondrion Balaenoptera physalus (finback whale, common rorgual) C;Species: mitochondrion Balaenoptera physalus (finback whale, common rorgual) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002 C;Accession: A58851, 234920 R;Arnason, U.; Gullberg, A.; Widegren, B. A.; Annason, U.; Gullberg, A.; Widegren, B. A;Title: The complete nucleotide sequence of the mitochondrial DNA of the fin whale, Bal A;Reference number: A58850; MUID:92139449; PMID:1779436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-98 <ARN>
A;Residues: 1-98 SARN>
A;Crosa-references: GB:X61145; NID:g12772; PIDN:CAA43447.1; PID:g12779
A;Note: submitted to the EMBL Data Library, August 1991
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels
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Search completed: February 17, 2004, 10:58:14 Job time : 6.43564 sec8

1 NVLMAMNI 8 |:||| :: 7 NILMAFSM 14

8 8

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 17, 2004, 10:50:13; Search time 2.85149 Seconds (without alignments) 148.428 Million cell updates/sec Run on:

US-09-900-147-2 42 1 NVLMAMNII 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

13973 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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		Description	P59486 tropheryma	O99826 rhipicephal	P31807 escherichia	Q9zjz9 helicobacte	Q9njp7 mesobuthus	Q9u8d1 mesobuthus	P39603 bacillus su	P41301 balaenopter	O21333 dasypus nov		Q9ppy4 ureaplasma					P17345 candida par		-	thermoplas			-	P03902 bos taurus		027127 methanobact		P28487 drosophila		-	P38389 arabidopsis	P72712 synechocyst	Q9y9f0 aeropyrum p	Q58620 methanococc
SUMMARIES		ΩI	Y010 TROWT	NULM RHISA	YCHH ECOLI	C553_HELPJ	SCP2_MESMA	SCP3 MESMA	YWCE_BACSU	NULM BALMU	NULM DASNO	YV31_CAEEL	ACPH_UREPA	FXY3_HUMAN	YFRC_PROVU	NULM BALPH	NULM_DIDMA	ATP8_CANPA	Y666_CHLTR	Y710_CHLPN	RPOH_THEAC	RL31_HALN1	VAPD_HAEIN	Y736_ARCFU	NULM_BOVIN	NULM_SHEEP	RL3E_METTH	YF16_METJA	ADHR_DROYA	YJJZ_ECOLI	C2_OXYNO	S61B_ARATH		Y069_AERPE	YC23_METJA
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		Match Length	69	91	92	96	99	99	87	98	98	59	77	87	96	98	98	48	83	84	87	91	91	95	98	86	86	66	32	78	82	82	96	91	92
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025825 helicobacte 051168 borrelia bu 029273 hippopotamu 029709 hylobates I P56632 sus scrofa P56010 pisaster oc P47475 mycoplasma P45807 escherichia 029796 methanococc P4873 cyanophora 029291 rickettsia
C553 HELPY Y143_BORBU NULM_HTPAM NULM_HTLIA NULM_PIG NULM_PIG Y233 MYGGE Y233 MYGGE Y2446 MRTJA Y33 CYAPA Y33 CYAPA CSPA_RICCN
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ALIGNMENTS

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REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Prote-obacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                     Mitochondrion.
Eukaryota, Matazoa, Arthropoda, Chelicerata, Arachnida, Acari,
Parasitiformes, Ixodida, Ixodidae, Rhipicephalus.
NCBI_TaxID=34632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.9%; Score 26; DB 1; Length 91; 50.0%; Pred. No. 62; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 91 AA; 10598 MW; D2E51EC5F1D056EE CRC64;
                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Prochetical protein ychH.
YCHH OR B1205 OR C1663 OR Z1976 OR ECS1710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 AA
                                                                                                                                             91 AA
                                                                                                                                                                                                                                                                            Rhipicephalus sanguineus (Brown dog tick).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12;
MEDLINE=92007806; PubMed=1833189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, T11163; T11163.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF081829; AAD05527.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1
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Best Local Similarity 50...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli,
Escherichia coli 06, and
Escherichia coli 0157:H7.
                                                                                                                                             STANDARD;
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82 LMMSMNLI 89
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50 NILIAFGII 58
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            1 NVLMAMNII
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YCHH ECOLI
ID _YCHH_ECOLI
                                                                                                                                               NULM RHISA
099826;
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marcia-Villegas M.R., de la Vega F.M., Galindo J.M., Segure M.,

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      the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99120557; PubMed=9923682; Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G. Tummino P.J., Caru, Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8F75344F0C72525C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.9%; Score 26; DB 1;
44.4%; Pred. No. 62;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome C-553 precursor (C553).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 AA.
                                                                                                                                                                                                                    EMBL; AD00219; AAC4289.1; --
EMBL; AE000219; AAC4289.1; --
EMBL; AE0016759; AAA80028.1; --
EMBL; AE0016759; AAA80028.1; --
EMBL; AP002538; AAG5603.1; --
EMBL; AP002556; BAB35133.1; --
PIR; EG8700; C85700.
PIR; F90842; F90842.
ECOGGEN; EG11533, ych4.
Hypothetical protein; Complete proteome.
SEQUENCE 92 AA; 10486 MW; 8F75344F0C72
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INCETPro; IPR003088; Cyt_CI.
INCETPro; IPR003229; Cyt_CIC.
INCETPro; IPR000345; Cyt_Cheme_bind.
Pfam; PF00034; cytochrome c; I.
PRINTS; PR00605; CYTCHROMECIC.
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                                                                                                                                                                                                    EMBL; X61941; CAA43947.1; -.
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Best Local Similarity 44...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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CSS3 HELPJ
CSS3 HELPJ
TZS9;
             a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Venom gland;
MEDLINE=99402983; PubMed=10471839;
MEDLINE=99402983; PubMed=10471839;
Shu S.-Y., Li W.-X., Zeng X.-C., Jiang D.-H., Mao X., Liu H.;
"Molecular cloning and sequencing of two 'short chain' and two 'long chain' K(+) channel-blocking peptides from the Chinese scorpion Buthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu Y.Q., Wu J.H., Ped J.M., Shi Y.Y., Ji Y.H., Tong Q.C.;
"Solution structure of BmP02, a new potassium channel blocker from the
"Solution structure of BmP02, a new potassium channel blocker from the
venom of the Chinese scorpion Buthus martensi Karsch.";
Biochemistry 39:13669-13675(2100).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: BELONGS TO THE SCORPION LEIUROTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 42, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Neurotoxin BmP02 precursor (Potassium ion channel blocker P02P).
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
ProDom; PD004020; Cyt C bact; 1.
PROSITE; PS00190; CYTOCHROME C; 1.
Electron transport; Heme; Signal; Periplasmic; Complete proteome.
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1 19 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                              CYTOCHROME C-553.
HEME (COVALENT).
IRON (HEME AXIAL LIGAND) (1
SIMILARITY).
IRON (HEME AXIAL LIGAND) (1
SIMILARITY).
                                                                                                                                                                                                                                                                                                     3E607AE5D422AD82 CRC64;
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PDB, 1DU9, 28-MAR-01.
Toxin, Neurotoxin, Ionic channel inhibitor;
Potassium channel inhibitor; Signal, 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEUROTOXIN BMP02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 AA.
                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 65;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                        Score 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20530297; PubMed=11076505;
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                                                                                                                                                                                                                                                                                                     10354 MW;
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62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
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                                                                                           19
29
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15 NVLMATDV 22
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                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                     96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=34649;
                                                                                                                                                                                                                                               73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MESMA
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                                                                                                                   CHAIN
BINDING
BINDING
METAL
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10 IVLAMNVM 17
                                                                                                        01-FEB-1995
                                                                                                                      01-FEB-1995
28-FEB-2003
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                                                                         BACSU
                                                         YWCE_BACSU
                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the TWBL outstation the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not remoyed. Usage, by and for commercial,
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                                                                ö
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB=Venom gland;
MNEDLINE=9931319; PubMed=10386622;
MN J.J., Dai L., Lan Z.D., Chi C.-W.;
ML Grannic organization of three neurotoxins active on small conductance "Genomic organization of three neurotoxins active on small conductance ca2+-activated potassium channels from the scorpion Buthus martensi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Venom gland;
MEDLINE=99402983; PubMed=10471839;
MEDLINE=99402983; PubMed=10471839;
Zhu S.-Y., Li W.-X., Zeng X.-C., Jiang D.-H., Mao X., Liu H.;
"Molecular cloning and sequencing of two 'short chain' and two 'long chain' K(+) channel-blocking peptides from the Chinese scorpion Buthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                Gaps
                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurocoxin BmP03 precursor (Potassium ion channel blocker P03).
Mesobuthus martensli (Manchurian scorpion) (Buthus martensii):
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          martensii Karsch.";
FEBS Lett. 457:509-514(1999).
-!- FUNCTION: Blocks small conductance Calcium-activated potassium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the venom gland.
SIMILARITY: BELONGS TO THE SCORPION LEIUROTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 56;
62;
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                              Score 25; DB 1; Length 56;
Pred. No. 62;
                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70953032007E8672 CRC64;
   70953032042F8672 CRC64;
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BY SIMILARITY.

NEUROTOXIN BMP03.

BY SIMILARITY.

BY SIMILARITY.
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                                                                                                                                                                                                        56 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                 5; Mismatches
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Pred. No. 6
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                                    59.5%;
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        6015 MW;
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                                                                                                                                                                                                          STANDARD;
                                                                   3; Conservative
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                                                                                                                   10 IVLAMNVM 17
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Best Local Similarity
Matches 3; Conserv
                                                                                                  2 VLMAMNII 9
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34
38
56 AA;
                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
        56 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REDIINE-98044013; PubMed=9384377;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Kunst F., Ogasawara N., Moszer I., Brans A., Braun M., Briganell S.C., Bron S.,

Borriss R., Bourderler L., Brans A., Braun M., Briganell S.C., Bron S.,

Borriss R., Bourdeier L., Brans A., Braun M., Briganell S.C., Bron S.,

Ra Bornise R., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,

RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,

RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,

RA Chiaseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kuita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudaga B., Park S.H.,

RA Persecan B., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Seto T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Setouchi M., Taconi B., Schroeter R., Serror P., Sain B.S., Sata K.,

RA Setouchi M., Tamakoshi A., Tankaka H., Parkensum K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarcti A.,

RA Voshida K., Yoshikawa H.P., Zumstein B., Yoshikawa H., Danchin A.,

RA Winters P., Wippt A., Yamamoco of the Gram-posttive bacterium Bacillus M., The complete genome sequence of the Gram-posttive bacterium Bacillus
                                                                                                                                                                                                                                                                                             Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rappoport G., Danchin A.,
"Bacillus subtlins genome project: cloning and sequencing of the 97
"b region from 325 degrees to 333 degrees.";
Mol. Microbiol. 10:371-384 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:249-256(1997).
                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Bacillus.
                                      (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 41, Last annotation update)
87 AA.
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or send an email to license@isb-sib.ch).
                                                                                                          Hypothetical protein ywcE precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                  MEDLINE=95020537; PubMed=7934828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X73124; CAA51597.1; -. EMBL; Z99123; CAB15839.1; -.
    STANDARD;
                                                                                                                                 YWCE OR IPA-41R.
Bacillus subtilis.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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4; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                              WCBI_TaxID=9361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YV31 CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-9441932; PubMed=8308901;
Arnason U., Gullberg A.;
"Comparison between the complete mtDNA sequences of the blue and the
fin whale, two species that can hybridize in nature.";
J. Mol. Evol. 37:312-322(1993).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti; Balaenopteridae, Balaenoptera.
                           Transmembrane, Signal, Complete proteome.
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                                                                                                                        Score 25; DB 1; Length 87;
Pred. No. 98;
3; Mismatches 1; Indels
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                                                       HYPOTHETICAL PROTEIN YWCE
                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10747 MW; 9F770651FE65ED1B CRC64;
                                                                                              CC74135F423940CB CRC64;
                                                                                                                                                                                                                                                                                98 AA.
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                                                                     POTENTIAL.
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Balaenoptera musculus (Blue whale)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001133; Oxidored 4L. InterPro; IPR003214; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00420; oxidored q2; 1. ProDom; PD000359; Oxidred4L; 1.
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62.5%;
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                                                                                                                         59.5%;
                                                                                                                                        50.0%;
                                                                                              87 AA; 9959 MW;
              BG10587; ywcE
                                                                                                                                      Local Similarity 50.0
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Matches 5; Conservative
                                                                                                                                                                                                                                                                              STANDARD;
                                          53
                           Hypothetical protein;
PIR; S39696; S39696.
Subtilist; BG10587;
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59 ILFAVNVI 66
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55
                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion.
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                                                       CHAIN
TRANSMEM
                                                                                              SEQUENCE
                                                                                                                         Query Match
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                                                                               TRANSMEM
                                          SIGNAL
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NULM DASNO
ID NULM DA
AC 021333
DT 15-JUL
                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=97357423; PubMed=9214749;
Arnason U., Gullberg A., Janke A.;
Phylogenetic analyses of mitochondrial DNA suggest a sister group relationship between Kranthra (Edentata) and Ferungulates.";
Mol. Biol. Evol. 14:762-768(1997).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Edentata, Dasypodidae, Dasypus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leimbach D.; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE UPPO057 (PMP3) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
WANNAL OR ND4L OR NADH4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10840 MW; D0FF9BC309048774 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               020516;
15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Hypothetical 6.8 kDa protein F47B7.1 in chromosome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.5%; Score 25; DB 1; I 50.0%; Pred. No. 1.1e+02; ive 3; Mismatches 1;
                                                                                                                                                              Dasypus novemcinctus (Nine-banded armadillo)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001133; Oxidored 4L. InterPro; IPR003214; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y11832; CAA72524.1; -. PIR; T11449; T11449.
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37 LSAMNLI 43

S F T T S

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HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 407:57-762(2000).

Nature 407:57-762(2000).

Nature 407:57-762(2000).

Nature 407:57-762(2000).

Nature 40.

Nature 40.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHOPANTETHEINE (BY SIMILARITY). 3CDB655FBFA968C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
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MEDLINE=20500219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria, Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24; DB 1; Length 77;
Pred. No. 1.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                  Length 59;
                                                                                                                                                                                                                                    POTENTIAL.
DCE8905FCE3A660D CRC64;
                                                                                                                                                                                                                                                                                                               Score 24; DB 1; 1
Pred. No. 1.1e+02;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Acyl carrier protein homolog (ACP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00550; pp-binding; 1.
PROSITE; PS50075; ACP_DOMAIN; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
                                                                                                                                                                                                        POTENTIAL.
                           WormPep; F47B7.1; CE02743.

MormPep; F47B7.1; CE02743.

InterPro; IPR00612; UPP0057.

PROSITE; PS01309; UPP0057; 1.

Hypothetical protein; Transmembrane.

TRANSMEM 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE002149; AAF30918.1; -.
InterPro; IPR006163; Pp_bind.
InterPro; IPR006162; Ppantne_attach.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%;
71.4%;
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                                                                                                                                                                                                                                                                                                                        57.1%;
EMBL; U39646; AAA80373.1; -.
PIR; T16386; T16386.
                                                                                                                                                                                                                                                                59 AA; 6840 MW;
                                                                                                                                                                                                                                                                                                                                                    55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                    Local Similarity 55.6
hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 NMHVAVNII 38
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NVLMAMNII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UREPA
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                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PPY4;
                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REDILINE_2388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Schemen C.R., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
RA Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., WcKernan K.J., Malek J.A., Gunarane P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Nillalon D.K., Munzhy D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Batkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Batkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Generation and initial analysis of more than 15,000 full-length
RT human and mouse CDNA sequences.";
REDICTION: Induces a hyperpolarization-activated chloride current
C. -1- FUNCTION: Induces a hyperpolarization-activated chloride current
C. -1- FUNCTION: Longer CDNA Sequences.";
Ry Departs C. Maria M.A., Compus coordent R.A., Ry Schul C.C., Compus C.C., When expressed in xenopus coortessed and contractive channels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activating endogenous oocyte channels.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUE SPECIFICITY: Expressed in a subset of human breast tumors.
-!- MISCELLANEOUS: Marker of a cell type preferentially transformed by
                                                                                                                                                                                                                                                                                                                                                                                                       Morrison B.W., Moorman J.R., Kowdley G.C., Kobayashi Y.M., Jones L.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mat-8, a novel phospholemman-like protein expressed in human breast tumors, induces a chloride conductance in Xenopus oocytes."; J. Biol. Chem. 270:2176-2182(1995).
                          014802; 013211;
15-701-1998 (Rel. 36, Last sequence update)
15-301-1998 (Rel. 42, Last annotation update)
15-5EP-2003 (Rel. 42, Last annotation update)
FXYD domain-containing ion transport regulator 3 precursor (Chloride
conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein)
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neu or ras oncoprotein.
SIMILARITY: Belongs to the FXYD family.
87 AA.
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95138184; PubMed=7836447;
       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung carcinoma;
                                                                                                                                                                                                 FXYD3 OR MATS OR PLML.
                                                                                                                                                                                                                             (Human)
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                             Homo sapiens
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PROSITE; PS01097; HUPF_HYPC; 1.
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                  NULM_BALPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                             FXYD DOMAIN-CONTAINING ION TRANSPORT REGULATOR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S -> SEWRSSGEQAGRGWGSPPLTTQLSPTG (IN
                                                                                                                                GO, GO:0005897; C:integral to plasma membrane; TAS.
GO, GO:0005254; F:chloride channel activity; TAS.
GO; GO:0006821; P:chloride channel activity; TAS.
GO: GO:0006821; P:chloride transport; TAS.
InterPro; IPR000272; ATPIGI PLM MATB.
PRAM; PPG02039; ATPIGI PLM MATB; 1.
PROSTITE; PSO1310; PXYD; 1.
Transmembrane; Signal; Ionic channel; Chloride channel; Chloride;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Proteus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence and comparative analysis of the frd operon encoding the fumarate reductase of Proteus vulgaris. Extensive sequence divergence of the membrane anchors and absence of an frd-linked ampt cephalosporinase gene.";

Eur. J. Blochem. 167:481-488(1987).

-! SIMILARITY: BELONGS TO THE HUPF/HYPC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 1; Length 87;
Pred. No. 1.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL). MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6D674D668EB32493 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
FRD operon hypothetical protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 AA
                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X06151; CAA29511.1; -.
PIR; S00119; S00119.
InterPro; IPR001109; HupF HypC.
Pfam; PF01455; HupF HypC; 1.
PINSF; PIRSF0005618; HupF HypC; 1.
PRINTS; PR00445; HUPFHYPC; 1.
ProDom; PD003112; HupF HypC; 1.
TIGRFAMS; TIGR00074; hypC_hupF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=88004470; PubMed=3308458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REF.
EMBL; X93036; CAA63604.1; -.
EMBL; U28249; AAA73922.1; -.
EMBL; BC005238; AAH05238.1; -.
BTR; A55571; A55571.
Genew; HGNC:4027; FXYD3.
MIM; 604996; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 AA; 9263 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.v.,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                               20
87
                                                                                                                                                                                                                                                                                                                                                                             38
59
37
58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VLMAMNII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteus vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                21,
39,
36,
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=585;
                                                                                                                                                                                                                                                                                          Ion transport
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YFRC PROVU
P20927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cole S.T.;
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
    DDR B DDR B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRANIE-ISOLATE No. 27 / Anno 1987; TISSUE-Liver;
MEDLINE-92139449; PubMed=1779436;
Arnason U., Gullberg A., Widegren B.;
Arnason U., Gullberg A., Widegren B.;
"The complete nucleotide sequence of the mitochondrial DNA of the fin
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Cetacea; Mysticeti;
Balaenopteridae; Balaenoptera.
NCBI_TaxID=9770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           whale, Balaenoptera physalus.";
J. Mol. Evol. 33:556-568(1991).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                        Score 24, DB 1; Length 96;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Balaenoptera physalus (Finback whale) (Common rorqual).
                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
MADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
MTND4L OR ND4L OR NADH4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10763 MW; 0070D3D6C3AE805F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MTNDH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
Hypothetical protein.
SEQUENCE 96 AA; 10300 MW; EC094F1F37956EE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X61145; CAA43447.1; -.
BYR, ASBEST; S24920.
INTERPRO; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00420; oxidored q2; 1.
ProDom; PD000359; Oxidred4L; 1.
                                                                        57.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                  Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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7 NILMAFSM 14
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                                                                                                                                                                                   1 NVLMAM 6
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ID NULM DIDMA
AC P41307;
                                                                                                                                                                                                                                                                                                                                                                      NULM BALPH P24976;
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PIR; F71485; F71485.
PHCI-2DPAGE; 084673; -.
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                    :|:| |||
38 LLIARNII 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 NILTAVN 70
                                                                                                                                                                                     2 VLMAMNII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 83 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NVLMAMN 7
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               Protein CT666.
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ID Y710 CHLPN
AC Q9Z7J5;
                                                                                                                                                                                                                                                                     Y666 CHLTR
084673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
                                                                                                                                                                                                                                                          Y666 CHLTR
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                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                           MEDLINE-1933, MEDLINE-1933, PubMed-8056314; Janke A., Feldmaier-Fuchs G., Thomas K., von Haeseler A., Paabo S. "The marsupial mitochondrial genome and the evolution of placental
                       Eukaryoca; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                           Genetics 137:243-256(1994).
-1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (AGL)
 Didelphis marsupialis virginiana (North American opossum).
                                                                                                                                                                                                                                                                                                                                                                                    Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H(+)(Out).
-1- SUBCELLULAR LOCATION: Membrane-bound.
-1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10815 MW; F988F6026B0A4C59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 57.1%; Score 24; DB 1; L
62.5%; Pred. No. 1.8e+02;
ive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=90332440; PubMed=2143015;
                                                                                                                                                                                                                                                                                       PIR; S47878; S47878.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR001214; Oxidored4L.
Pfam; PF00420; oxidored 42; IPR000189; Oxidored 42; IPR000189; Oxidored 42; IPP0000189; Oxidored 42; IPP0000189; Oxidored 42; IPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Candida parapsilosis (Yeast).
                                                                                                                                                                                                                                                                                EMBL; Z29573; CAA82685.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VLMAMNII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 2 VLIKLNII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5480;
                                                      NCBI_TaxID=9267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP8 OR AAP1.
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                    Mitochondrion
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P17345;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin B.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis.";
Science 282:754-759(1998).
-!- SIMILMITY: BELONGS TO THE CHLAMYDIAL CPN0710/CT666/TC0037
-PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                          EMBL; X52115; CAA36361.1; -.
PIR; S10465; PWCK8P.
PIR, 44drogen ion transport; CF(0); Mitochondrion; Transmembrane.
TRANSMEM 1.2 POTENTIAL.
SEQUENCE 48 AA; 5492 MW; 0E7876341CAF0747 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         i, Indels
                                                                                                                                                                                                                                                                                                                                              Score 23; DB 1; Length 48;
Pred. No. 1.5e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FF227A1F3549AAE3 CRC64;
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Pred. No. 2.6e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=D/UW-3/Cx;
MEDLINE=99000809; Pubmed=9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001337; AAC68261.1; -.
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nes 4; Conservative
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Best Local Similarity 62.5%;
Matches 5; Conservative
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RESULT 19
RPOH_THEAC
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its wase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                    MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W. DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Bisen J., Praser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=J138;
Hirakawa H., Shirai M., Kuhara S.;
Hirakawa H., Shirai M., Kuhara S.;
"Genomic Sequence comparison of two unrelated isolates of Chlamydia pneumoniae from Japan and U.S.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0710/CT666/TC0037
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20330349; PubMed=10871362;
Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome genences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
                                                                                                                                              MEDLINE=99206606; PubMed=10192188;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein CDM0710/CP0036/CPj0710.
CPN0710 OR CP0036 OR CP00710.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiae; Chlamydiales; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 1; Length 84;
Pred. No. 2.6e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 AA; 9348 MW; 50A9CC271A5CB693 CRC64;
                                                                                                                                                                                                                                                                                                                                                  pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AE001652; AAD18849.1; -. EMBL, AE002167; AAF37931.1; -. EMBL, AP002547; BAA98917.1; -. EMBL, AB035952; BAA88660.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; C86579; C86579.
PIR; F72046; F72046.
PHCI-2DPAGE; Q9Z7J5; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                      SEQUENCE FROM N.A.
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                                                                                           NCBI_TaxID=83558;
                                                                                                                                    STRAIN=CWL029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; CP0036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 407:508-513 (2000).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klenk H.-P., Renner O., Schwass V., Zillig W., "Nucleotide sequence of the genes encoding the subunits H, B, A' and A' of the DNA-dependent RNA polymerase and the initiator tRNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPOH / EUKARYOTIC RPBS RNA POLYMERASE SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                            Archaea; Buryarchaecta; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 1; Length 87;
Pred. No. 2.7e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL445064; CACII533.1; ALT_INIT.

PIR; S26721; S26721.

HSSP; O27122; 18.

HAMAP; MF 00025; -; 1.

InterPro; IPR000783; RNA_pol H_23kD.

Pfam; PF01191; RNA_pol RbS C; 1.

ProDom; PE01515; RNA_pol H_23kD; 1.

PROSITE; PS01110; RNA_POL H_23KD; 1.

Transferase; Transcription; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 87 AA; 9927 MW; 9C5B1F39ABAC6F4E CRC64;
                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase subunit H (EC 2.7.7.6)
      87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 20:5226-5226(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-DSM 1728;
MEDLINE-93027268; PubMed=1408839;
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Similarity 50.0%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X68198; CAA48279.1;
                                                                                                                                                                                                                        Thermoplasma acidophilum.
         STANDARD;
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                              RPOH OR TA0389.
RPOH THEAC
003588;
01-JUN-1994 (
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RL31 HALN1 RESULT 20

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Gaps

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2; Mismatches

4; Conservative

Matches

65 NILTAVN 71

1 NVLMAMN 7

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SEQUENCE OF 76-80.
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029522;
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                                                                                                                                                                                                                                                                                            MEDLINE=2050483; PubMed=11016950; Berquist B., Pan M., Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shrogna J., Shukla H.D., Lasky S.R., Baliga N.S., Thorseon V., Sbrogna J., Swartzall S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Leithauser B., Kaller K., Cruz R., Krebs M.P., Angevine C.M., Dale H., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Sham M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Bbhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; Genon sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12181(2000).
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STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Ploistochmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
Relavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
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15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Virulence-associated protein D.
VAPD OR HI0450.
NAPD OR HI0450.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
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                                                                                                                                                           Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.8%; Score 23; DB 1; Length 91; 100.0%; Pred. No. 2.8e+02; cive 0; Mismatches 0; Indels
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InterPro; IPR000054; Ribosomal_L31e.

PERO; PF01198; Ribosomal_L31e; 1.

PR051TE; PS01144; RIBOSOMAL_L31E; 1.

Ribosomal protein; Complete protecome.

RINT MET 0 0 BY SIMILARITY.

SEQUËNCE 91 AA; 10092 MW; 25003B509C7F98D5 CRC64;
                                          16-OCT-2001 (Rel. 40, Created)
26-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L31e.
RPL31E OR VNG2467G.
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           91 AA
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           PRT;
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                STANDARD;
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Best Local Similarity
Matches 5; Conserv
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AMNII 33
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                   RL31 HALN1
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Klenk H.-P., Clayton R.A. Tomb J.-F., White O., Nelson K.E.,
Klenk H.-P., Clayton R.A. Tomb J.-F., White O., Nelson K.E.,
Kletchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Fleischmann R.D., McKenney K., Adama M.D., Loftus B.,
Kirkness E.F., Dougherty B.A., McKenney K., Adama M.D., Loftus B.,
Kirkness E.F., Godsyne J.D., Weidman J.F., McDonald L., Utterback R.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                  "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
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Nature 390:364-370(1997).
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C. Fine L.D., Fritchman J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20137488; PubMed=10675023;
Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
Langen H., Fountoulakis M.;
Two-dimensional and Define protecome of Haemophilus influenzae.";
Electrophoresis 21:411-429(2000).
-- SIMILARITY: BELONGS TO THE VAPD FAMILY.
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44.4%; Pred. No. 2.8e+02;
tive 2; Mismatches 3; Indels
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Archaeoglobus archaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;
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Pfam; PF04605; VapD_N; 1.
Virulence; Complete proteome.
SEQUENCE 91 AA; 10543 MW;
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4; Conservative
                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995).
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Matches 4; Conserv
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J01394; AAB59276.1;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Complete sequence of bovine mitochondrial DNA. Conserved features of
                                                                                                                                                                                                                                                                                                                    Gaps
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Anderson S., de Bruijn M.H.L., Coulson A.R., Eperon I.C., Sanger F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
 SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE UPF0132 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=65, 66, D, and F;
Wetrstein P.J.;
"Bos taurus mitochondrial protein coding regions.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-! - CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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                                                                                                                                                                                                                                                                                       Score 23; DB 1; Length 95;
Pred. No. 3e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                               Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                        P03902; Q8SFX7;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
MTND4L OR ND4L.
Bos taurus (Bovine).
                                                                                                                                                                                                                                                  POTENTIAL.
310B66160F26858A CRC64;
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                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                   EMBL; AE001054; AAB90510.1; -. PIR; H69341; H69341.
                                                                                                                                                                                                                                     32 52
55 75
95 AA; 10475 MW;
                                                                                                                                                                        InterPro; IPR005348; UPF0132.
Pfam; PF03675; UPF0132; 1.
ProDom; PD015391; UPF0132; 1.
                                                                                                                                                                                                                                                                                       54.8%;
62.5%;
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55 VVMAFSII 62
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MEDLINE=98440761; PubMed=9767689;
Hiendleder S., Lewalski H., Wassmuth R., Janke A.;
The complete mitochondrial DNA sequence of the domestic sheep (Ovis aries) and comparison with the other major ovine haplotype.";
J. Mol. Evol. 47:441-448(1998).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                   Match 54.8%; Score 23; DB 1; Length 98; Local Similarity 37.5%; Pred. No. 3.1e+02; Indels 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                               65 65 V -> A (IN STRAIN 66).
98 AA; 10797 MW; 4DB48B7DA59C1881 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MJMH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
MTND4L OR ND4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidored4u; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10837 MW; ECOC943C752F8691 CRC64;
                                                                                                                                                                                                        Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
VARIANT 65 65 V -> A (IN STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
EMBL; AF490528; AAM08325.1; -... EMBL; AF490529; AAM08338.1; -... EMBL; AF493541; AAM12297.1; -... EMBL; AF493542; AAM12810.1; -... PIR, AOM429; QXBO4L.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AP010406; AAD10103.1; -. PIR, TI1058; TI1058. Cxidoxed 4L. InterPro; IPR00133; Oxidoxed 4L. InterPro; IPR003214; Oxidred4L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Best Local Similarity
13; Conserva
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7 NIMMAFTV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 NIMMAFTV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NVLMAMNI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NVLMAMNI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1990) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
                                       jannaschii.";
Science 273:1058-1073(1996).
-- SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila yakuba (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DCT-1996 (Rel. 34, Last annotation update)
Alcohol dehydrogenase related 31 kDa protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 34 F4 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
B837A92FA94002FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.8%; Score 23; DB 1; L
71.4%; Pred. No. 3.1e+02;
iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 AA
[1]
SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 AA; 11483 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U67592; AAB99536.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF05154; TM2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; C64489; C64489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LMAMNII 9
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1 MMAMNEI 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; MJ1516; -.
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ADHR DROYA
TOHR DROYA
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                                                                                                                                                                                                                                                                                                                                             MEDIATE-SOJ514; PubMed=9371463; MEDIATE-SOJ514; Dubode JD., COOK R., Gilbert K., Aldredge T., Bashirzadeh R., Blakely D., COOK R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Aldredge T., Harrison D., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noalling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum delthan; functional analysis and comparative genomics."; J. Bacceriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                       Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriaces;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h Similarity 71.4%; Score 23; DB 1; Length 98; Similarity 71.4%; Pred. No. 3.1e+02; 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Merhanococcus jannaschii.
Archaea; Buryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A098F7AB1B29D2F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ1516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 AA.
                                                                                                               15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
510S ribosomal protein L30e.
                                                                          98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP: MF 00481; -; 1.
InterPro; IPR004013; Ribosomal Ligoe.
InterPro; IPR0040138; Ribosomal Ligo.
Ffam; PF01248; Ribosomal Ligo; Probom; PF001248; Ribosomal Ligo; 1.
PROSITE: PS00093; RIBOSOMAL LigoE 1; 1.
PROSITE: PS00993; RIBOSOMAL LigoE 2; 1.
Ribosomal protein; Complete protecme.
SEQUENCE 98 AA; 10506 MW; A098F7ABIB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000876; AAB85544.1; -.
PIR; A69007; A69007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVMASNI 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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ID YF16 METJA
AC Q58911;
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RESULT 26

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Сарв

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Evolutionary conservation of components of the protein translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Columbia;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Pujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=84156523; PubMed=6323015;
Klobutcher L.A., Jahn C.L., Prescott D.M.;
Internal sequences are eliminated from genes during macronuclear development in the ciliated protozoan Oxytricha nova.";
Cell 36:1045-1055(1984).
                                                                                                  Bukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Oxytricha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=94150683; PubMed=8107851;
Hartmann B., Sommer T., Prehn S., Goerlich D., Jentsch S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB 1; Length 82;
Pred. No. 4.3e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO: IPR004217; Znf Tim10/DDP.
Pfam; PF02953; Zf-Tim10 DDP; 1.
SEQUENCE 82 AA; 9028 MW; 297AFFBC17079438 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
10-CT-2001 (Rel. 40, Last annotation update)
Protein transport protein SEC61 beta subunit.
01-NOV-1988 (Rel. 09, Last sequence update) 01-NOV-1988 (Rel. 09, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; K02624; AAA64886.1; -.
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EMBL; K02628; AAA64888.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 367:654-657(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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AT2G45070 OR T14P1.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NVLMAMNII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                             NCBI_TaxID=5945;
                                                                                Oxytricha nova.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rapoport T.A.;
                                       protein.
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S61B ARATH
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Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
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                                                                                                    NAD OR NADP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12 / MG1655;
MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EcoGene; EG13348; yjjZ.
Hypothetical protein; Complete proteome.
SEQUENCE 78 AA; 8697 MW; B466F1E01231D334 CRC64;
                                                                                                  11 >32 NAD OR NADP (BY SIMILAR:
32 32
32 AA; 3412 MW; 9302949AFCBE7D4F CRC64;
                                                                                                                                                                                     Score 22; DB 1; I
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                 ol-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypotherical protein yjjZ.
Escharich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                              0; Mismatches
                 FlyBase; FBgn0013164; Dyak\Adhr.
InterPro; IPR002198; ADH short.
PROSITE; PS00061; ADH_SHÖRT; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U14003; -; NOT ANNOTATED CDS.
EMBL; AE000507; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished observations (OCT-1996).
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P05526;
01-NOV-1988 (Rel. 09, Created)
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57.1%;
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71.4%;
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Matches 4; Conservative
                                                                                                                                                                                                                                5; Conservative
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69 MLMIMUL 75
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Best Local Similarity
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                                                                              Oxidoreductase.
NP BIND 11
NON TER 32
SEQUENCE 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
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RESULT 29 C2 OXYNO ID C2 OX AC P0552 DT 01-NO

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Y069_AERPE
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                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
28.FBB-2003 (Rel. 41, Last annotation update)
Photosystem I reaction center subunit psaK 1 precursor (Photosystem
                                                                                                            -1- FUNCTION: NECESSARY FOR PROTEIN TRANSLOCATION IN THE ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 3:109-136(1996).
-!- FUNCTION: THE EXACT FUNCTION OF PSAK IN PHOTOSYSTEM I (PSI) IS
      Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thalians.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                             -i-SUBLITI: HETEROTRIMERIC COMPLEX COMPOSED OF SEC61-ALPHA, SEC61-BETA AND SEC61-GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22; DB 1; Length 82;
Pred. No. 4.3e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Cyanobacteria; Chroccoccales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
SCA3EC83818EFD2F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR005609; Sec61 beta.
Pfam; PF03911; Sec61 beta; 1.
Protein transport; Translocation; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 AA.
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PSAKI OR PSAK OR SSR0390.
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                                                                                                      Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endoplasmic reticulum
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Best Local Similarity
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P72712;
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                     (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. PHOTOSYSTEM I REACTION CENTER SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99310319; PubMed=10382966; Kawarabayasi Y., Haino Y., Horikawa H., Yamazaki S., Haikawa Y., Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi Hogoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H., Nomura N., Sako Y., Kikuchi H., Nomura P., and Sako Y., Kikuchi H., Mague Sequence Of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 1; Length 86;
Pred. No. 4.5e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                EMBL; D90900; BAA16719.1; -.
PIR, S74567; S74567.
HAMAP; MF_00474; -; 1.
InterPro; IPR001549; PSI P8aG/K.
Pfam; PF01241; PSI PSAK; 1.
PROSITE; PS01026; FHOTOSYSTEM I PSAGK; 1.
Photosystem I; Photosynthesis; Transmembrane; Thylakoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein, Complete proteome.
SEQUENCE 91 AA, 10080 MW, B6EDE0AF50AFD94A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
SFOBEAD1B9E99E3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-!- SIMILARITY: Belongs to the UPF0147 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SCP-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0147 protein APES069.
APES069.
modified and this statement is not removed. entities requires a license agreement (See h or send an email to license@isb-sib.ch).
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HAWAP; MF 00342; -; 1.
Interpro; IPR065354; UPF0147.
PÉm; PF03685; UPF01471.
ProDom; PD029943; UPF0147; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 AA; 8644 MW;
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                                                                                                                                                                                                                                                                                                                                   Complete proteome.
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SEQUENCE FROM N.A.

SETAAIN=26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White D., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

MCKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

McKenney K., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: Natural electron acceptor for a formate dehydrogenase.
-i- SUBCELLULAR LOCATION: Pertiplasmic.
-i- PTM: BINDS ONE HEME GROUP PER MOLECULE.
-i- SIMILARITY: BELONGS TO THE CLASS I CYTOCHROME C FAMILY.
                         Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                            The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                      MEDIJNE=20536487; PubMed=10965034; Koyanagi S., Nagata K., Tamura T., Tsukita S., Sone N.; Purification and characterization of cytochrome c-553 from
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 20-28, AND CHARACTERIZATION.
 Cytochrome C-553 precursor (C553). HP1227.
                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori.";
J. Biochem, 128:371-375(2000).
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TIGR; HP1227; -
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les 3; Conserv
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                                                                              NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                   Jenter J.C.;
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                                                                                                                                                                                                                                                                                                                                                      STRAINS-JAL-1 / DSW 2661 / ATCC 43067;
STRAINS-JAL-1 / DSW 2661 / ATCC 43067;
MEDLINE-96337999; Pubmed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlawage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Raich C.I.,
Overbeek R., Kirkness E.F., Weinstcock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidamn J.F., Puhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 273:1058-1073(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO M.THERMOAUTOTROPHICUM MTH1250.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22; DB 1; Length 92;
Pred. No. 4.8e+02;
2; Mismatches 2; Indels
Score 22; DB 1; Length 91;
Pred. No. 4.7e+02;
1; Mismatches 0; Indels
   Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                              Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
DDBCA78E28CCF164 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CTT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ1223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
 52.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9739 MW;
                                                                                                                                                                                                                                                               MJ1223.
Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 55.6
les 5; Conservative
                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein;
TRANSMEM 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 NVLVGESII 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NVLMAMNII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F64452; F64452.
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 AA;
                                                              4 MAMNI 8
                                                                              1 | | | | :
1 MAMNL 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; MJ1223; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C553 HELPY .
025825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (
28-FEB-2003 (
28-FEB-2003 (
                                                                                                                                                                    YC23 METJA
Q58620;
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C553_HELPY
ID C553_HI
AC 025825,
DT 28-FEB-
DT 28-FEB-
DT 28-FEB-
                               Matches
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                                                                                                                                      RESULT 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Electron transport; Heme; Signal; Periplasmic; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22; DB 1; Length 96;
Pred. No. 5e+02;
4; Mismatches 1; Indels
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HEME (COVALENT).
IRON (HEME AXIAL LIGAND) (
SIMILARITY).
IRON (HEME AXIAL LIGAND) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGEEFEA2AE5B8428 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002329; Cyt_CIC.
InterPro; IPR000345; CytC heme_bind.
Pfam; PF00034; cytochrome_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0665; CYTCHROMECIC.
Prodom; PD004020; CYT C bact; 1.
PROSITE; PS00190; CYTOCHROME C;
                                                                                                                                                                                                                         EMBL; AE000628; AAD08272.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 AA; 10346 MW;
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ilarity 37.5%;
Conservative
                                                                                                                                                                                                                                                                                                                            InterPro; IPR003088; Cyt_CI
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332
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MEDLINE=99098146; PubMed=9881471;
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Matches
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                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=ATCC 35210 / B31;

STRAIN=ATCC 35210 / B31;

MEDLINE=98065943; PubMed=9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Hickey E.K., Gwinn M.,

Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,

van Vugt R., Palmer N., Adams M.D., Goodyne J.D., Weidman J.,

Utterback T., Watchey L., McDonald L., Artiach P., Bowman C.,

Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,

Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Hippopotamidae, Hippopotamus.
NCBI_TaxID=9833;
                                                                                                  Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.4%; Score 22; DB 1; Length 96; 50.0%; Pred. No. Se+02; ...ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                   sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Complete proteome.
SEQUENCE 96 AA; 11367 MW; 3829071FCE919815 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
MTND4-ubjaninone oxidoreductase chain 4L (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                           Nature 390:580-586(1997).
                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0161 protein BB0143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 AA.
                                   96 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hippopotamus amphibius (Hippopotamus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD004225; DUF37; 1.
TIGRFAMS; TIGR00278; TIGR00278; 1.
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE001125; AAC66526.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF 00386; -; 1.
InterPro; IPR002696; DUF37.
Pfam; PF01809; DUF37; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| : ||
57 ILMTLRII 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G70117; G70117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VLMAMNII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] -
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NULM HIPAM
Q9ZZY3;
                                     Y143 BORBU
051168;
               RESULT 35
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                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to licenseeisb-sib.ch).
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Arnason U., Gullberg A., Managan W.;
A complete mitochondrial DNA molecule of the white-handed gibbon,
Hylobates lar, and comparison among individual mitochondrial genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Ursing B.M., Arnason U.;
"Analyses of mitochondrial genomes strongly support a hippopotamus-whale clade.";
"Male Clade.";
Proc. R. Soc. Lond., B. Biol. Sci. 265:2251-2255(1998).
Proc. R. Soc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hylobatidae; Hylobates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         all hominoid genera.";
Hereditas 124:185-189(1996).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٠.
                                                                                      Proc. R. Soc. Lond., B, Biol. Sci. 265:2251-2255(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22; DB 1; Length 98; Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidared4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10739 MW; 158CEEABC1614E67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NULM HYLLA

ID NULM HYLLA STANDARD; PRT; 98 AA.

1D NULM HYLLA

Q95709;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

NATNO-1097 (Rel. 35, Last sequence update)

ON MYND-10 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00420; oxidored q2; 1.
Probom; PD000359; Oxidored4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10776 WW; 5F09598BCE0622F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X99256; CAA67636.1; --
PIR; T11841; T11841.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AJ010957; CAA09436.1; -.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.4%;
71.4%;
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion.
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J. Bacteriol. 175:7918-7930(1993)
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54 NLILSNNLI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NVLMAMNII 9
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                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxiD=2097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y233 MYCGE
P47475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Landrace; TISSUB=Heart;
MEDLINE=99365306; PubMed=10433971;
Lin C.S., Sun Y.L., Liu C.Y., Yang P.C., Chang L.C., Cheng I.C.,
Mao S.J.T., Huang M.C.;
"Complete nucleotide sequence of pig (Sus scrofa) mitochondrial genome and dating evolutionary divergence within artiodactyla.";
Gene 236:107-114(1999).
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98404150; PubMed=9732457;
Ursing B.M., Arnason U.;
"The complete mitochondrial DNA sequence of the pig (Sus scrofa).";
J. Mol. Evol. 47:302-306(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 236:107-114(1999).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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52.4%; Score 22; DB 1; Length 98; 57.1%; Pred. No. 5.1e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    828C7F511A4E3AFA CRC64;
                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J; Ubiquinone; Mitochondrion.
10824 MW; 828C7F511A4E3AFA
                                                                                                                                                                                                                                          98 AA.
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(Rel. 21, Last sequence update)
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InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00420; oxidored q2; 1.
ProDom; PD000359; Oxidred4L; 1.
Oxidoreductase; NAD; Ubiquinone
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                                                                                                                                                                                                                                                                                                                                                                         MIND4L OR ND4L OR NADH4L.
                    Best Local Similarity 57.1
Matches 4; Conservative
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LVYMNII 9
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                                                                                    1 NVLMAMN 7
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wes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion
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01-MAR-1992
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P25000;
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P56632;
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Query Match
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NULM PIG
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SEQUENCE FROM N.A.
SETALIRE-96026346; PubMed=7569993;
REDILINE-96026346; PubMed=7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fleischmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Tomb. S. Smith H.O., Hutchison C.A. III, Vencer J.C.,
"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=91012605; PubMed=1976816;
Smith M.J., Banfield D.K., Doteval K., Gorski S., Kowbel D.J.;
"Nucleotide sequence of nine protein-coding genes and 22 tRNAs in the
"Inchondrial DNA of the sea star Pisaster ochraceus.";
J. Mol. Bvol. 31:195-204(1990).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Pisaster.
NCBI_TaxID=7612;
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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MEDLINE=94075230; PubMed=8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.4%; Score 22; DB 1; Length 98; 33.3%; Pred. No. 5.1e+02; ive 5; Mismatches 1; Indels
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InterPro; IPR001133; Oxidored 4L.
Pfam; PF00420; oxidored 42; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10965 MW; 499EB65E8ADBAE05 CRC64;
01-MAR-1992 (Rel. 21, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3)
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01-FEB-1996 (Rel. 33, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MG233.
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                                                                                                                  Pisaster ochraceus (Sea star).
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50.0%;
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PIR; B64368; B64368.
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Best Local Similarity 50.0°
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Q57966;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Detection of new genes in a bacterial genome using Markov models for "Detection of new genes";
three gene classes.";
Nucleic Acids Res. 23:3554-3562(1995).
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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SEQUENCE FROM N.A.
STRAIN-KIZ / MGIGES5;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y., Shao Y., Shao P.J., Mau B., Shao Y., Shao Y., Shao P.J., Shao 
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Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
Buncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lew H., Lin D., Namath A., Oeffner P., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 1; Length 99;
Pred. No. 5.2e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OGT-2001 (Rel. 40, Last annotation update)
Hypothetical protein ybaM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION.
MEDLINE=96032851; PubMed=7567469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91310687; PubMed=1856227;
         SIMILARITY: TO B.SUBTILIS YSXB
                                                                                                                                                                                           EMBL; U39703; AAC71454.1; -. EMBL; U02141; AAD12419.1; -. PIR; G64225; G64225.
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68 NVAVAFSVI 76
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Prodom; PD00061; Cold_shock; 1.
SMART; SM00357; CSP; 1.
PROSTIR; PS00325; COLD SHOCK; 1.
Transcription regulation; DNA_binding; Activator; Complete proteome.
                                                                                                                                   Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                             "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Exiksentz-Ponten T., Minkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 396:133-140(1998).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=782;
                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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Pred. No. 6e+02;
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30-MAY-2000 (Rel. 39, Last sequence update)
36-FBB-2003 (Rel. 41, Last annotation update)
Cold shock-like protein cspA.
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STRAIN-Madrid E;
MEDLINE-99039499; PubMed=9823893;
                                                                                                            STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSD
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InterPro; IPR002059; Cold_shock.
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Matches 4; Conser
                                                                                     SEQUENCE FROM N.A.
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MATNIV 6
                                          NCBI_TaxID=781;
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Q9ZCP9;
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STRAINSUTEX IB 555 / Pringsheim;
Loeffelhardt W. Stirewalt V.L., Michalowski C.B., Annarella M.,
Loeffelhardt W. Stirewalt V.L., Michalowski C.B., Annarella M.,
Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
(In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa."; Plant Mol. Biol. Rep. 13:327-332(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=UTEX LB 555 / Pringsheim;
Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
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                                                                                                                                                                                                                                                                                                                                                                                         Būkaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
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  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyanelle, Hypothetical protein.
SEQUENCE 65 AA; 7635 MW; EAFDD0C8B6233CE3 CRC64;
                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 7.6 kba protein ycf33.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cold shock-like protein cspA.
CSPA OR RC1021.
Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE YCF33 FAMILY.
                                                                                                                                                                                                65 AA.
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U30821; AAA81285.1; -. PIR; T06942; T06942.
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2; Conservative
                                                                                                                                                                                                STANDARD;
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14 NIILGIKVI 22
                                        1 NVLMAMNII 9
                                                                                                                                                                                                                                                                                                                                                Cyanophora paradoxa.
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                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2762;
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092GV1;
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(1997)

CSPA_RICCN

SERVICE

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                             EMBL; AJ235272; CAA15108.1; ...

DR PIR; B71673; B71673.

DR PIR; B71673; B71673.

DR PRSP; P41016; 116.

DR PRINTS; PR0002059; Cold_shock.

DR PRINTS; PR000505; ColdSHOCK.

DR PCDDm; P0001621; CGP; 1.

DR PCDDm; P0001621; CGP; 1.

DR PCDSTE; P800357; CSP; 1.

DR PCDSTE; P800357; CSP; 1.

Transcription regulation; DNA-binding; Activator; Complete proteome.

GT DOMAIN

SEQUENCE 70 AA; 7785 MW; P49FBPZFB344903E CRC64;
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7%; Pred. No. 66+02;
Matches 4; Conservative 1; Mismatches 1; Indels
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Search completed: February 17, 2004, 10:57:01 Job time : 4.85149 secs

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                                                                                                                                     February 17, 2004, 10:50:13; Search time 6.50495 Seconds (without alignments) 58.540 Million cell updates/sec
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Sequence 13, 1
Sequence 13, 1
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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-09-134-001C-4976
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                                                                                                                                                                                                                                                                                                                                                                                                      328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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18, Appl
30061, A
4499, Ap
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Sequence 5, Application US/09308935

Fatent No. 6268334

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

FILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/308,935

CURRENT FILING DATE: 1999-02-27

EARLIER APPLICATION NUMBER: PCT/GB97/03506

EARLIER FILING DATE: 1997-12-22

EARLIER FILING DATE: 1996-12-20

HOWBER OF SEQ ID NOS: 18
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                               Sequence 6, A
Sequence 6, A
Sequence 6, A
Sequence 18,
Sequence 4499
Sequence 27,
Sequence 27,
Sequence 27,
Sequence 27,
Sequence 27,
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APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPERBUCE: 620-67
CURRENT FILING DATE: 1999-05-27
CURRENT FILING DATE: 1999-05-27
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1996-12-20
EARLIER FILING DATE: 1966-12-20
SOFTWARE: PATON NOS: 18
SOFTWARE: PATON NOS: 18
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Seguence 4
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 42; DB 3; Length 9; 100.0%; Pred. No. 2.5e+05; ive 0; Mismatches 0; Indels
                              US-08-487-811A-6
US-09-060-694-6
US-09-370-6
PCT-US93-07370-6
US-09-215-221-18
US-09-134-001C-4499
US-09-134-01C-4499
US-09-103-478-27
US-09-103-478-27
US-09-193-931C-27
           -07-928-611-6
-08-333-977-6
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US-09-213-392-4
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                                                                                                                                                                    US-08-725-531-4
                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09308935; Patent No. 6268334; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 9; Conserv
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STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-078-596-13
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                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-308-935-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: ANXON & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUTRY: U.S.A.
COMPUTER: Virginia
COUTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25 (BPO)
SOFWARE: Patentin Release #1.0, Version #1.25 (BPO)
SOFWARE: J3-UN-1995
CLASSIFICATION NUMBER: 23-JUN-1995
CLASSIFICATION NUMBER: 25.327
REFERENCE/DOCKET NUMBER: 25.327
REFERENCE/DOCKET NUMBER: 25.327
REFERENCE/DOCKET NUMBER: 117-181
TELECHONE: (703) 816-4000
ITELEPHONE: (703) 816-4000
ITELEPHONE: (703) 816-4000
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Score 42; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                      Length 16;
                                                                                                                                                                                                   Query Match

100.0%; Score 42; DB 3;

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 9; Conservative 0; Mismatches 0
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Sequence 13, Application US/08428131
Setent No. 586378
Patent No. 586378
Patent No. The Application Setent No. Trube OF INVENTION: Transcription Factor DP-1
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-078-596-13
; Sequence 13, Application US/09078596
; Patent No. 6150116
; Patent No. 6150116
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas Barrie
                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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1 NVLMAMNII 9
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                                                                                                                                 GENERAL INFORMATION:
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                                                                JS-09-308-935-6
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GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholás B
APPLICANT: La Thangue, Nicholás B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
TITLE OF INVENTION: 9-67
CURRENT APPLICATION WUMBER: US/09/308,935
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: PCT/GB97/03506
EARLIER APPLICATION NUMBER: GB 9626589.7
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTING DATE: 1996-12-20
SOFTWARE: PATENTING DATE: 1996-12-20
SOFTWARE: PATENTING DATE: 1996-12-20
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT PILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: ECT/GB97/03506
EARLIER PILING DATE: 1997-12-22
EARLIER PILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 20
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 42; DB 3; Length 19; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 9; Conservative 0; Mismatches 0; Indels
  0; Indels
0; Mismatches
                                                                                                                                                   RESULT 6
US-08-308-935-16
; Sequence 16, Application US/09308935
; Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09308935; Patent No. 6268334; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 9; Conservative
  9; Conservative
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                                                                                9 NVLMAMNII 17
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US-09-308-935-4
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  Matches
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Fatent No. 626834
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
TITLE OF INVENTION:
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: PCT/GB97/03506
EARLIER APPLICATION NUMBER: PCT/GB97/03506
EARLIER APPLICATION NUMBER: GB 9626589.7
EARLIER APPLICATION NUMBER: GB 9626589.7
EARLIER PLING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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                                                          APPLICANT: La Thandaue, Nicholas B
APPLICANT: La Thandaue, Nicholas B
APPLICANT: Bandara, Lesantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPREBUCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT PILING DATE: 1999-05-27
EARLIER PILING DATE: 1997-12-22
EARLIER PILING DATE: 1997-12-22
EARLIER PILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-1
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US-08-428-131-11
; Sequence 11, Application US/08428131
Sequence 6, Application US/09308935 Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 30
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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100.0%; Score 42; DB 4; Length 74;
100.0%; Pred. No. 0.068;
tive 0; Mismatches 0; Indels 0; Gaps
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US-08-894-139-10
is Sequence 10, Application US/08894139
is Sequence 10. Application US/08894139
sequence 10. Application US/08894139
sequence 10. Application US/08894139
sequence 10. Application US/08894139
APPLICANT: HIANGUE, NICHOLAS B. APPLICANT: HIANGUE, RENE
APPLICANT: HIANGUE, SERNORE
ITITE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: 25
CORRESPONDENCE ADDRESS: 25
CORRESPONDENCE ADDRESS: 100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COUNTRY: U.S.A.
ZIP: 22201-4714
COUNTRY: U.S.A.
SIPPLICATION SAFE
COMPUTER: PREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PREADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: PARABLE POWN:
CORRESTICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLEEPAN: (703) 816-4100
TELEFPHONE: (703) 816-4100
TELEFPHONE: (703) 816-4100
TELEFPHONE: (703) 816-4100
TELEFPHONE: CHARACTERISTICS:
LENGTH. AA MANIE AA MANI
                                                          ATTOKNITY AGENT IN CATACOM NAME: Archur R. CZEWFORD REGISTRATION NUMBER: 25,327
REPERCOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4100
INFORMATION FOR SEO ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 72 amino acids TYPE: amin
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Best Local Similarity 100.0
Lange 9; Conservative
                          ATTORNEY/AGENT INFORMATION:
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US-08-894-139-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NVLMAMNII 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-078-596-11
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GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas Barrie
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Nivon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/428,131
FILING DATE: 23-UNN-1995
CLASSIFICATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: 72 amino acid8
TYPE: amino acid8
TYPE: amino acid8
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Sequence 11, Application US/09078596

Patent No. 6150116

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
CITY: Arlington
STREET: 1000 No. 6150116th Glebe Road, 8th Floor
CITY: Arlington
STREET: 100 No. 6150116th Glebe Road, 8th Floor
CITY: Arlington
STREET: 100 No. 6150116th Glebe Road, 8th Floor
COUNTRY: U.S. A.
ZIP: 22201-4714
COUNTRY: U.S. A.
COUNTRY: U.S. A.
COUNTRY: U.S. A.
CONPUTER: Ploppy disk
COMPUTER: IBW PC Comparible
COMPUTER: Ploppy Gleb
SOFWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/09/078,596
FILING NAMP.
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Best Local Similarity 100.0%; Score 42; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 NVLMAMNII 23
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APPLICANT: La Tranque, Nicholas B
APPLICANT: La Tranque, Nicholas B
APPLICANT: La Endara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1999-05-27
EARLIER PILING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-20
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

81.0%; Score 34; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08194338
Patent No. 5474898
Sequence 11, Application US/09308935
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 NVLMAMN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NVLMAMN 7
                        Patent No. 6268334
GENERAL INFORMATION:
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                                                     RESULT 13
US-09-308-935-15

is Sequence 15, Application US/09308935

j Patent No. 626834

igeneral INFORMATION:
    APPLICAMY: La Thangue, Nicholas B
    APPLICAMY: La Thangue, Nicholas B
    APPLICAMY: Bandara, Lasantha R
    TITLE OF INVENTION: Peptide antagonists of DP transcription factors
    TITLE OF INVENTION: Peptide antagonists of DP transcription factors
    TITLE APPLICATION NUMBER: US/09/308,935
    CURRENT FILING DATE: 1999-0.27
    EARLIER APPLICATION NUMBER: CT/GB97/03506
    EARLIER FILING DATE: 1999-12-22
    EARLIER FILING DATE: 1999-12-20
    NUMBER OF SEQ ID NOS: 18
    SOFTWARE: PatentIn Ver. 2.1
    SEQ ID NO 15
    LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09308935

Patent No. 626834

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT PILING DATE: 1999-05-27
EARLIER PILING DATE: 1999-12-22
BARLIER PILING DATE: 1999-12-22
FRALIER PILING DATE: 1999-12-22
MUMBER OF SEQ ID NOS: 18
SOFTWARF: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide US-09-308-935-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide US-09-308-935-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.5%; Score 38; DB 3; Length 19;
88.9%; Pred. No. 0.097;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.5
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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|NVRMAMNII 17
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|NALMAMNII 17
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Best Local Similarity
54 NVLMAMNII
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US-09-308-935-11
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LENGTH: 19
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STRANDEDNESS: single

Matches

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Length 14; Indels

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US-09-134-001C-3434
US-09-134-001C-3434
US-09-134-001C-3434
US-09-134-001C-3434

Sequence 3444, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: UNMERS: US/09/134,001C

TITLE OF INVENTION: UNMERS: US/09/134,001C

CURRENT PELING DATE: 1998-08-13

PRIOR PELING DATE: 1998-08-13

PRIOR PELING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

WUMBER OF SEQ ID NOS: 5574

SEQ ID NO 3434

LENGTH: 100
                                                                                                                                                                  Sequence 3697, Application US/09134001C
Sequence 3697, Application US/09134001C
Sequence 3697, Application US/09134001C
Sequence 3697, Application US/09134001C
Sequence 3697, Application US/09134,001C
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPERBNCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3697
LENGTH: 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB 4;
Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.0%; Score 29; DB
85.7%; Pred. No. 43;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3933, Application US/09107532A patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 85.7
Matches 6; Conservative
                                |||::|||
55 NVLVPINII 63
  NVLMAMNII 9
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Best Local Similarity
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US-09-107-532A-3973
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                                                                                                                                                                     JS-09-134-001C-3697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Black, Michael
APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Hodgson, John
APPLICANT: Kowales, David
APPLICANT: Lonetto, Michael
APPLICANT: Nicholas, Richard
APPLICANT: Reschard, Richard
APPLICANT: Reschard, Richard
APPLICANT: Reschard, Martin
APPLICANT: Reschard, Martin
APPLICANT: Rosenberg, Martin
APPLICANT: Rosenberg, Martin
APPLICANT: Rosenberg, Martin
APPLICANT: Somenberg, Martin
APPLICANT: Ward, Julie
APPLICANT: 
                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                 78.6%; Score 33; DB 1; Length 63; 66.7%; Pred. No. 3.9;
                                                                                                                                                                                                                                             Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FRASEGO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513:
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SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610-270-5090
                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7'
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                             internal
                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                              |||:|:||:
| NVLVALNIL 11
                                                                                                                                                                                                                                                                                                        1 NVLMAMNII 9
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
TOPOLOGY: linear
                                                                               ANTI-SENSE: NO FRAGMENT TYPE: US-08-194-338-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-936-165A-513
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APPLICANT: Succliffe, J Gregor
APPLICANT: Strander, Mark G
APPLICANT: Erlander, Mark G
APPLICANT: Lovenberg, Timothy W
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA ENCODING
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 4; Length 92;
Pred. No. 1e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5968817th Torrey Pines Road, TPC 8 CITY: LA Jolla STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
AURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,538
FILING DATE: 19930315
                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ARIAIGLO, PRAMEA Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
TELEFRANCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...92
SEQUENCE DESCRIPTION: SEQ ID NO: 4069:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                  OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 68, Application US/08031538
Patent No. 5968817
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 NILFKWNI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NVLMAMNI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECTUM FOR DIAGNOSTICS AND THERAPEUTICS
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 63;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature;
; LOCATION: (B) LÖCATION 1...60;
; SEQUENCE DESCRIPTION: SEQ ID NO: 3973:US-09-107-532A-3973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                    ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3973:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 60 amino acids
                                                                                              NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                            STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.48;
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Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Waltham
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19 NILYSLNIL 27
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US-09-107-532A-4069
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EARLIER APPLICATION NUMBER: 60/048,912
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,997
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,998
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,882
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,899
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,893
                                                              REPLING DATE: 1997-06-06
RR APPLICATION NUMBER: 60/048, 896
RR FILING DATE: 1997-06-06
RR APPLICATION NUMBER: 60/048, 895
RR APPLICATION NUMBER: 60/048, 895
RR APPLICATION NUMBER: 60/048, 895
RR FILING DATE: 1997-06-06
RR APPLICATION NUMBER: 60/048, 894
RR FILING DATE: 1997-06-06
RR APPLICATION NUMBER: 60/048, 894
RR FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/094,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,972
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,900
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,892
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/048,894
FILING DATE: 1997-06-06
                   ILING DATE: 1997-00-00
PPLICATION NUMBER: 60/048,880
TITMS DATE: 1997-06-06
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Sequence 3106, Application US/09134001C
Batent No. 6380370
BARRAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn UNBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3106
LENGTH: 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                       59.5%; Score 25; DB 2; Length 31; 44.4%; Pred. No. 76; 1; Pred. 4; Mismatches 1; Indels
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Sequence 1030, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
TITLE OF INVENTION: 207 Human Secreted Proteins
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205, 258
CURRENT FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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                TSR5099P
             REFERENCE/DOCKET NUMBER: TSRE;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 44.4.
                                                                                                                                                                                                                                      MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                  NAME/KEY: Region
LOCATION: (78)
OTHER INFORMATION:
OTHER INFORMATION:
US-08-031-538-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || :||:::
21 NVFIAMDVM 29
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US-09-134-001C-3106
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US-09-205-258-1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT PEPLICATION NUMBER: US/09/205,258
CURRENT PEPLICATION NUMBER: US/09/205,258
CURRENT PELLING DATE: 1998-10-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER APPLICATION NUMBER: 60/048,375
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1032, Application US/09205258 Patent No. 6525174
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1030
LENGTH: 66
                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PZ007P1
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Sequence 4976, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BUIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BUIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UNDER: US/09/134,001C
CURRENT PELLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-14

PRIOR FILING DATE: 1997-14

PRIOR FILING DATE: 1997-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4976

LENGTH: 93

LENGTH: 93
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44.4%; Pred. No. 2.3e+02;
tive 3; Mismatches 2; Indels
                                               EARLIER APPLICATION NUMBER: 60/049,373
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER PILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1998-07-15
EARLIER PILLING DATE: 1998-07-15
EARLIER FILLING DATE: 1998-07-130
NUMBER OF SEQ ID NOS: 1227
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4976
APPLICATION NUMBER: 60/
FILING DATE: 1997-06-06
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US-09-205-258-1032
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Best Local Similarity
Matches 4; Conserv
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Pagenence No. 5594108

GENERAL INFORMATION:
APPLICANT: Van Tol, Hubert H.M.
APPLICANT: Civelli, Olivier
TITLE OF INVENTION: A No. 5594108el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/07928611

Patent No. 5569601

GENERAL INFORMATION:
APPLICANT: An Tol, Hubert H.M.
APPLICANT: Civelli, Olivier
TITLE OF INVENTION: A No. 5569601el Human Dopamine Receptor and Uses
TITLE OF INVENTION: A No. 5569601el Luman Dopamine Receptor and Uses
CORRESPONDENCES: 22
CORRESPONDENCES 12

STREET: Ald South Wacker Drive, Suite 3000
                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                     Score 24; DB 1; Length 37;
Pred. No. 1.5e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE Patentin Release #1.0, Version #1.25
SOFTWARE Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,611
FILING DATE: 19920810
FILING DATE: 19920810
FLING DATE: 19920810
FLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5569601nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-B
TELEPENCH/DION INFORMATION:
TELEPENCH/SORVETION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amir.
                                                                                                               Query Match 57.1%;
Best Local Similarity 44.4%;
Matches 4; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 37 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 44.4
Matches 4; Conservative
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                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-626-618A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 DALMAMDVM 22
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14 DALMAMDVM 22
                                                                                                                                                                                                               1 NVLMAMNII 9
amino acid
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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US-08-333-977-6
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Patent No. 6562958

GENERAL INPORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPRENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8011
LENTH: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-626-618A-6

y Sequence 6, Application US/07626618A

y Sequence 6, Application US/07626618A

y Batent No. 542265

generate in Sequence 6, Application US/07626618A

generate in Sequence 7

APPLICANT: Civelli, Olivier 1

APPLICANT: Civelli, Olivier 2

APPLICANT: Civelli, Olivier 3

TITLE OF INVENTION: A No. 5422265el Human Dopamine Receptor and Uses

TITLE OF INVENTION: A No. 5422265el Human Dopamine Receptor and Uses

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS: Allegretti & Witcoff, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STRIE: 11linois

COUNTRY: USA.
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Pred. No. 2.7e+02;
3; Mismatches 1; Indels
                                      Length 93;
                                    59.5%; Score 25; DB 4; Length 93;
55.6%; Pred. No. 2.6e+02;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER TO USA.

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER. Floppy disk.
SOFTWARE: PACFOLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/626,618A
FILING DATE: 7 DEC 1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. $422655nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
ELENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 50.0
Matches 4; Conservative
                                              Query Match 59.5
Best Local Similarity 55.6
Matches 5; Conservative
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27 NVLLVIGII 35
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9 IVMAANVI 16
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Gaps

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GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: A No. 6203998el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                Score 24; DB 2; Length 37;
Pred. No. 1.5e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%; Score 24; DB 3; Length 37; 44.4%; Pred. No. 1.5e+02; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elab PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,694
FILING DATE: 15-APR-1998
CLASSIFICATION: 530
ATTORNEY/AGENTIND: 530
ATTORNEY/AGENTIND: AND REVINE RESULT ON NUMBER: 3500
REGISTRATION NUMBER: 3500
REGISTRATION NUMBER: 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90,1092-MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: McDonnell Boennen nu
STREET: 300 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-060-694-6; Sequence 6, Application US/09060694; Patent No. 6203998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                       57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.1%;
Best Local Similarity 44.4%;
Matches 4; Conservative
                           TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 37 amino acids
                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear;
MOLECULE TYPE: protein
US-09-060-694-6
                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                        14 DALMAMDVM 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 DALMAMDVM 22
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                                                                                                                                                        amino acid
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                                                                                                                                                                                                                             US-08-487-811A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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US-09-378-074-6
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Parent No. 5883226
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: 2 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 37;
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,977
FILING DATE: 03-NOV-1994
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/626,618
FILING DATE: 7 DEC 1990
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5594108nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092
TELECOMMUNICATION INFORMATION:
TELECHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: BR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,811A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5883226nau, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .5e+02;
                       E: Allegretti & Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.1%; Score 24; Best Local Similarity 44.4%; Pred. No. 1 Matches 4; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 312-715-1234
TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-333-977-6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 DALMAMDVM 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                           STREET: 10 South
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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US-08-487-811A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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Score 24; DB 5; I
Pred. No. 1.5e+02;
                                                          4; Mismatches
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               Ouery Match
Best Local Similarity 44.4%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Ver. 2.1
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Best Local Similarity 62.5
Matches 5; Conservative
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14 DALMAMDVM 22
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7 NVLIAPNM 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NVLMAMNI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
SEQ ID NO 18
LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Murine sp.
US-09-215-221-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 36
US-09-252-991A-30061
                                                                                                                                                                                                                                 US-09-215-221-18
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Sequence 6, Application US/09378074
Patent No. 643711A.
GENERAL INFORMATION:
APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: A No. 6437114el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
TITLE OF INVENTION: A Novel Human Dopamine Receptor and Uses NUMBER OF SEQUENCES: 22
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                  COMPUTER KEAUMALE FURNT

WEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CONTWARE: Patentin Release #1.0, Version #1.25

SOTTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/378,074

FILING DATE: 20-Aug-1999

FILING DATE: CONTOWNDATA:

APPLICATION NUMBER: 07/928,611

FILING DATE: CUNKNOWNDATA:

NAME: NO. 6437114 Man. Kevin E

REFERENCE/DOCKET NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 90,1092-B

TELECOMMUNICATION INPRAMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.1%; Score 24; DB 4; Length 37; 44.4%; Pred. No. 1.5e+02; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SUFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
INCREMIT APPLICATION NUMBER: PCT/US93/07370
INFORMATION FOR SEQ ID NO: 6:
SEGURENCE CHARACTERISTICS:
LENGTH: 37 aming acids
                                                                                                                                                                           ADDRESSE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear MOLECULE TYPE: protein ;
SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-378-074-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US93-07370-6; Sequence 6, Application PC/TUS9307370; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                          ZIP: 60606
COMPUTER READABLE FORM:
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Best Local Similarity 44.4
Matches 4; Conservative
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14 DALMAMDVM 22
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GY: linear
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Sequence 30061, Application US/09252991A
; Sequence 30061, Application US/09252991A
; Patent No. 6551795
; GRNERAL INFORMATION:
    TITLE OF INVENTION:
    TORRENT PELING DATE: 1999-02-18
    CURRENT FILING DATE: 1999-02-18
    PRIOR APPLICATION NUMBER: US 60/074,788
    PRIOR APPLICATION NUMBER: US 60/094,190
    PRIOR PELING DATE: 1998-07-27
    PRIOR FILING DATE: 1998-07-27
    SEQ ID NO 30061

LENGTH: 69

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                                                                                                                                                                                                                                                   Sequence 18, Application US/09215221

Sequence 18, Application US/09215221

Sequence 18, Earles Application US/09215221

GENERAL INFORMATION:
APPLICANT: BILERS, MARTIN
APPLICANT: BURGIN, ANDERA
APPLICANT: BURGIN, HANS-HARALD
APPLICANT: SEDLACEK, HANS-HARALD
TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF FILE REPRENCE: 026083/0192
CURRENT APPLICATION NUMBER: 18/09/215,21
CURRENT APPLICATION NUMBER: 197 56 975.7
PRIOR PILING DATE: 1999-12-18
PRIOR PILING DATE: 1997-12-20
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                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
Length 37;
                                               1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.1%; Score 24; DB 3; I
62.5%; Pred. No. 1.6e+02;
iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.1%; Score 24; DB 4; Best Local Similarity 62.5%; Pred. No. 38+02; Matches 5; Conservative 2; Mismatches
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APPLICANT: Goldberg, Robert B.
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: Fischer, Robert L.
APPLICANT: The Regents of the University of California
TILLE BEFERENCE: 023070-077620
CURRENT APPLICATION NUMBER: US/09/193,931C
CURRENT FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 09/103,478
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
PRIOR RILING DATE: 1998-02-19
PRIOR FILING DATE: 1998-02-19
SROR FILING DATE: 1998-02-19
SROR FILING DATE: 1998-02-19
SRORTWARE: PATCH NUMBER: US 08/804,534
FRIOR FILING DATE: 1998-02-19
SOFTWARE: PATCH NOS: 29
SOFTWARE: PATCH NOS: 29
SOFTWARE: PATCH NOS: 29
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 85;
                                                                                                                                                                        CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,478
FILING DATE: 24-JUM-1998
CLASSIFICATION 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-077611US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 3.864; Mismatches
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                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%;
44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Masa-aki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||:|:| :
60 DVLLALNTL 68
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                      Calofornia
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Best Local Similarity
Matches 4; Conserv
                                                                   94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: DOMAIN
                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-193-931C-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-103-478-27
                                               COUNTRY:
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                   Sequence 4499, Application US/09134001C

Sequence 4499, Application US/09134001C

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WUGLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WUMBER: US/09/134,001C
CURRENT PELING DATE: 1998-08-13
FRIOR PELLING DATE: 1999-11-08
FRIOR FILING DATE: 1997-11-08
FRIOR FILING DATE: 1997-11-08
FRIOR FILING DATE: 1997-0-08-14
SEQ ID NO 4499
LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-328-352-5816

Sequence 5816, Application US/09328352

Sequence 5816, Application US/09328352

Sequence 5816, Application US/09328352

Sequence 5816, Application US/09328352

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 5816
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APPLICANT: Ohto, Masa-aki
APPLICANT: Ohto, Masa-aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: Fischer, Robert L.
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%; Score 24; DB 4; Length 77; 50.0%; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 24; DB 4; I Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/09103478
Patent No. 6235975
GENERAL INFORMATION:
APPLICANT: Harada, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT CORGANISM: Acinetobacter baumannii US-09-328-352-5816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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1 NLVLKMNI 8
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Best Local Similarity
Matches 4; Conserv
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US-09-103-478-27
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RESULT 43
US-08-738-127-4
i Sequence 4, Application US/08738127
j Patent No. 5919655
j GENERAL INFORMATION:
APPLICANT: Bandman, Olga
i APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
CITY: Palo Alto
SIPP: CA
APPLICANT: GO11, Surya K.

TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSE: 16
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
CITY: Palo Alto
COUNTRY: U.S.
COUNTRY: U.S.
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

57.1%; Score 24; DB 1; Length 87;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
SURRENT APPLICATION NUMBER: US/08/725,531
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
PILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIOMATICATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415-855-055
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 amino acids
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STRANDEDNESS: sir
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CLONE: 1085026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; CLONE: 1
US-08-725-531-4
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                                  LOCATION: (1)...(85)

OTHER INFORMATION: S. pombe HAP3 subunit of CCAAT box-binding factor;
OTHER INFORMATION: (CBF) protein B domain homolog
US-09-193-931C-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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-APPLICANT: Morrison, Briggs W.

APPLICANT: Leder, Philip
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2223
COMPUTER: U.S.A.
ZIP: 02110-2223
COMPUTER: IBM PS/2 Model 50Z or 55SX
OMPUTER: MS-DOS (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 11, 1994
APPLICATION NUMBER:
FILING DATE: AUGUST 11, 1994
APPLICATION NUMBER: 39,109
REGISTRATION NUMBER: 39,109
REGISTRATION NUMBER: 39,109
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 39,109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.1%; Score 24; DB 1; Length 87; Best Local Similarity 75.0%; Pred. No. 3.9e+02; Antches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                   Length 85;
                                                                                                                                                                                                      1, Indels
                                                                                                                                                   Query Match
57.1%; Score 24; DB 4; I
Best Local Similarity 44.4%; Pred. No. 3.8e+02;
Matches 4; Conservative 4; Mismatches 1
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US-08-725-531-4
; Sequence 4, Application US/08725531
; Patent No. 5756310
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08289247B Patent No. 5728579 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-289-247B-4
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60 DVLLALNTL 68
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Length 87;

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Sequence v. Application US/09083661

Patent No. 5955283

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STREET: U.S.

ZIP: 93304
                                                                       Score 24; DB 2; Length 87;
Pred. No. 3.9e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,661
                                                                         57.1%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 75.0
Est Local Similarity 75.0
                                                                         Query Match 57.1
Best Local Similarity 75.0
Matches 6; Conservative
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CLONE: 1085026
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US-09-213-392-4
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LIBRARY:
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US-09-083-661-4
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Fatent No. 5945505
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%; Score 24; DB 2; Length 87; 75.0%; Pred. No. 3.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
       APPLICATION NUMBER:
FILING DATE:
ATCONEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0141 US
TELEPANICATION INFORMATION:
TELEPANICATION 18F-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/083,661
APPLICATION NUMBER: 09/083,661
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0128 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARPELICATION DATA:
APPLICATION NUMBER: US/09/213,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 87 aming acids
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECTLE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1085026
US-08-738-127-4
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PRIOR APPLICATION DATA:
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US-09-213-392-4
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Pred. No. 3.9e+02;
0; Mismatches 2;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,531
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0128 US
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
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Job time : 6.50495 secs
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Oggca4 samia cynth Q8x2f escherichia Q8x2f escherichia Q8w9t7 leptasteria Q8x30 salmonella Q96de8 homo sapien Q81wu8 macroscelid

Q8cqi6 staphylococ

Q89945 brucella me Q86189 brucella su Q86189 brucella su Q8mil9 cicindela v Q9mij9 cicindela su Q9mij6 cicindela su Q9mij6 cicindela bu Q9mij8 cicindela bu Q9mij8 cicindela bu Q9mij8 cicindela bu Q9mij8 cicindela bu Q9mik0 cicindela bu Q9mik0 cicindela bu Q9mik0 cicindela bu Q9mij8 musculu Q9kmij bacillus ha Q9kmij aprococcus Q9vz5 staphylococ Q8uzi3 pyrococcus Q9vz5 staphylococ Q8uzi3 pyrococcus Q9vz8 streptococc Q8min9 daktulospha Q8hmið daktulospha Q8hmið daktulospha

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MEDLINE-19.

MEDLINE-2297686; PubMed-12368813;

MEDLINE-2297686; PubMed-12368813;

Medalberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,

Read T.D., Eisen J.A., Sebhadri R., Ward N., Methe B., Clayton R.A.,

Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,

DeBoy R.T., Dodson R.J., Umayam L.A., White O., Wolf A.M.,

Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,

Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,

Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;

"Genome sequence of the dissimilatory metal ion-reducing bacterium

Shewanella
                                                                                                                                                                                                                                                                                                                                                                                                               Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.4%; Score 30; DB 16; Length 83; 77.8%; Pred. No. 80; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome.
SEQUENCE 83 AA; 9075 MW; AC5D08F38ACB345C CRC64;
                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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                                   Q8X3F6
Q8Z697
Q8W9T7
Q8ZP30
Q96DE8
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Q9MIJ9
Q9MIJ5
Q9MIJ6
Q9MIJ4
Q9MIX0
Q8M1J4
Q26413
Q9K8Y3
Q9K8Y3
Q9VX5
Q9UZJ3
Q9TZ3
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Q8G1S9
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Query Match
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Q8v857 proteus mir
O21757 pygathrix b
O21705 pygathrix b
O21712 pygathrix r
Q8cg6 steaphylococ
Q8cg6 steaphylococ
Q8x8c1 escherichia
Q8fbe9 escherichia
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QBnwtO staphylococ
QBnwsO staphylococ
QBogsE staphylococ
QBcp32 staphylococ
QBu94 staphylococ
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                                                               February 17, 2004, 10:50:12; Search time 12.7426 Seconds (without alignments) 182.261 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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Q8X8C1 Q8FBE9

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RESULT 2
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SEQUENCE FROM N.A.
SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINES=2131952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Naba T., Takeuchi F., Kuroda M., Yuzawa H., Kuroda H., Cui L., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamuto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB 16; Length 70;
Pred. No. 1.1e+02;
1; Mismatches 0; Indels
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TRUNCATED(TNP) OR TRUNCATED-TNP OR SAV1195 OR SA1038.
Staphylococcus aureus (strain MuSO / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria, Firmicutes, Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 70 AA; 8186 MW; 87AD7A20448962DE CRC64;
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SEQUENCE 64 AA; 7522 MW; 1FD45452DB1E5A22 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                         Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus
NCBI_TaxID=196620;
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PRT;
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EMBL; AP004826; BAB95160.1; -.
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85.7%;
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                                                     01-OCT-2002 (TrEMBLrel, 22, 01-OCT-2002 (TrEMBLrel, 22, 01-OCT-2002 (TrEMBLrel, 22, Truncated transposase. TRUNCATED TNP OR MM1295.
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Best Local Similarity 85...
6; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acquired MRSA.";
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MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Takeuchi N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoco K., Hiramatau K.,
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iakeuchi F., Kuroda M., Yuzawa H., Kuroda H., Cui L., Yagai Y., Iwama N., Asamo K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatau K., 'Genome and virulence determinants of high virulence community-
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Pred. No. 99;
1; Mismatches 0; Indels
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Complete protecome.
SEQUENCE 64 AA; 7522 MW; 00DD9F52CELC4580 CRC64;
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SEQUENCE 61 AA; 7173 MW; C2DB0FAD5256D876 CRC64;
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Last annotation update)
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Last annotation update)
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Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus (strain MM2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
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EMBL; AP004825; BAB94943.1; -.
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85.7%;
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01-OCT-2002 (TrEMBLrel. 22,
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Lancet 359:1819-1827(2002).
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TRUNCATED TNP OR MW1078.
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TRUNCATED TNP OR MW1278.
                                                                                                                                                           PRELIMINARY;
                    28 NPLMAMGII 36
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STRAIN=ATCC 29906;
Weigel L.M., Anderson G.J., Tenover F.C.;
"gyrA and parC Mutations Associated with Fluoroquinolone Resistance in
                                                                                                                                                                                                                                                                                                                                                                  STRAIN=N;
MEDLINE=9929341; PubMed=10368952;
Campbell N.J.H., Barker S.C.;
"The novel micochondrial gene arrangement of the cattle tick,
"The novel micochondrial gene arrangement of a coding region.";
Boophilus microplus: fivefold tandem repetition of a coding region.";
Mol. Biol. Evol. 16:732-740(1999).
EMBL; AFIIOGA: AAD28382.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Proteus.
                                                                                                                                                                                                                                Mitochondrion.
Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari,
Parasitiformes, Ixodida, Ixodidae, Boophilus.
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Pred. No. 2.5e+02;
2; Mismatches 1; Indels
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF397169; AAL57340.1; -.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                            Boophilus microplus (Cattle tick).
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illarity 62.5%;
Conservative
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
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                                             PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6941;
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Matches
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Q9XNQ4
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MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N. K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus.";
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Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
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Pred. No. 1.4e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE016748; AA004818.1; -. Complete proteome. SEQUENCE 89 AA; 10671 MW; 32E07301FE24162D CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Truncated transposase.
TRUNCATED-SA OR SAV1390 OR SA1222.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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SEQUENCE 98 AA; 11619 MW; 4853E89EE4C8EF17 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                  Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 AA
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Pfam; PF01609; Transposase_11; 1.
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                                                              (TrEMBLrel. 23, C (TrEMBLrel. 23, L (TrEMBLrel. 23, L
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85.7%;
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es 6; Conservative
                     PRELIMINARY;
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                                                                                                                                       Truncated transposase.
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Best Local Similarity
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01-MAR-2003
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44 NTLMALNM 51
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                                         1 NVLMAMNI 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarthini, Cercopithecidae, Colobinae,
                                                                                                                                                                    Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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STRAIN=DJ7 AND DJ1 AND DJ4, and DJ5;
STRAIN=DJ7 AND DJ1 AND DJ3,
Wang W, Forstner W.R.J., Zhang Y., Lui Z., Wei Y., Huang H., Hu H.,
Wang W, Mu D., Melnick DJ.;
Int. J. Primatol. 0:0-0(1997).
EMBL; U92956; AAD08834.1; --
EMBL; U92957; AAD08825.1; --
EMBL; U92958; AAD08825.1; --
EMBL; U92958; AAD08825.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 AA; 10902 MW; 78796F27726E9AE0 CRC64;
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                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADH dehydrogenase subunit 4L.
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                                  98 AA
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EMBL, U92956; AAD08822.1; -
InterPro, IPR001133; Oxidored 4L.
InterPro; IPR003314; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
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ProDom; PD000359; Oxidred4L; 1.
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ProDom; PD000359; Oxidred4L; 1.
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Best Local Similarity 62.5
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                                      PRELIMINARY;
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44 NTLMALNM 51
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NCBI_TaxID=61621;
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021705
RESULT 10
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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STRAIN=CJ3, and CJ1;

Wang W., Forstner M.R.J., Zhang Y., Lui Z., Wei Y., Huang H., Hu H.,

Xie Y., Wu D., Melnick D.J.;

Int. J. Frimatol. 0.0-0 (1997).

EMBL; U92563; AAD04666.1; -.

EMBL; U92961; AAD04660.1; -.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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  Length 98;
                                                     1; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADH dehydrogenase subunit 4L.
                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Query Match
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1;
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EMBL, U92962; AAD04663.1; -
InterPro; IPR00113; Oxidaced 4L.

InterPro; IPR00314; Oxidaced-E.

Pfam; PF00420; Oxidaced-G.

ProDom; PD000359; Oxidaced-L.
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Matches 5; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE 1
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Q8FBE9
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SEQUENCE FROM N.A.

RX MEDLINE=21074935; PubMed=11206551;

RX MEDLINE=21074935; PubMed=11206551;

RA Perra N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

RA Rose D.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Rapodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

A Welch R.A., Blattner F.R.;

I "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

Naure 409:529-533(2001).
                                                                                                                                                                                                                                                                                                           Gaps
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STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.,
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016747; AAO04602.1; -.
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Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                  Query Match 66.7%; Score 28; DB 8; Length 98; Best Local Similarity 62.5%; Pred. No. 2.5e+02; Matches 5; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                      98 AA; 10923 MW; 71683E3FF63B8572 CRC64;
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SEQUENCE 47 AA; 5498 MW; 170FAA03C09426DD CRC64;
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Last annotation update)
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Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
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InterPro; IPR001133; Oxidored 4L. InterPro; IPR002314; Oxidored4L. Pfam; PP00420; Oxidored 42; 1. ProDom; PD000359; Oxidred4L; 1.
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01-MAR-2002 (TrEMBLrel. 20, Li
01-MAR-2003 (TrEMBLrel. 23, Li
01f, hypothetical protein.
YIE OR 25431 OR ECS4815.
Bscherichia coli 0157:H7.
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85.7%;
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les 6; Conservative
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                                                                                                                                    Mitochondrion.
                                                                                                                                                                      SEQUENCE
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OGCPD5
OCCPD
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DF Trunc
GN SEB100
OX NGEI
OX NGEI
RR SEQUE
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09X8C1
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AC 08X8C
DT 01-MA
DT 0
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STRAIN=0157.HT / RIMD 0509952;
MBDLINE=21156231; PubMed=11258795;
MBDLINE=21156231; PubMed=11258795;
MBDLINE=21156231; PubMed=11258795;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiha T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterchemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
EMBL, ARGO9650; AAG59082.1; -.
EMBL, AR002567; BAB38238.1; -.
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"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
EMBL, AE016770; AANS591.1.
BHYPOthetical protein; Complete protecome.
SEQUENCE 81 AA, 9452 MW, 378572149DF160BB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=217992;
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Pred. No. 3.4e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 16; Length 81; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Voltage-gated potassium channel subunit MiRP2.
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Last annotation update)
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STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
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                                                                                                                                                                                                                                                                                                      InterPro; IPR002145; HTH_CopG.
Pfam; PF01402; HTH_4; 1.
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Best Local Similarity 62.5%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
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SEQUENCE 81 AA;
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Gaps

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Saturniidae; Saturniinae; Attacini; Samia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LECURENCE FROM N.A.

Wei Z., Zhao Q., Zhang Z., Wang Z., He J.;

Wei Z., Zhao Q., Zhang Z., Wang Z., He J.;

But Silkworm Mitcochondrial Cytochrome Oxidase Subunit III, tRNA-Gly
and Partial NADH Dehydrogenase Subunit 3 genes.";

Submitted (UUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF288145; AAG01169.1; -.

Interpro; IPR000440; Oxidored_q4.

Mitcchondrion.
                                                       STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016144; AA003660.1; -.
Complete protecome.
SEQUENCE 40 AA; 4792 MW; FEE13BA49163D7F9 CRC64;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                          Score 26; DB 16; Length 40;
Pred. No. 3e+02;
2; Mismatches 0; Indels
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Pred. No. 3.6e+02;
3; Mismatches 1; Indels
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SEQUENCE 50 AA; 5711 MW; BB7A3D4768A49F2D CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    50 AA.
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55.6%;
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71.4%;
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Guery Match
Best Local Similarity 71...,
Best Local Similarity 71...,
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15 NLLMILSII 23
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Best Local Similarity
Matches 5; Conservat
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1 MLMALNI 7
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                 NCBI_TaxID=1282;
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Q9GCA4;
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SEQUENCE FROM N.A.

SEQUENCE TRON N.A.

SEQUENCE 35092 / DSM 1617 / P2;

STRAIN=ATCC 35092 / DSM 1617 / P2;

MEDITR=2132295; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

Amors A., Erlecher C., Gordon P.M.K., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Thi-Ngoc H.P., Regan M.A., Sensen C.W., Van der Oost J.;

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

Agrich Garple genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

REMBL, ALGOG744; AAK41533.1;

SM Hypothetical protein; Complete proteome.
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                                                                                                                                         "Endogenous Xenopus oocyte MiRPs govern mammalian K+ channel function and phenotypic variability."; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AFS45501; AAN77245.1; -. Ionic channel. SEQUENCE 99 AA; 11332 MW; 53A06B045F73FAE3 CRC64:
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                                                                                                                    Anantharam A., Lewis A., Panaghie G., McCrossan Z.A., Lerner D.J., Abbott G.W.;
           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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44.4%; Pred. No. 4.1e+02;
.ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                64.3%; Score 27; DB 13; Length 99; illarity 71.4%; Pred. No. 4.1e+02; Conservative 2; Mismatches 0; Indel9
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Last annotation update)
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein SSO1296.
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Best Local Similarity 44...
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75 NIIISMNAI 83
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                                                       Xenopodinae; Xenopus.
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Best Local Similarity
Est Conserve
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16 NVLLAIN 22
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                                                                                                              SEQUENCE FROM N.A.
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                                                                      NCBI_TaxID=8355;
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Q8CQ16;
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McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney B., Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Scomplete genome sequence of Salmonella enterica serovar Typhimurium
                               Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Leptasterias.
NCBI_TaxID=59564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
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                                                                                                                                                                                   Hrincevich A.W., Rocha-Olivares A., Foltz D.W., "Phylogenetic analysis of molecular lineages in a species-rich subgenus of sea stars (Leptasterias subgenus Hexasterias)."; Am. Zoologist 40:365-374(2000).
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Pred. No. 6.2e+02;
Transparents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.9%; Score 26; DB 8; Length 84;
44.4%; Pred. No. 5.7e+02;
tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                Hrincevich A.W., Rocha-Olivares A., Foltz D.W.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162110; AAL61885.1; -.
InterProy, IPR001133; Oxidored 4L.
Pfam; PF00420; oxidored q2; 1.
Mitochondrion.
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EMBL, AR008779; AAL20697.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 92 AA; 10469 MW; 270E355575AFF3F4 CRC64;
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84 AA; 9151 MW; AADAFD859FE82405 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative inner membrane protein.
YCHH OR STM1782.
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STRAIN-LT2 / SGSC1412 / ATCC 700720;
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01-DEC-2001 (TrEMBLrel. 19, Created)
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Best Local Similarity 44.4%;
Matches 4; Conservative
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NILLSNNLI 62
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                  Mitochondrion.
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Matches
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STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
EMBL: AP0020525; BAB36907:1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 3.8e+02;
3; Mismatches 1; Indels
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EMBL, AL62721; CAD02137.1; -
HYPOChetical protein; Complete proteome.

SEQUENCE 73 AA; 7846 MW; 74C42318C53CCA58 CRC64;
                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 53 AA; 6018 MW; 653FBE5407E4B98F CRC64;
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Last annotation update)
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NCBI_TaxID=601;
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50.0%;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
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43 NIVAAMNL 50
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RESULT 22
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002697
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DT 01-MA
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RESULT 23 08W9T7 1D Q8W9T DT 01-MA, DT 01-MA, DT 01-MA, DT 01-OC DE NADH, GN LEPLA.

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-16M / ARCC 23456 / Biotype 1;
STRAIN-16M / ARCC 23456 / Biotype 1;
STRAIN-16M / ARCC 23456 / Biotype 1;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
DelVecchio V.G., Kapatral V., Redkar R.J., Vykidis A., Reznik G.,
Ivanova N., Anderson I., Blattacharyas A., Lykidis A., Reznik G.,
Jablonnski L., Larsen N., Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov B., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
Haselkorn R., Kyrpides N., Overbeek R.;
Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
Brock Ar009568; Alls 2498-11;
Hypotherical protein; Complete proteome.
SRQUENCE 98 AA; 10766 MW; 999E92EBIDEAC40D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29461;
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                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBL_TaxID=29459;
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Pred. No. 6.6e+02;
3; Mismatches 1; Indels
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01-NAR-2003 (TrEMBLrel. 23, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
 01-WAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein BMEI1317.
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55.6%;
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Matches 5; Conservative
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25 NRLVAINIV 33
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BR0625.
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25 NRLVAINIV 33
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                                                                                                     Brucella melitensis.
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Matches 5; Conserved
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Q8G1S9;
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MEDLINE=22056029; PubMed=12034869;
Arnason U., Adegove U.A., Bodin K., Born E.W., Esa Y.B., Gullberg A.,
Annason W., Short R.V., Xv Xv, Janke A.;
"Mammalian mitogenomic relationships and the root of the eutherian
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Macroscelidea; Macroscelididae; Macroscelides
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 6.6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                      61.9%; Score 26; DB 4; Length 95; 55.6%; Pred. No. 6.4e+02; Live 2; Mismatches 2; Indels
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                   Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC009524; AAH09524.1; -. InterPro; IRR003639; Mov34_1. ProDom; PD363422; Mov34_1; 1.
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                                                                                                                                                                                                                                                                                     95 AA; 11009 MW; D70270AD00529A18 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
NADH dehydrogenase subunit 4L.
     01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Similar to 26S proteasome;associated padl homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:8151-8156(2002).
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InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
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ProDom; PD000359; Oxidred4L; 1
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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Matches 5; Conservative
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DVLMTSNIV 82
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SEOUENCE FROM N.A.
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Q8YG45

RESULT 27 Q8YG45 ID Q8YG4

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DT 01-0C
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DT 01-MADH
GN MADH
GN MADH
GN MADH
GN MADH
OC BURAT
OC BU

Q9XNR1;

Q9XNR1

RESULT 29

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Barraclough T.G., Hogan J.E., Vogler A.P.;
"Testing whether ecological factors promote cladogenesis in a group of tiger beetles (Coleoptera: Cicindelidae).";
Proc. R. Soc. Lond., B. Biol. Sci. 0:0-0(2000).
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"Testing whether ecological factors promote cladogenesis in a group of tiger beetles (Coleoptera: Cicindelidae).";
Proc. R. Soc. Lond., B. Biol. Sci. 0:0-0(2000).
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Neoptera, Endopterygota, Coleoptera, Adephaga, Cicindelidae,
Cicindela.
                                                                                                                   Mitochondrion.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Adephaga; Cicindelidae;
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Pred. No. 2.7e+02;
4: Mismatches · 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 8; Length 21;
Pred. No. 2.7e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 21 AA; 2247 MW; EB3165AA3EAFAD45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TH-2001 (TrEMBLrel. 17, Last annotation update)
NADH dehydrogenase subunit III (Fragment).
Cicindela sperata.
Mitochondrion.
                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
NADH dehydrogenase subunit III (Fragment).
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21 AA.
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PRT;
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50.0%;
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PRELIMINARY;
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                                                                                                      Cicindela cuprascens.
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5 IIMALSII 12
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5 IIMALSII 12
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                                                                                                                                                                                           NCBI_TaxID=93357;
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                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
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Q9MIJ2;
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Barraclough T.G., Hogan J.E., Vogler A.P.;
"Testing whether ecological factors promote cladogenesis in a group of tiger beetles (Coleoptera: Cicindelidae).",
Proc. R. Soc. Lond., B, Biol. Sci. 0.0-0(2000).
                                                                                                                                                                                                                                                                                          MEDINE=99297341; PubMed=10368952; Campbell N.J.H., Barker S.C.; Campbell N.J.H., Barker S.C.; "The novel mitochondrial gene arrangement of the cattle tick, Boophilus microplus: fivefold tandem repetition of a coding region."; Mol. Biol. Bvol. 16:732-740 (1999).
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                                                                                                                                                                       Mitochondrion.

Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari,
Parasitiformes, Ixodida, Ixodidae, Boophilus.

NCBI_TaxID=6941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Coleoptera, Adephaga, Cicindelidae,
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Pred. No. 2.7e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.9%; Score 26; DB 8; Length 99; 50.0%; Pred. No. 6.6e+02;
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99 AA; 11987 MW; 7AEADEFSFB76C500 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
NADH dehydrogenase subunit III (Fragment).
                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) NADH dehydrogenase subunit 4 (Fragment).
                                                 99 AA.
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                                                                                    Created
                                                                                                                                                        Boophilus microplus (Cattle tick)
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Matches 4; Conservative
                                                 PRELIMINARY;
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IIMALSII 12
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Gaps

Mitochondrion.

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Query Match

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Gaps

Mitochondrion.

SEQUENCE

Query Match

RESULT 31

Mitochondrion

Q9MIJ8

Cicindela.

RESULT 30
09MIJ38
1D Q9MIJ3
AC Q9MIJ3
DT 01-0C
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Neoptera; Endopterygota; Coleoptera; Adephaga; Cicindelidae;
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Best Local Similarity 50.0
Matches 4; Conservative
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5 IIMALSII 12
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5 IIMALSII 12
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Mitochondrion.
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SEQUENCE FROM N.A.
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                                        Cicindela.
NCBI_TaxID=93360;
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SEQUENCE
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Q9MIK0
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Barraclough T.G., Hogan J.E., Vogler A.P.;

"Testing whether ecological factors promote cladogenesis in a group of tiger beetles (Coloptera: Cicindelidae).";

Proc. R. Soc. Lond., B, Biol. Sci. 0:0-0(2000).

EMBL; AF133032; AAF89133.1; -.
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Barraclough T.G., Hogan J.E., Vogler A.P.;

Barraclough T.G., Hogan J.E., Vogler A.P.;

"Testing whether ecological factors promote cladogenesis in a group tiger beetles (Coleoptera: Cicindelidae).";

Froc. R. Soc. Lond., B. Biol. Sci. 0:0-0(2000).

EMBL; AF133026; AAF89122.1;
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Neoptera, Endopterygota, Coleoptera, Adephaga, Cicindelidae,
                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Adephaga; Cicindelidae;
Cicindela.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%; Score 25; DB 8; Length 21; 50.0%; Pred. No. 2.76+02; tive 4; Mismatches 0; Indels
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Q9MIJ4;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
C1-CT-2000 (TrEMBLrel. 15, Last sequence)
C1-CT-2000 (TrEMBLrel. 15
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NON TER 21 21 SEQUENCE 21 AA; 2226 MW; EB2A641A3EAFAD45 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
NADH dehydrogenase subunit III (Fragment).
           01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
NADH dehydrogenase subunit III (Fragment).
Cicindela marutha.
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50.0%;
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Best Local Similarity 50...
A; Conservative
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5 IIMALSII 12
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5 IIMALSII 12
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=93356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cicindela blanda.
                                                                                                                                                                                                                          NCBI_TaxID=93364;
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                                                                                                             Mitochondrion
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SEQUENCE
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Q9MIJ6
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SEQUENCE FROM N.A.

Barraclough T.G., Hogan J.E., Vogler A.P.;

Barraclough T.G., Hogan J.E., Vogler A.P.;

"Testing whether ecological factors promote cladogenesis in a group of tiger beetles (Coleoptera: Cicindelidae).";

Figer beetles (Coleoptera: Cicindelidae).";

Proc. R. Soc. Lond., B. Biol. Sci. 0:0-0(2000).

EMBL; AF133027; AAF89124.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                         Gape
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Barraclough T.G., Hogan J.E., Vogler A.P.;

Barraclough T.G., Hogan J.E., Vogler A.P.;

"Testing whether ecological factors promote cladogenesis in a group riger beetles (Coleoptera: Cicindelidae).";

Proc. R. Soc. Lond., B. Biol. Sci. 0:0-0(2000).

EMBL; AF133024; AAF89118.1; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Neoptera; Endopterygota; Coleoptera; Adephaga; Cicindelidae;
Cicindela.
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Pred. No. 2.7e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                Score 25; DB 8; Length 21;
Pred. No. 2.7e+02;
4; Mismatches 0; Indels
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21 21
21 AA, 2243 MW; BB3165AA3F664D45 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
11-CCT-2002 (TrEMBLrel. 22, Last annotation update)
TNR OR TERMSCIN-R.
Mus musculus (Mouse)
                                                                                                                                                                                                                                      NON TER 21 21
SEQÜENCE 21 AA; 2261 MW; EB3165AA3EBD3D45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
NADH dehydrogenase subunit III (Fragment).
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MEDLINE=21311952; PubMed=11418146; MEDLINE=21311952; PubMed=11418146; MEDLINE=21311952; PubMed=11418146; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aokti K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kantori M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramateu K., Hiramateu K., Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
EMBL; AP001516; BAB06588.1; + Hypothetical protein; Complete proteome.
SEQUENCE 59 AA; 7032 MW; 47AFFCFDC9EEF843 CRC64;
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MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Cui L.,
Yamamoto K., Hiramateu K.;
"Genome and virulence determinants of high virulence community-
                   SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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1-JOCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SAV0618 (Hypothetical protein MW0582).
SAV0618 OR SA0575 OR MW0582.
                                                                                                                                                                                                                                                                                                                                                                                                                     Match 59.5%; Score 25; DB 16; Length 59; Local Similarity 37.5%; Pred. No. 6.9e+02; les 3; Conservative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.5%; Score 25; DB 16; Length 74; 55.6%; Pred. No. 8.4e+02; ive 2; Mismatches 2; Indels
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Hypothetical protein; Complete proteome.
SEQUENCE 74 AA; 8228 WW; 35AFAB2F9FF612AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus (strain Mus0 / ATCC 700699),
Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain MM2).
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NCBI_TaxID=158878, 158879, 196620;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lancet 359:1819-1827(2002).
EMBL; AP003359; BAB56780.1; -.
EMBL; AP003131; BAB41807.1; -.
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Matches 5; Conserv
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Matches
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AACOOS SON AACOO A
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                   MEDLINE=99274730; PubMed=10341229; Weber P., Bartsch U., Rasband M.N., Czaniera R., Lang Y., Bluethmann H., Margolis R.U., Levinson S.R., Shrager P., Montag D.; Mice deficient for tenascin-r display alterations of the extracellular matrix and decreased axonal conduction velocities in the CNS.";
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MEDLINE=95102611; PubMed=7804230;
Christopher L.J., Dykstra C.C.;
"Identification of a type II topoisomerase gene from Cryptosporidium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 3.1e+02;
4; Mismatches 1; Indels
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Pred. No. 5.4e+02;
1; Mismatches 3; Indels
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NCBI_TaxID=86665,
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Bukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
Cryptosporidiidae, Cryptosporidium.
NCBI_TaxID=5807;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Last annotation update)
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EMBL; S76665; AAB32916.2; -.
HSSP; P06786; 1BGW.
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                                                                                                                                                                                                    J. Neurosci. 19:4245-4262 (1999).
EMBL; AJ005844; CAA06739.1; -.
MGD; MGI:99516; Thr.
NON_TER 24
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BH2869.
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12 NMLIGVNLI 20
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RESULT 38
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AC 02641
DT 01-NO 01-NO 01
DT 01-NO 01-NO 01
COC CYPPE.
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Q9K8Y3;

RESULT 39
COKRAY3
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GN BH286
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Q9K8Y3

Matches

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63 VLMANNLL 70

38 NALVDLNII 46

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30 ILMIMSII 37
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Best Local Similarity
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SEQUENCE
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SEQUENCE
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                                    Q8HNB1
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Matches
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  RESULT 43
Q8HNB1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                         Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                         STRAIN=Vol. / DSM 3638 / ATCC 43587 / JCM 8422;
STRAIN=Vol. / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
where complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AEO10199; AALS0965.1;
Hypothetical protein; Complete proteome.
SEQUENCE 75 AA; 8393 MW; A52E0F2EB1852AFI CRC64;
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Pred. No. 8.9e+02;
2; Mismatches 1; Indels
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Pred. No. 8.5e+02;
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SEQUENCE 79 AA; 9470 MW; 9651135ACEB74D09 CRC64;
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Last annotation update)
                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
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EMBL; AE007473; AAK75879.1; -. ·
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Best Local Similarity 62.5%;
Matches 5; Conservative
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                                                                        Hypothetical protein PF0841
PF0841.
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NCBI_TaxID=2261;
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RESULT 41
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Mol. Ecol. 11:2013-2026(2002).
EMBL; AF534471; AAN37814.1; -.
                                                                                                                                                                                                                                                                                                                                                                               "Locating the sources of an invasive pest, grape phylloxera, using mitochondrial DNA gene genealogy."; Mol. Ecol. 11:2013-2026(2002).
EMBL, AF534470; AAN37812.1; -.
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                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Phylloxeroidea; Phylloxeridae; Daktulosphalra.
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2; Mismatches 1; Indels
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Pred. No. 9.1e+02;
2; Mismatches 1; Indels
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81 AA; 9706 MW; 87F8E9ED6DEA86E7 CRC64;
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Last annotation update)
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MEDLINE-22234187; PubMed-12296945;
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MEDLINE=22234187; PubMed=12296945;
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PRELIMINARY;
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Downie D.A.;
Locating the sources of an invasive pest, grape phylloxera, using a mitochondrial DNA gene genealogy.";
MOI. Ecol. 11:2013-2026(2002).
ENBL; AF5344-7; AAN37816.1; -.
Mitochondrion.
NON TER
81 81
SEQÜENCE 81 AA; 9744 MW; 87F8E9ED746E0FA3 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
COII.
Daktulosphaira vitifoliae (grape phylloxera).

Mitochondrion.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Phylloxeroidea; Phylloxeridae; Daktulosphaira.
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SEQUENCE FROM N.A.
STRAIN-ARIMAGARI;
MEDLINE-22234187; PubMed=12296945;
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30 ILMIMSII 37
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Q8HNA9;
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DT 01-MA,
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Search completed: February 17, 2004, 10:56:17 Job time : 14.7426 secs

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Human liver peptid Peptide #10461 enc Human brain expres Human bone marrow

Peptide #10814 enc

DP-1 transcription E2F activity inhib Soybean DP-1 prote

Fragment from a

Human peptide enco Soybean E2F protei DP-1 transcription DP-1 transcription Human DNA binding Repressor protein Human DNA binding Repressor protein Wast E2F derived E2F activity inhib E2F activity inhib DP-1 transcription Insulin-like growt Osteoblast prolife Osteoblast prolife Osteoblast prolife Polypeptide sequen Human prostate spe Novel human colon

Human digestive sy Tyrosine activatio Human immune/haema

Human liver peptid Peptide #8153 enco Protein #6903 enco

E2F activity inhib

Sequence:

Run on:

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Database

26456786

Result

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DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
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/note= "Claim 3"
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                      Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 91; DB 19; Length 1 Best Local Similarity 100.0%; Pred. No. 2.9e-10; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DP-1 transcription factor peptide H (DEF box).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW30501 standard; Peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRRVYDALNVLMAMNIISK 19
                                                                                                                    Claim 4; Page 44; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-GB03506
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              WPI; 1998-377596/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1998
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Peptide H (I) comprises residues 163-199, i.e. the DEF box region, of transcription factor DP1. Claimed fragments (II) (see AAM30502-07) (c) of transcription factor DP1. Claimed fragments (II) (see AAM30502-07) (c) (II) are capable of antagonising the heterodimerisation of a DP protein with an E2F protein. Also claimed are fusion proteins (I) or (III) and a membrane translocation sequence (III) comprising (I) or (III) and a membrane translocation sequence (see AAM30508), expression vectors encoding (I)-(III) and host cells. (c) specifically in tumour or cardiovascular cells, either in vivo or in specifically in tumour or cardiovascular cells, either in vivo or in c) (I)-(III) are used the respectively expression marrow. Surgical stents comprising or viro, e.g. for purging bone marrow. Surgical stents comprising control, e.g. for purging bone marrow. Surgical stents comprising control and an antagens who control by inactivating control in assays for the DNA-binding activity of DP/E2F dimerisation and as immunoassay controler and antagonists of DP-1/E2F dimerisation and as immunoassay controler capacide encoding (I)-(III) to control DP levels in cells, controler agents, AB profession (I)-(III) to control DP levels in cells, controlarly by gene therapy. When formulated with cytotoxic or cytostatic agents, (I)-(III) enhance cell killing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapв
 Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 91; DB 19; Length 37; 100.0%; Pred. No. 6.9e-10; Live 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yoshida T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E2F activity inhibiting compound Ib-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamasaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRRVYDALNVLMAMNIISK 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW57051 standard; peptide; 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
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28 AA;

Sequence

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This represents a compound that can inhibit E2F activity. The compound also of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                     This represents a compound that can inhibit E2F activity. The compound also fethe formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylozarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or anino, and A is an B2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibitors - for treatment and prevention of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2F activity; inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                                                Length 28;
                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                              DB 19; L 4.2e-09;
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                                                                                                                                                                                                    94.5%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "N-terminal lauroyl"
                                                                                                                                                        prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         E2F activity inhibiting compound Ib-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamasaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                            Example 3; Page 27; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                      AAW57055 standard; peptide; 28
                                                                                                                                                                                                                                                                                       11 RRRVYDALNVLMAMNIIS 28
                                                                                                                                                                                                                                                                      18
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                                                                                                                                                                                                                                          18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity inhibito
arteriosclerosis
 and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-240020/21.
                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                    28 AA;
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                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    AAW57055;
                                                                                                                                                                                                              Query Match
Best Local
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Gaps

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                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                  DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
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0
           Length 28;
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Pred. No. 9.5e-09;
0; Mismatches 2; Indels
           DB 19; L
'4.2e-09;
                                       Mismatches
                                                                                                                                                                                                                                                      DP-1 transcription factor peptide H2mt1.
           Score 86;
                                                                                                                                                                                                                                                                                                                                                                                                             'note= "V169A mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "V175A mutation"
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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94.5%; Scc...
100.0%; Pred
0; P
                                                                                                                                                                  AAW30515 standard; Peptide; 19 AA.
                                                                  18
                                                                                  11 RRRVYDALNVLMAMNIIS 28
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                   1 RRRVYDALNVLMAMNIIS
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                                                                                                                                                                                                                           (first entry)
                                       18; Conservative
                                                                                                                                                                                                                                                                                                              surgical stent; therapy
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           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 10
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                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                               AAW30515;
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                                       Matches
                                                                                                                                      RESULT 5
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1 RRRVYDALNVLMAMNIISK 19

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tumour;

bp-1; transcription factor; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; surgical stent; therapy.

'note= "R167A mutation" /note= "D171A mutation"

Location/Qualiflers

Misc-difference 2 fisc-difference

lomo sapiens

Synthetic

WO9828334-A1.

12-JUL-1998

bp-1 transcription factor antagonist peptide H2mt2.

(6-0CT-1998 (first entry)

RESULT 6

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Peptide HZmt3 is based on peptide H2 (see AAW30504) from the DEF box (see AAW30501) of transcription factor DP1. In HZmt3, amino acid residues of H2 that correspond to DP1 residues Leu173 and Leu176 are subscriptioned by Arg residues. H2 is an antagonist of the heterodimerisation of DP1 with E2F. H2mt3 has none of the antagonistic activity of H2. H2 and other calaimed peptides (see AAW30504-07) from the DEF box region of DP1 can be used to induce apoptosis, specifically in tummour and cardiovascular cells, e.g. for the prevention of restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                               DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 86.8%; Score 79; DB 19; Local Similarity 89.5%; Pred. No. 5.4e-08; Les 17; Conservative 0; Mismatches 2;
                                                                                         DP-1 transcription factor peptide H2mt3
                                                                                                                                                                                                                                                                       /note= "L176R mutation"
                                                                                                                                                                                                                                               note= "L173R mutation"
                                                                                                                                                                                                                 Location/Qualifiers
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          AAW30517 standard; Peptide; 19 AA
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                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 AA;
                                                                                                                                                                                                                                Misc-difference 8
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                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-1996;
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                                                                 26-OCT-1998
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                                       AAW30517;
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Matches
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AAW3051
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                                                                                                                                                                                                                                                                                                                                                                                         Peptide HZmt2 is based on peptide H2 (see AAW30504) from the DEF bc (see AAW30501) of transcription factor DP1. In HZmt2, amino acid tresidues of H2 that correspond to DP1 residues Arg167 and Asp171 are substituted by Ala residues. H2 is an antagonist of the heterodimerisation of DP1 with E2F. H7mt2 retains some, but not all, of this antagonistic activity. H2 and other claimed peptides (see AAW30504-07) from the DEF box region of DP1 can be used to induce apoptosis, specifically in tumour and cardiovascular cells,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 77; DB 19; Le
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g. for the prevention of restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW30506 standard; Peptide; 16 AA
                                                                                                                                                                                                                                                                                                                                                                           Example D; Page 26; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RARVYAALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.6%;
89.5%;
                                                                                                                                                                                                                             97WO-GB03506
                                                                                                                                                                                                                                                                                          La Thangue NB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Conservative
                                                                                                                                                                                                                                                                     (PROL-) PROLIFIX LTD.
                                                                                                                                                                                                                                                                                                               WPI; 1998-377596/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AA;
                                                                                                                                                                                                                              2-DEC-1997;
                                                                                                                                                                                                                                                 20-DEC-1996;
                                                                                                                                                                                                                                                                                           Bandara LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW30506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.

DP-1 transcription factor antagonist peptide H5.

26-OCT-1998 (first entry)

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Gaps

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Length 19; 2; Indels

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Peptide H7 comprises amino acid residues 170-199 in the DEF box (I) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07) containing one or both of 2 motifs (see AAW30504-03) of the DEF box are capable of antagonising the heterodimerisation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially concenting substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and and 175 of DP-1, fusion sequence (see AAW30508), expression vectors conceding (I)-(III) and host cells. (I)-(III) are used therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging C bone marrow. Surgical stens comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding cactivity of DP/E2F heterodimers. They are also used as research reagents, as positive controls in assays for identifying angagonists of DP-1/E2F dimerisation and as immunoassay agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           described is the use of sequences antisense to nucleic acids ding (I)-(III) to control DP levels in cells, particularly by therapy. When formulated with cytotoxic or cytostatic agents,
                  DP-1; transcription factor; antagonist, E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
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                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                    3..9 "Claim 3" /note= "Claim 3" 5..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB67766 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                     5..15
/note= "Claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 44; 55pp; English

    (I) - (III) enhance cell killing.

                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-GB03506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96GB-0026589.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDALNVLMAMNIISK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROL-) PROLIFIX LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
ses 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-1996;
                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                            WO9828334-A1
                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bandara LR,
                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB67766
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                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                     Peptide
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB67766
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide H5 comprises amino acid residues 168-183 in the DEF box (II) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07) containing one or both of 2 motifs (see AAW30502-03) of the DEF box are capable of antagonising the AAW30502-03) of the DEF box are capable of antagonising the chercodimerisation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and a membrane translocation sequence (see AAW30508), expression vectors correctly (I) (III) and host cells. (I)-(III) are used to therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging treat or prevent restences in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding cactivity of DP/E2F heterodimers. They are also used as research reagents as positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunoassay agents. Also described is the use of sequences antisense to nucleic acids encoding (I)-(III) to control by inactivating the DAM-binding caccides are controls in the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              When formulated with cytotoxic or cytostatic agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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Pred. No. 1.6e-07;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DP-1 transcription factor antagonist peptide H7.
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW30507 standard; Peptide; 30 AA
                                                                                                                                /note= "Claim 3"
                                                                                                                                                                    7..16
/note= "Claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 44; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (I) - (III) enhance cell killing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.5%; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVYDALNVIMAMNIIS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVYDALNVLMAMNIIS 16
                                                                                                                                                                                                                                                                                                                                            97WO-GB03506
                                                                                                                                                                                                                                                                                                                                                                                              96GB-0026589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bandara LR, La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity 100...
Local Similarity 100...
Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROL-) PROLIFIX LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-1998
                                         Homo sapiens
                                                                                                                                                                                                                                         WO9828334-A1
                                                                                                                                                                                                                                                                                                                                            22-DEC-1997;
                                                                                                                                                                                                                                                                                          02-JUL-1998
                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW30507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                Peptide
                                                                                                                                                               Peptide
                                                                                           Key
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Peptide H6 comprises amino acid residues 167-180 in the DEF box region (see AAM30501) of transcription factor DP1. Unlike claimed peptides (see AAM30504-07) that contain one or both of 2 motifs (see AAM30502-03) of the DP1 DEF box, peptide H6 is not capable of antagonising the heterodimerisation of a DP protein with an B2F protein. The claimed peptides, their variants and fusion proteins can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g. to prevent restenosis.
                                                                                                                                                                                                                                                Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E2F activity; inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.8%; Score 69; DB 19; Length 14
100.0%; Pred. No. 2.8e-06;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yoshida T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E2F activity inhibiting compound Ib-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamasaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW57052 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                  Example C; Page 41; 55pp; English.
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                                                                    97WO-GB03506
                                                                                                       96GB-0026589
                                                                                                                                                                                 La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RRVYDALNVLMAMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRVYDALNVLMAMN 14
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata K,
                                                                                                                                              PROL-) PROLIFIX LTD
                                                                                                                                                                                                                     WPI; 1998-377596/32.
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Modified-site
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                                                                                                           20-DEC-1996;
WO9828334-A1
                                                                                                                                                                                     Bandara LR,
                                   02-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and alter plant cell proliferation characteristic such as to alter plant cell proliferation characteristic such as to alter plant cell, organ or tissue shape, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB67764-68 represent fragments of a wheat E2F-dimerisation partner
(DP) protein. The protein acts as a plant E2F transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                        E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                       Fragment from a wheat E2F-dimerisation partner (DP) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70; DB 22; Length 56;
Pred. No. 1.1e-05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                              (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF
                                                                                                                                                                                                                                                                                                                                                                                                     Ramirez-Parra E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP-1 transcription factor peptide H6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.9%;
68.4%;
                                                                                                                                                                                                                                                                       25-SEP-2000; 2000WO-EP09325.
                                                                                                                                                                                                                                                                                                         99ES-0002127.
99ES-0002474.
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       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 68.4
hes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Gutierrez-Armenta C,
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-257972/26.
N-PSDB; AAF80148.
                                                                                                                                                            Triticum monococcum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AA
                                                                                                                                                                                               WO200121644-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
Homo sapiens
                                                                                                                                                                                                                                                                                                           24-SEP-1999;
11-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-1998
         11-JUN-2001
                                                                                                                                                                                                                                    29-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches

RESULT 11

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Gaps

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Length 14;

08-APR-1999;

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                                                                            This represents a compound that can inhibit E2F activity. The compound alkanoyl, alloyl, hetero-arylcarbonyl, alloyl, arylcxycarbonyl, alloyl, hetero-arylcarbonyl, alkoxycarbonyl, arylcxycarbonyl, hetero-arylcxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                                    Gaps
                      E2F activity inhibitors - for treatment and prevention of tumours
                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                           74.7%; Score 68; DB 19; Length 15; 100.0%; Pred. No. 4.8e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       DP-1; soybean, cell cycle regulatory protein;
transcription factor; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "encoded by CNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "encoded by GNC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "encoded by ANT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "encoded by GNC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "encoded by GGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "encoded by CNT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "encoded by NAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "encoded by ANG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "encoded by NAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "encoded by NAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "encoded by NAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "encoded by GNG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "encoded by NTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                         Example 4; Page 28; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                           AAY32163 standard; Protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 Soybean DP-1 protein fragment
                                                                                                                                                                                                Query Match
Best Local Similarity 100.00
These 14; Conservative
                                                                                                                                                                                                                                                           1 RRRVYDALNVLMAM 14
                                                                                                                                                                                                                                                                                  2 RRRVYDALNVLMAM 15
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                       15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max
                                                                                                                                                                                                                                                                                                                                                                    AAY32163;
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                    RESULT 13
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                                                                                                                                                                                                                                                     This sequence represents 42% of the middle region of soybean cell cycle regulatory protein DP-1, as deduced from an isolated cycle regulatory protein DP-1, as deduced from an isolated come (see AAZ34579). The invention relates to nucleic acid fragments (see AAZ34575-8) encoding plant CDC-16, DP-1, DP-2 and E2F cell cycle regulatory proteins (see AAY32159-67). It also celates to the construction of a chimeric gene encoding all or a portion of the cell cycle regulatory protein, in sense or antisense orientation, where expression of the chimeric gene results in producton of altered levels of the cell cycle regulatory protein in consection for the construction of altered levels of the cell cycle regulatory protein in consection for the chimeric gene results in the sense constitutes studies of cell cycle regulation in plants, convide genetic tools to enhance cell growth in tissue culture, increase gene transfer efficiency and provide more stable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The proteins may also provide targets to and/or identification of cell cycle regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.5%; Score 66; DB 20; Length 83; 83.3%; Pred. No. 0.0001; ive 1; Mismatches 2; Indels
                                                                                                                 Klein TM, Morakinyo LO, Odell JT, Sakai H;
                                                                                                                                                                                              Plant-derived cell cycle regulatory proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins that may be useful as herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human liver peptide, SEQ ID No 37013.
                                                                                    (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG58365 standard; Peptide; 96 AA.
                                                                                                                                                                                                                             Claim 10; Page 41; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RRRVYDALNVLMAMNIIS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
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2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                       98US-0081132.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 83.3
les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transformations. The pro
facilitate design and/or
                                                                                                                                                WPI; 1999-633830/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 AA;
                                                                                                                                                                  N-PSDB; AAZ34579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157273-A2.
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03-AUG-2000;
21-SEP-2000;
                                                       09-APR-1998;
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG58365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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AAM63859;
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                                                                                                                                                  Seguence
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                                                                                                                                                                                                                                                                             RESULT 16
                                                                                                                                                                                                                                                                                      AAM63859
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                                                                                                                                                                                                                                         셤
                                                                                                                         The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult

1 iver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high specification is ampleaded acid molecule expressed in the human adult stringency to a nucleic acid molecule expressed in the human adult claver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, is associated with coronary heart disease. ABG593910 represent hyperlipoprotechinaemia, hyperlipidaemia and hypercholesterolaemia which hyperlipoprotechinaemia, hyperlipidaemia of the invention.

3. Chuman liver single exon encoded peptides of the invention.

3. Chuman liver single exon encoded peptides of the invention.

3. Chuman liver supplementation for this patent does not appear in the norm with the legumence information for this patent does not appear in the liver wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #10461 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                   ö
                                                                    Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver -
                                                                                                                                                                                                                                                                                                                            63.7%; Score 58; DB 22; Length 96; 47.4%; Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                      8; Mismatches
                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Я;
                             DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank
                             Rank
                                                                                                            Claim 27; SEQ ID No 37013; 658pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                            1 RRRVYDALNVLMAMNIISK 19
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RRRIYDIVNVLESLHLVSR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB42955 standard; Peptide; 96
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      (MOLE-) MOLECULAR DYNAMICS INC
                              Chen W,
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2000US-0608408.
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2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0234687
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                                                                                                                                                                                                                                                                                                                                           Local Similarity 47.4 tes 9; Conservative
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                              Hanzel DK,
                                                   WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel
                                                                                                                                                                                                                                                                                                           96. AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2002
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                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                               Query Match
                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB42955
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8X4X8X8X8X8X8X8X8X8X8X8X8X8X8X8
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human brain expressed single exon probe encoded protein SEQ ID NO: 35964.
                                                                          measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO: 35964; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                           probe for
Claim 27; SEQ ID NO 35590; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                              63.7%; Score 58; DB 22; Length 96;
47.4%; Pred. No. 0.004;
ive 8; Mismatches 2; Indels
                                                           exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM63859 standard; Protein; 96 AA.
                                                                    The invention relates to a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RERVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RRRIYDIVNVLESLHLVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                             96 AA;
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The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                     Peptide #10814 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human peptide encoded by genome-derived single exon probe SEQ ID 35546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromacrosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary cillary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 22; Length 96; Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID No 37046; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG45881 standard; Peptide; 96 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||:|| :||| :|||
RRRIYDIVNVLESLHLVSR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.78;
                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.48;
                                                                                                                                                                                                                                                                                                                       2000US-0207456
2000US-0608408
                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                   2000GB-0024263
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 AA;
                                                                                                                         genetic disorder
                                                                                                                                                                                               WO200157272-A2
                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000;
                                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-2002
                                   17-0CT-2001
                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG45881;
AAM36777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG45881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                           Human bone marrow expressed probe encoded protein SEQ ID NO: 36978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO: 36978; 658pp + Sequence Listing; English.
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                                                                       ö
                              Score 58; DB 22; Length 96;
Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.7%; Score 58; DB 22; Length 96; 47.4%; Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing gene expression in human bone marrow
                                                0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Mismatches
                                                                     8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM36777 standard; Protein; 96 AA.
                                                                                                                                                                                                                                 AAM76672 standard; Protein; 96 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                         1 RRRVYDALNVLMAMNIISK 19
                                                                                                                           3 RRRIYDIVNVLESLHLVSR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||:|| :|| :||| ::::|:
RRRIYDIVNVLESLHLVSR
                                 63.7%;
illarity 47.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 47.4 les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG, Hanzel DK,
                Query Match
Best Local Similarity
''hea 9; Conservê
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 AA;
 96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                        06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                    AAM76672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
 Sequence
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RESULT 17
AAM76672
LD AAM76672
XX
XX
XX
DT 06-NO
XX
KW Human
XX
Human
XX
Human
XX
HOWO
OS HOWO
XX
XX
HOWO
OS HOWO
XX
XX
KW M2200
XX
XX
KW M2200
XX
KW M0200
XX
KW M0200
XX
KW M0200
XX
XX
KW M0200
XX
XX
KW M0200
XX
XX
KW M01.9
RR 26-WR
PR 26-WR
PR 26-WR
PR 26-WR
PR 26-WR
PR 21-SE
PR

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Gaps

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RESULT 18
AAM36777
ID AAM36
XX

Matches

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Gaps

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Indels

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(MOLE-) MOLECULAR DYNAMICS INC.
                                     26-MAY-2000; 2000US-207456P.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-062346.
21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-236359P.
04-OCT-2000; 2000GB-0024263.
                          30-JAN-2001; 2001WO-US00665.
                                                                        Penn SG, Hanzel DK,
                                                                                WPI; 2002-114183/15.
           WO200186003-A2.
   Homo sapiens.
                                  04-FEB-2000;
                  15-NOV-2001.
                                                                                                                                                                                                                                                                            Sequence
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This sequence represents 10% of the middle region of soybean cell cycle regulatory protein B2F, as deduced from an isolated cell cycle regulatory protein B2F, as deduced from an isolated cell cycle regulatory proteins (see AAZ34583). The invention relates to nucleic acid fragments (see AAZ3455-83) encoding plant CDC-16, DP-1, DP-2 and E2F cell cycle regulatory protein, (see AAZ3159-67). It also relates to the construction of a chimeric gene encoding all or a relates to the construction of a chimeric gene results in correctation, where expression of the chimeric gene results in producton of altered levels of the cell cycle regulatory protein in producton of altered levels of the cell cycle regulatory protein in products a transformed host cell. The nucleic acids and proteins may be used to facilitate studies of cell cycle regulation in plants, increase gene transfer efficiency and provide nore stable transfer efficiency and provide targets to transformations. The proteins may also provide targets to transformations. The proteins may also provide targets to facilitate design and/or identification of cell cycle regulatory proteins that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                  soybean; cell cycle regulatory protein; transcription factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%; Score 56; DB 20; Length 80; ilarity 47.4%; Pred. No. 0.0076; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sakai H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant-derived cell cycle regulatory proteins
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Odell JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 44-45; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW30509 standard; Peptide; 11 AA.
                                                                                                                                                                                                                        AAY32167 standard; Protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 RRRIYDIVNVLESIGVLSR 71
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                                             1 RRRVYDALNVLMAMNIISK 19
                                                                                3 RRRIYDIVNVLESLHLVSR
                                                                                                                                                                                                                                                                                                                                                                                Soybean E2F protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US0763B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0081132
                                                                                                                                                                                                                                                                                                                                (first entry)
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     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-633830/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ34583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09953075-A2
                                                                                                                                                                                                                                                                                                                                01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                  AAY32167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW30509
ID AAW3
XX
        Matches
                                                                                                                                                                                     RESULT 20
                                                                                                                                                                                                          AAY3216
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                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes; the novel set of probes which hybridise at high extragency to a nucleic acid expressed in the human lung; measuring gene expression in a nucleic acid expressed in the human lung; measuring gene expression in a collection of detectably labeled nucleic acid ecroek from human lung. comprising (a) contacting the array with a collection of detectably labeled nucleic acid expression in a evaryotic genome, comprising the array; identifying exons in a eukaryotic genome, comprising the eukaryote; and (b) measuring the label detectably bound to each probe of the eukaryote; and (b) measuring the predicted exon, the probe is included anyone array identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (b) measuring the expression of each of the exons in several comprising (a) identifying exons from genomic sequence by the method comprising of the exons should be assigned to a single exon in several comprising of the exons should be assigned to a single gene, a peptide comprising or probes/per neading frames (ORF). The probes are used for gene of 12011 sequences, mentioned in the specification, or encoded by the comprising or in the special part of the exons should be assigned to a single gene, a peptide comprising or such as asthma. Jung cancer, chronic obstructive pulmonary disease (CDP), interstital lung disease (IDP), familial didopath gument places, Hermann-Pick disease, Hermannsky-budiak syndrome, sathma, lung cancer, chronic obstructive pulmonary dysplasis, primary cillary dysfaments in pulmonary dysplasis, primary cil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 23; Length 96; Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID No 35546; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.78;
                                                                                                                                                                                                                                                2000US-180312P.
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Gaps

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Query Match Best Local Similarity

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97WO-GB03506.
                                                                 96GB-0026589.
                                                                                                     La Thangue NB;
                                                                                   (PROL-) PROLIFIX LTD.
                                                                                                                        WPI; 1998-377596/32
                                                                 20-DEC-1996;
           WO9828334-A1
                                               22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                     Bandara LR,
                             02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU78095;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                        Peptide HI comprises amino acid residues 166-176 in the DEF box region (see AAW30501) of transcription factor DPI. Unlike claimed peptides (see AAW30504-07) that contain one or both of 2 motifs (see AAW30502-03) of the DPI DEF box, peptide HI is not capable of antagonising the heterodimerisation of a DP protein with an E2F protein. The claimed peptides, their variants and fusion proteins can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g. to prevent restenosis.
                                                                                                                                                                                                                                                    Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                       DP-1; transcription factor; antagonist, E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                               59.3%; Score 54; DB 19; Length 11; 100.0%; Pred. No. 0.0014; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DP-1 transcription factor antagonist peptide H3.
                                    DP-1 transcription factor peptide H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                          Example C; Page 41; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW30505 standard; Peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Claim 3"
                                                                                                                                                           97WO-GB03506.
                                                                                                                                                                             96GB-0026589
                                                                                                                                                                                                                 Bandara LR, La Thangue NB;
                   26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                          surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RRRVYDALNVL 11
                                                                                                                                                                                              (PROL-) PROLIFIX LTD.
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                  WPI; 1998-377596/32.
                                                                                                                                                                                                                                                                                                                                                                                              11 AA;
                                                                                                     Homo sapiens.
                                                                                                                       WO9828334-A1
                                                                                                                                                           22-DEC-1997;
                                                                                                                                                                             20-DEC-1996;
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                                                                                                                                        02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                            Synthetic.
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AAW30509;
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PT Polypoptide fragments of the DP-1 transcription factor - used for inducing apoptide fragments of the DP-1 transcription factor - used for dividing apoptide fragments of the DP-1 transcription factor DP-1 (all may apoptide).

Second of the DP-1 specifically in tumour and cardiovascular cells, No. 2 for preventing restenosis and cardiovascular cells and no process and cardiovascular cells and no process and cardiovascular cells and no process. The DP-1 cells and peptides (all Nava0502-03) of transcription factor DP-1 (all may person of the DP-1 by the DP-1 by the DP-1 cells and are variants of these peptides, especially containing and are variants of these peptides, especially containing and not 175 of DP-1, tusion proteins (III) comprising (I) (III) and host cells. (II) (III) are used conding (I) (III) and host cells. (IV) (III) are used conding (I) (III) and host cells. (IV) (III) are used conding (IV) (III) are used conding (IV) (III) function by inactivating the DRA-binding activity of DP-1 BZP binerisation and as ammunoassay agents. As an apparatus as positive controls in assays for identifying activity of DP-1 BZP dimerisation and as ammunoassay agents. As a positive controls in assays for identifying activity of DP-1 BZP dimerisation and as ammunoassay agents. As an acciding (I) (III) control DP lavels in cells, particularly by matches (III) control DP lavels in cells, particularly by matches (II) (III) enhance cell killing.

ON Sequence 20 AA, Score 51, DB 19; Length 20; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Munan Abbarding site; Mutchinson Gilford syndrome, Alborate Abbarding domain E2P-1.

Mature 1 telomerase reverse transcriptase; TERT; Site C; Progeria; burn; RW acquired immunodeficiency syndrome, cardiovascular acquired immunodeficiency syndrome, cardiovascular acquired immunodeficiency syndrome, ca
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The present invention relates to a new method of modulating expression of telomerase reverse transcriptase (TERT) from a TERT expression system of telomerase a TERT promoter and a Site C repressor binding site. The method of the invention involves modulating TERT transcription repression to the Site C repressor binding site. The method of the invention is by the Site C repression of TERT for producing a mammalian cantibody. The method is also useful in a variety of different applications, including immortalisation of cells, production of reagents for use in life science research, therapeutic applications and characteric shortening and/or increasing TERT expression delays natural telomeric shortening and/or increasing TERT expression cally useful for treating disease conditions such as Progeria or the utchinson-Gilford syndrome, acquired immunodeficiency syndrome (AIDS), cardiovascular disease, osteoporosis, in skin rejuvenation and to inhibit immune senescence. The method can be employed to lengthen telomeres of osteoblast and osteodolast stem cells, encouraging bone replacement and proper remodeling and reinforcement, and can thus be used in bone marrow transplants and as such the method improves the survival and effectiveness of bone marrow are as such the method improves the survival and effectiveness of the method the method improves the survival and effectiveness of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating expression of telomerase reverse transcriptase (TERT) in a cell, for regulating proliferative capacity of a cell, involves modulating TERT transcription repression by Site C repressor binding
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                                                                                                                                                                                                                                                                                                                                                                                                       Mohammadpour H;
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/label= DNA_binding_domain
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Location/Qualifiers
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55 KRRIYDITNVLEGIQLIAK
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01-SEP-2000; 2000US-230174P.
05-OCT-2000; 2000US-238345P.
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Domain
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Human; telomerase reverse transcriptase; TERT; Site C; Progeria; burn; repressor binding site; Hutchinson-Gilford syndrome; AIDS; cancer; acquired immunodeficiency syndrome; cardiovascular disease; osteoporosis; skin rejuvenation; immune senescence; bone marrow transplant; skin graft; neoplastic disease; TERT minimal promoter; DNA binding domain; E2F-4.
                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to modulating expression of telomerase reverse transcriptase (TERT) expression system that includes a TERT promoter and a Site C repressor binding site. The method involves modulating TERT transcription repression by the Site C repressor binding site. The methods and compositions of the present invention are useful for the immortalization of cells, production of reagents in life science research, therapeutic agent screening applications, diagnosis and treatment of disorders associated with abserrant telomerase activity such as cancer, progeria, immune senescence, HIV, and in skin rejuvenation.
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                                                                                                                                                                                                                                                                                               Modulating expression of telomerase reverse transcriptase TERT by blocking repression of TERT transcription, useful for the diagnosis treatment of disorders associated with aberrant telomerase activity such as cancer and HIV -
cytostatic; immunostimulant; anti-HIV; vulnerary; telomerase; human; repressor protein; B2F-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.0%; Score 51; DB 24; Length 85; 47.4%; Pred. No. 0.072; ive 5; Mismatches 5; Indels
                                                                                                                                                                                                                                         Mohammadpour H, Andrews WH;
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/label= DNA_binding_domain
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55 KRRIYDITNVLEGIQLIAK 73
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                                                                                                                                                  06-JUN-2002; 2002WO-US17959.
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Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                               (SIER-) SIERRA SCI INC
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                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is useful for treating disease conditions such as Progeria or thuchinson-Gilford syndrome, acquired immunodeficiency syndrome (AIDS), cardiovascular disease, osteoporosis, in akin rejuvenation and to inhibit immune senescence. The method can be employed to lengthen telomeres of osteoblast and osteoclast stem cells, encouraging bone replacement and proper remodeling and reinforcement, and can thus be used in bone marrow transplants for the treatment of cancer and skin grafts for burn victims and as such the method improves the survival and effectiveness of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating expression of telomerase reverse transcriptase (TERT) in a cell, for regulating proliferative capacity of a cell, involves modulating TERT transcription repression by Site C repressor binding
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cytostatic; immunostimulant; anti-HIV; vulnerary; telomerase; human;
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Similarity 47.4%;
9; Conservative
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Best Local Similarity
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28-FEB-2002.
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RESULT 26 ABB82987

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                                                                                                                                                                                      Modulating expression of telomerase reverse transcriptase TERT by blocking repression of TERT transcription, useful for the diagnosis and treatment of disorders associated with aberrant telomerase activity
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Pred. No.
                                                                                                                             Mohammadpour H,
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                                       06-JUN-2002; 2002WO-US17959.
                                                                      17-JUN-2001; 2001US-296992P
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Matches 9; Conservative
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                                                                                                                             Foster CA, Fraser S,
                                                                                                                                                            WPI; 2003-167401/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 27
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29 AA;
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1996;
                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                         WO9814474-A1
                                                                                                                                                                                                                                                                28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mizukami T,
                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                 AAW57049;
                                                                                                                        Sequence
                                                                                                                                      Query Match
                                                                                                                                                       Matches
                                                                                                                                                                                                                RESULT 29
                                                                                                                                                                                                                          AAW57049
                                                                                                                                                                                                                                 8
                                                                                                                                                                                      요
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0
                                                                                                                                              The present sequence is a peptide comprising DNA-binding domain of wheat E2F protein that was identified in a wheat cDNA library by yeast two-hybrid screening. The E2F is a transcription factor that interacts with plant retinoblastom (Rb) and is involved in cell cycle regulation. The present sequence has the ability to bind to E2F binding site in plant DNA and is used to control plant growth, cellular DNA replication, cell cycle progression, differentiation and development by altering its DNA-binding
                                                                                                                                                                                                                                                                   Gaps
                                                                                                Regulating plant growth and/or cellular DNA replication and/or cell cycle progression, differentiation and development using a plant E2F polypeptide -
                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                           E2F activity; inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                                                                                 Score 49; DB 21; Length 28;
Pred. No. 0.042;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamasaki M, Yoshida T;
                                                 (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                  Ramirez Parra E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-terminal lauroyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                            E2F activity inhibiting compound Ia-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            AAW57054 standard; peptide; 29 AA
                                                                                                                                                                                                                                                                                                   20
                                                                                                                                  Claim 8; Page 26; 45pp; English
                                                                                                                                                                                                                                                                                   RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                    53.8%;
                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-JP03442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96JP-0259432
                                                                  Xie Q,
                         98ES-0000975
        99WO-EP03158
                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                   Query Match 53.8
Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shibata K,
                                                                  Gutierrez-Armenta C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-240020/21.
                                                                                   WPI; 2000-116290/10
                                                                                                                                                                                                                                   28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             28-AUG-1998
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          07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-1998.
                           08-MAY-1998;
                                  11-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                             AAW57054;
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                     activity
                                                                                                                                                                                                                                                                                                                             RESULT 28
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ID AAW
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                                                                                                                                         This represents a compound that can inhibit E2F activity. The compound is of the formula R1 - A - R2 where R1 is an optionally substituted allangui, alloyl, hetero-arylcarbonyl, atkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E2F activity inhibitors - for treatment and prevention of tumours and arteriosclerosis
B2F activity inhibitors - for treatment and prevention of tumours and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E2F activity; inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 19; Length 29;
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yoshida T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E2F activity inhibiting compound Ia-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamasaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 24; 52pp; Japanese.
                                                                                                      Example 6; Page 31; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW57049 standard; peptide; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||:|| ||| ::|:
12 KRIYDITNVLEGIQLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96JP-0259432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-JP03442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-240020/21.
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les 8; Conserva
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stress such as pathogen attack, to modulate e.g. enhance crop yields,
                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                RESULT 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel cell cycle protein (CCP) and the polynucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for medulating the cell polypeptide and an anti-CCP antibody is useful for medulating the cell of CCP in a sample. A CCP medulator is useful for medulating the cell of CCP in a sample. A CCP medulator is useful for medulating the cell of CCP in a sample of CCP medulator is useful as medulating the cell of CCP protein or production of CCP protein forms which have decreased or certain or production of CCP protein forms which have decreased or cell of CCP protein or production of CCP protein forms which have decreased or cell of CCP polypeptide are useful as herbicides or plant growth regulators. The polymucleotide is useful for medifying cell fate, plant development, cc farmulation or enhancement of cell division, DNA replication, promoction, stimulation and/or development, nodule function, dwarfism in plants.

Seed size, seed development, nodule function, dwarfism in plants, enescence, tolerance or resistance to stress. CCP, the polymucleotide is useful in agriculture to modulate the coll cycle and the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due to environmental conditions, including ablotic stress such as
                                                                               ö
                                                                                                                                                                                                                                                                                                       Cell cycle protein; CCP; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield; motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators -
                                                                               Gaps
                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Magyar Z;
                                                  Score 46; DB 19; Length 29;
Pred. No. 0.16;
                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acosta JAT,
prevention of tumours and arteriosclerosis.
                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 25, 316pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Veylder L,
                                                                                                                                                                                                   AAU72601 standard; Peptide; 35 AA
                                                                                                       1 RRRVYDALNVLMAMNIIS 18
                                                                                                                      :||:|| ||| ::|:
12 KRRIYDJTNVLEGIQLIA 29
                                                                                                                                                                                                                                                                              DEF domain consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-2001; 2001WO-IB01307.
                                                      50.5%;
                                                                   44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-2000; 2000US-204045P.
                                                                                                                                                                                                                                                       (first entry)
                                                                Local Similarity 44.4 les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CROP-) CROPDESIGN NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boudolf V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-062249/08
                          29 AA;
                                                                                                                                                                                                                                                                                                                                                                                          WO200185946-A2
                                                                                                                                                                                                                                                     26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                            AAU72601;
                           Sequence
                                                     Query Match
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                                                                                                                                                                      RESULT 30
AAU72601
SXS
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and attenuate plant architecture, plant quality traits, plant reproduction and seed development, endoreduplication in storage cells, storage tissues and/or storage organs of plants or its parts. Cells, useful as an immunogen to generate antibodies. CCP protein is useful to screen for naturally occurring CCP substrates. The polymucleotide is useful for expressing CCP protein, to detect CCP mRNM, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence represents a motif which may be found in a CCP protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMW30303) of the DEF box, are antagonists of the heterodimeriation of a DP protein with an EZP protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and a membrane translocation sequence (see AAW3068), expression vectors encoding (I)-(III) and host cells. (I)-(III) are used therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding activity of DP/EZF heterodimers. They are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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Pred. No. 0.32;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DP-1; transcription factor; antagonist; E2F protein; cell proliferation; cardiovascular cell; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DP-1 transcription factor antagonist peptide motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRRVYDALNVLMAMNII 17
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                                                                                                                                                                                                                                                                                                                                                                                                    Match 49.5%;
Local Similarity 64.7%;
les 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 RXRVXDALNVXMAXXXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell proliferation; car
surgical stent; therapy
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                                                                                                                                                                                                                                                                                                                                    35 AA;
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Sequence
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                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel insulin-like growth factor binding protein (IBP) constructed using the formula R1-C-X1-PNC-X2-QC-X3-CWCV-X4-C-K2 where cyclic, glycosylated, phosphorylated, acetylated, amidated, culphated derivatives and fragments of these with the physiological ability of IBP are included and RINH2 = an amino acid or peptide with a sequence of up to 41 amino acid residues, X1 = a peptide consisting of 24-31 amino acids, X2 = a peptide consisting of peptide consisting of 10 amino acids, X4 = a peptide consisting of 18-24 amino acids, R2COH = CONH2 or a peptide with up to 12 amino acids. The products of the invention have immunoprotective, antiproliferative, anti-inflammatory and cytostatic activity. The IBP peptides, complexes, antibodies, inhibitors and (antisense) nucleic acids are all useful in the treatment of muscle loss/shrinkag/wastage, osteoporosis, diabetes, inflammatory processes, cancer, inflammatory and neoplastic diseases, inflammatory processes, cancer, inflammatory and neoplastic diseases, inflammatory processes, cancer, inflammatory and neoplastic diseases, inflammatory and wound or bone healing. The nucleic acids and antisense
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                                                                                                                                                                                                                                                                                                                                                                             Insulin-like growth factor binding protein; IBP; immunoprotective; antiproliferative; anti-inflammatory; cytostatic; treatment; muscle loss; shrinkage; wastage; osteoporosis; diabetees; amyloid lateral sclerosis; neuropathy; inflammation; cancer; neoplastic disease; growth disturbance; muscle; bone apparatus; wound healing; bone healing; gene therapy; diagnosis; nervous system; lymph gland; stommach; intestinal tract.
                                                                                                                                                    Gaps
used as research reagents, as positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunoassay agents. Also described is the use of sequences antisense to nucleic acids encoding (I)-(III) to control DP levels in cells, particularly by gene therapy. When formulated with cytotoxic or cytostatic agents, (I)-(III) enhance cell killing.
                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Opitz H;
                                                                                                                      46.2%; Score 42; DB 19; Length 9; 100.0%; Pred. No. 9.3e+05; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                           AAY25475 standard; peptide; 24 AA
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                                                                                                              Query Match
Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-372233/32
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Staendker L;
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oligonuclectides can be used in somatic or non-somatic gene therapy. The peptides, etc., can be used in diagnosis of functional deficiencies in bones, muscles, nervous systems, lymph glands, etcmach/intestinal tracts, immune systems, for diabetes, inflammatory and neoplastic processes and also as a marker for cancer. This sequence represents a specific claimed example of a peptide which can occupy the XI position of the IBP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is an N-terminal fragment from a protein which has a mol. wt. of 15 kD by SDS-PAGE under reducing conditions, strong affinity to cation exchanger and heparin and osteoblast proliferating activity which is reduced after 10 mins. at 70 degrees C, and is lost after after 10 mins. at 90 degrees C. The protein, which was obtd. from the human foetal fibroblast cell inc IMR-90 (ATCC-CC1186), can be used to treat bone reducing diseases, e.g. osteoporosis, and as an antigen for the immunological diagnosis of such diseases.
                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 1.7;
4; Mismatches 6; Indel8
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Ueda M, Washida N, Yamaguchi K, Yano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "undefined"
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Tsuda E,
                                                                                                                                                                                           nvention
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44.0%; Score 40; DB 17; Length 25;

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                                                                                                                                                                            February 17, 2004, 10:50:13; Search time 13.7327 Seconds (without alignments) 58.540 Million cell updates/sec
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Sequence 11,
Sequence 11,
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-308-935-1
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US-09-078-596-13
US-09-308-935-15
US-09-308-935-16
US-09-308-935-17
US-08-894-139-7
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 100
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Match 1
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28 40 44.0 42 6 52582874	Patent No. 5258287 Sequence 9, Appli Patent No. 5258287 Sequence 4216, App Sequence 14, Appl Sequence 13, Appl Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl Sequence 31, Appl Sequence 31, Appl Sequence 17, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 525, Appli		ption factors	ngth 19; Indels 0; Gaps 0;		ption factors
28 29 29 30 31 31 32 33 33 34 34 35 36 36 36 36 36 37 38 39 39 39 39 39 39 39 39 39 39 39 39 39	5258287-4 US-08-664-965E-9 5258287-1 US-09-134-01016-42 US-09-134-01016-42 US-08-194-338-14 US-08-194-338-14 US-08-378-1654-51 US-08-318-14 US-08-318-14 US-08-318-14 US-09-308-318-7 US-08-318-7 US-08-318-7 US-08-318-7 US-08-318-7 US-09-205-258-525 US-09-205-258-525 US-09-205-258-525 US-09-708-732-10-903	ALIGNMENTS	B agonists of DP 09/308,935 /GB97/03506 9626589.7	Score 91; DB 3; Le Pred. No. 7.3e-10; 0; Mismatches 0;	і .	1308935 Las B Antagonists of DP US/09/308,935 PCT/GB97/03506 1-22 GB 9626589.7
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ία ι το Φιτά το	 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		8-935-3 ce 3, Applic No. 626833 No. 626833 No. 626833 ONT. Banda OF INVENTI REFERENCE: REFERENCE: RE APPLICATI RE OF SEQ ID ARE: PATH PRI 19 : PRI RE 19 : PRI RE 19 : PRI RE 19 : PRI RE 19 :	imi '		8-935-1 ce 1, Applic no. 626933 no. 626933 LINCOMATICANT: CANT: Bandal CANT: Bandal OF INVENTICAT NOT APPLICAT NOT PILING D) ER APPLICAT ER PILING D) ER APPLICAT
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ATTORNEY/AGENT INFORMATION
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                                                      FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-308-935-1
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Best Local Similarity 100.0%; Score 91; DB 3; Length 37;
Best Local Similarity 100.0%; Fred. No. 1.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels
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100.0%; Score 91; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 19; Conservative 0; Mismatches 0;
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; Sequence 11, Application US/09078596
; Parent No. 6150116
; Parent No. 6150116
; APPLICANT: La Thangue, Nicholas Barrie
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                                  TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 37
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100.0%; Score 91; DB 3; Length 72
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels
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                                       NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
CITY: Arlington
STRIE: Virginia
COUNTR: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPAT
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Batent No. 6448376

CENERAL INFORMATION:
APPLICANT: BERNARDS, REMAINS B.
APPLICANT: HIJMANS, ELEANORE M.
APPLICANT: HIJMANS, ELEANORE M.
APPLICANT: ALGANS, ELEANORE M.
APPLICANT: ALGANS, ELEANORE M.
APPLICANT: ALGANS ENSENS:
CORRESPONDENCE ADDRESS:
ADDRESSER: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUBER: US/08/894,139 FILING DATE: U13-AUG-1997 CLASSIFICATION: 536
Transcription Factor DP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 25,327
REGISTRATION NUMBER: 25,327
REPRENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-UIN-1995
ATTORNEY/AGENT INFORMATION:
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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OPERATURE SYSTEM: PC-LOUS/MS-LOUS
SOFTWARE: PACEDIA MS-LOUS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILLING DATE: 23-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFREENCE/POCKET UNTORENTION:
TELECHONE: (703) 816-4000
TELECHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO.: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
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APPLICATION NUMBER: US/09/078,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09078596
Patent No. 6150116
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSS:
ADDRESSES: Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.0%; Score 81; DB 2;
100.0%; Pred. No. 3.8e-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.08; ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Patent No. 626834

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lesantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FITE REPRENENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT PILING DATE: 1999-05-27
FARLIER APPLICATION NUMBER: PCT/GB97/03506
FARLIER APPLICATION NUMBER: PCT/GB97/03506
FARLIER APPLICATION NUMBER: 1997-12-20
FARLIER PILING DATE: 1996-12-20
FORTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LINGHH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide
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                                                                                                                                                                                                                                                                                                                                              Length 74;
                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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89.5%; Pred. No. 1.9e-08;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
ATTLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRESSEE: ADDRESSEE: 1100 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                              Score 91; DB 4; I Pred. No. 3.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPRAN: (703) 816-4000
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KESULT 7
US-08-428-131-13
; Sequence 13, Application US/08428131
; Patent No. 5863757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RRRVYDALNVLMAMNIISK 19
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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Matches 17; Conservative
                                                                                                                                                                                 LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-894-139-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-308-935-15
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89.5%; Pred. No. 2.2e-07;
tive 0; Mismatches 2;
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; Pred. No. 3e-06;
0; Mismatches 0
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Sequence 6, Application US/09308935
Patent No. 6268334
                                                                                                                                                                                            JG-09-308-935-5
; Sequence 5, Application US/09308935
; Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              youry match 79.1%; 8 Best Local Similarity 100.0%; Matches 15; Conservative 0;
                                                                                       1 RRRVYDALNVLMAMNIISK 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
    Best Local Similarity 89.5 Matches 17; Conservative
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-308-935-6
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                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/09308935
; Sequence 17, Application US/09308935
; Patent No. 6268334
; GENERAL INFORMATION:
APPLICANT: Bandadara, Lasantha R
; APPLICANT: Bandadara, Lasantha R
; APPLICANT: Bandadara, Lasantha R
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
CURRENT APPLICATION NUMBER: US/09/308,935
; CURRENT PILING DATE: 1999-05-27
EARLIER FILING DATE: 1999-12-22
EARLIER FILING DATE: 1996-12-20
; RARLIER PILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 17
; LENGTH: 19
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Sequence 16, Application US/09308935

Facture 216, Application US/09308935

Patent No. 626834

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/308,935

CURRENT PILING DATE: 1999-05-27

SARLIER APPLICATION NUMBER: GB 9626589.7

EARLIER FILING DATE: 1997-12-22

EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTIN OFF: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide
US-09-308-935-16
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86.8%; Score 79; DB 3; Length 19;
Best Local Similarity 89.5%; Pred. No. 9.9e-08;
Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                  Score 81, DB 3; Length 17;
Pred. No. 3.8e-08;
O: Mismatches 0; Indels
                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RRRVYDALNVLMAMNIISK 19
                                                                                                       Query Match 89.0%; Sct
Best Local Similarity 100.0%; P:
Matches 17; Conservative 0;
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                                                                                                                                                                                        2 RRVYDALNVLMAMNIIS 18
                                                                                                                                                                                                                               1 RRVYDALNVLMAMNIIS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-078-596-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-308-935-17
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84.6%; Score 77; DB 3; Length 19;

Query Match

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APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT FILING DATE: 1999-05-27
EARLIER FILING DATE: 1999-05-27
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1996-12-20
EARLIER FILING DATE: 1996-12-20
SALIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                        APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: PCT/GB97/03506
EARLIER PILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: GB 9626589.7
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
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83.5%; Score 76; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
     Indels
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APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1999-05-27
EARLIER PELING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE 14
CORRESPONDENCE SEQUENCES: 1
ADDRESSE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arington
STRATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGRAT INFORMATION:
REFERENCE/DOCKET NUMBER: 25,327
REFERENCE/OOCKET NUMBER: 25,327
TELEPHONE: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.0%; Score 51; DB 2; Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
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; Sequence 12, Application US/08428131
; Patent No. 5863757
; GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
; TITLE OF INVENTION: Transcription Factor DP-1
; NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 56.0%; Score 51; DB 3; Best Local Similarity 100.0%; Pred. No. 0.01; Matches 11; Conservative 0; Mismatches
Sequence 4, Application US/09308935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 20
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 NVLMAMNIISK 19
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                                                     GENERAL INFORMATION:
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                                                                                     WS-09-308-935-11

WS-09-308-935-11

Sequence 11, Application US/09308935

Patent No. 6268334

GENERAL INFORMATION:

APPLICANT: La Thanque, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

CURRENT PAPLICATION NUMBER: US/09/308,935

CURRENT APPLICATION NUMBER: US/09/308,935

CURRENT APPLICATION NUMBER: US/09/103506

EARLIER PILING DATE: 1999-12-22

EARLIER PILING DATE: 1996-12-22

EARLIER PILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO.11

LENGTH: 14

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: PGT/GB97/03506
EARLIER APPLICATION NUMBER: GB 9626589.7
EARLIER FILING DATE: 1996-12-22
EARLIER FILING DATE: 1996-12-22
SOFTWARE: PAPELON ONS: 18
SOFTWARE: PAPELING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 9
LENGTH: 11
TYPE: PRT

CORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.3%; Score 54; DB 3; Length 11;
100.0%; Pred. No. 0.0014;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 9, Application US/09308935
; Patent No. 6268334
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
1 YDALNVLMAMNIISK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RRVYDALNVLMAMN 15
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Best Local Similarity 100.
Matches 11; Conservative
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US-09-308-935-9
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Pred. No. 0.048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 7, Application US/08894139
sequence 7, Application US/08894139
sequence 7, Application US/08894139
sequence 8
sequence 8
sequence 8
sequence 8
sequence 9
sequence 9
sequence 9
sequence 9
sequence 9
sequence 100 North Glebe 8
sequence 100 North Glebe 8
sequence 8
sequence 100 North Glebe 9
sequence 100 North 
                                                                                                                                        COMPUTE: IN PC Compatible
COMPUTE: IN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REFERENCE/DOCKET NUMBER: 620-22
REFERENCE/DOCKET NUMBER: 620-22
TELEPONE: (703) 816-4100
TELEPONE: (703) 816-4100
TELEPAK: (703) 816-4100
TELEPAK: (703) 816-4100
TELEPAK: (703) 816-4100
TELEPAK: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
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CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 47.4
Matches 9; Conservative
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MOLECULE TYPE: peptide
US-08-894-139-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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US-08-894-139-7
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; Sequence 12, Application US/09078596
; Patent No. 615016;
; Patent No. 615016;
; Fatent No. 615016;
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TORRESPONDENCES: 14
; CORRESPONDENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye
; STREET: 1100 No. 6150116th Glebe Road, 8th Floor
CITY: Arlington
; STATE: 'virginia
; COUWTRY: U.S.A.
; Z1P: 22201-4714
; COMPUTER: Floppy disk
; COMPUTER: IBM PC compatible
; COMPUTER: IBM PC compatible
; COMPUTER: PLOPPY disk
; COMPUTER: PLOPPY disk
; COMPUTER: PLOPPY disk
; COMPUTER: BATCHICH Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/078,596
; RITING NARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.0%; Score 51; DB 3; Length 73; 47.4%; Pred. No. 0.047; tive 5; Mismatches 5; Indels
                                     5; Indels
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             Best Local Similarity 47.4%; Pred. No. 0.04
Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRRVYDALNVLMAMNIISK 19
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7 KRRIYDITNVLEGIQLIAK 25
                                                                                        1 RRRVYDALNVLMAMNIISK 19
                                                                                                                           :||:|| ||| ::|:|
7 KRRIYDITNVLEGIQLIAK 25
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Best Local Similarity 47.4
Matches 9; Conservative
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US-08-894-139-5
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US-09-078-596-12
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Score 50; DB 4; Length 69;
Pred. No. 0.067;
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ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM:

OPERATING SYSTEM:

OPERATION DATA:

APPLICATION NUMBER: US/08/894,139

FLING DATE: 13-40G-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 620-22

TELECOMMUNICATION INFORMATION:

MATHER TOWNEY/AGENT NUMBER: 620-22

TELECOMMUNICATION INFORMATION:

MATHER TOWNEY/AGENT NUMBER: 620-22

TELECOMMUNICATION INFORMATION:

MATHER TOWNEY/AGENT NUMBER: 620-22
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CITY: ARLINGTON
STATE: VEGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRET APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08894139
Patent No. 6448376
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: HIJMANS, RELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
  APPLICANT: BERNARDS, RENE
APPLICANT: HIJMANS, ELEANORE M.
ITILE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1997
13-AUG-1997
13-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RRRVYDALNVIMAMNIISK 19
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TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide US-08-894-139-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                            DB 4; Length 74;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: VINGINIA

CONDUTRY: U.S.A.

ZIP: 22201-4714

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION 1000RATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100

INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                    RESULT 20
US-08-894-139-9
; Sequence 9, Application US/08894139
; Patent No. 6448376
; GENERAL INFORMATION:
; APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                   0.048;
                                                                                                                                                         Query Match 56.0%; Score 51; DB Best Local Similarity 47.4%; Pred. No. 0.04 Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 21
US-08-894-139-8
; Sequence 8, Application US/08894139
; Patent No. 6448376
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                 1 RRRVYDALNVLMAMNIISK 19
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LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                       , MOLECULE TYPE: peptide US-08-894-139-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-894-139-9
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Sequence 14, Application US/08428131

Sequence 14, Application US/08428131

Patent No. S863757

GENERAL INFORMATION:

TITLE OF INVENTION: Transcription Factor DP-1

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon & Vanderhye

STREET: 1100 No. 5863757th Glebe Road, 8th Floor

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk

COMPUTER: 1BM FC compatible

COMPUTER: 1BM FC compatible

CONPUTER: 1BM FC compatible

CONFORTER: 1BM FC compatible

CLASSIFICATION NUMBER: 117-181

TELEPAX: (703) 816-4100

TELEPAX: (703) 816-4100

INPORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino Aride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

8est Local Similarity 47.1%; Pred. No. 0.14;

Matches 8; Conservative 4; Mismatches 5; Indele
                                                                                                                                                                                                                                                                                                                                         DB 4; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                            Score 49; DB 4
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
REFERENCE/DOCKET NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPRAM: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 KRIYDITNVLEGIQLIRK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRRVYDALNVLMAMNIISK 19
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RRIYDITNVLEGIQLIA 17
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-428-131-14
                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-139-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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RESULT 24

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US-09-308-935-2
Sequence 2, Application US/09308935
Sequence No. 626834
Sequence No. 626834
GENERAL INFORMATION:
PAPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha B
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
TITLE OF INVENTION: 1990-18-27
CURRENT FILING DATE: 1999-12-27
EARLIER PILING DATE: 1997-12-22
EARLIER PILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Sequence 14, Application US/09078596

Sequence 14, Application US/09078596

Patent No. 6150106

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 12201-4714
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/078.596
FILING DATE: CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-40N-1995
FILING DATE: 23-40N-1995
FILING DATE: 33-40N-1995
FILING DATE: 33-40N-1995
FILING DATE: 33-40N-1995
FILING DATE: 13-100
TELEPRAK: (703) 816-4100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISICS:
LINGMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISICS:
LINGMATION ADMARIANCE ATHACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 3; Length 17;
Pred. No. 0.14;
4; Mismatches 5; Indels
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ORCANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 48.4%;
Best Local Similarity 47.1%;
Matches 8; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-078-596-14
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TYPE: amino acid
STRANDEDNESS: sir
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Best Local Similarity
Matches 8; Conserv
                                                  JS-08-604 965E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-604-965E-2
                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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5258287-4
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                                                                                              Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Satake, Toshiko
APPLICANT: Morinaga, Tomonori
APPLICANT: Worinaga, Tomonori
APPLICANT: Ucda, Masatsugu
APPLICANT: Higashio, Kanji
TITLE OF INVENTION: Basic Osteoblast Growth FactorII (bOGF-
TITLE OF INVENTION: 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                      Score 42; DB 3; Length 9;
Pred. No. 2.5e+05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 370 Lexington Avenue, Suite 2105
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB:
Pred. No. 1.2;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,965E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burgess, Ryan and Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01270
FILLING DATE: June 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WAYDE, Milton J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 5 1/4 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10017
                                                                                                                                                                                                                                                           Sequence 1, Application US/08604965E
Patent No. 6046033
GENERAL INFORMATION:
                                                      Query Match
Best Local Similarity 100.0%; F
Matches 9; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RRRVYDALNVLMAMNIIS 18
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RREMEDTLNHLKFLNVLS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Wayne, Milton J.
REGISTRATION NUMBER: 17,906
REFERENCE/DOCKET NUMBER: U-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 212-683-8150
                                                                                                                                                                                                                                                                                                                                                                       Kobayashi, Fumie
Yamaguchi, Kyoji
Washida, Naohiro
Satake, Toshiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.48;
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(ano, Kazuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                    Goto, Masaaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 423794
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212-532-4285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                               9 NVLMAMNII 17
                                                                                                                                                                  1 NVLMAMNII 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                        RESULT 26
US-08-604-965E-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-604-965E-1
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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APPLICANT: Ueda, Masatsugu
APPLICANT: Ueda, Masatsugu
APPLICANT: Higashio, Kanji
TITLE ON INVENTION: Basic Osteoblast Growth FactorII(bOGF-
TITLE OF INVENTION: II)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FATERIT NO. 5258287

APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM I.

TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION

FOF INSULIN-LIKE GROWTH PACTOR BINDING PROTEIN BP53

NUMBER OF SEQUENCES: 58

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 40;
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                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Burgess, Ryan and Wayne
STREET: 370 Learington Avenue, Suite 2105
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,965E
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01270
FILING DATE: June 27, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U-Wp-5212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10017
COMPUTER READMBLE FORM:
MEDIUM TYPE: 5 1/4 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                           NEW YORK
: UNITED STATES OF AMERICA
Sequence 2, Application US/08604965E
Patent No. 6046033
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RRRVYDALNVLMAMNIIS 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-683-8150
TELEFAX: 212-532-4285
                                                                                                                               Kobayashi, Fumie
Yamaguchi, Kyoji
Washida, Naohiro
Satake, Toshiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                      Tsuda, Eisuke
Yano, Kazuki
                                                                    Goto, Masaaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 423794
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wayne, Milton J.
REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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MOLECULE TYPE: peptide
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PARENT NO. 5258287
PARENT: BAXTER, ROBERT C.; WOOD, WILLIAM I.
TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION
TITLE OF INVENT FACTOR BINDING PROTEIN BP53
NUMBER OF SEQUENCES: 58
CURRENT APPLICATION DATA:
APPLICATION UNDBER: US/07/171,623
FILING DATE: 22-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 6; Length 60;
Pred. No. 12;
5; Mismatches 6; Indels
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Sequence 455, Application US/09205258
Sequence 455, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,020
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,876
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
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R APPLICATION NUMBER: 60/049,375
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,881
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,880
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EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/048,882
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,899
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,901
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APPLICATION NUMBER: 60/048,896
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9 RKEMEDTLNHLKFLNVLS 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-06-06
                        8 RREMEDTLNHLKFLNVLS 25
1 RRRVYDALNVLMAMNIIS 18
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 38.9%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                     LENGTH: 60
                                                                                                                                                                                                                                                                                                                 SEQ ID NO:1:
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                                                                                                       RESULT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Morinaga, Tomonori
APPLICANT: Ueda, Masatsugu
APPLICANT: Higashio, Kanji
APPLICANT: Higashio, Kanji
TITLE OF INVENTION: Basic Osteoblast Growth FactorII (bOGF-
TITLE OF INVENTION: II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.0%; Score 40; DB 3; Length 85;
44.4%; Pred. No. 5.1;
iive 4; Mismatches 6; Indels
                                                                                                                           44.0%; Score 40; DB 6; Length 42; ilarity 44.4%; Pred. No. 2.2; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Burgees, Ryan and Wayne
F: 370 Lexington Avenue, Suite 2105
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: NEW YORK
STATE: NEW YORK
COUNTX: UNITED STATES OF AMERICA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: 5 1/4 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,965E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JD95/01270
FILING DATE: June 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WAYDE, MILLON J.
REGISTRATION NUMBER: 17,906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U-Wp-5212
        , APPLICATION NUMBER: US/07/171,623
; FILING DATE: 22-MAR-1988
; SEQ ID NO:4:
; LENCTH: 42
                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08604965E
Patent No. 6046033
GENERAL INFORMATION
APPLICANT: Teuda, Eisuke
                                                                                                                                                                                                                                              | | : | | | : | ::|
9 RREMEDTLNHLKFLNVLS 26
                                                                                                                                                                                                                        1 RRRVYDALNVLMAMNIIS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: U
TELECOMMUNICATION INFORMATION
TELEPHONE: 212-683-4150
TELEPAX: 212-532-4285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamaguchi, Kyoji
Washida, Naohiro
Satake, Toshiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kobayashı, Fumie
                                                                                                                                                                                                                                                                                                                                                                                                                               Goto, Masaaki
Tsuda, Eisuke
Yano, Kazuki
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Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 423794
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burgess, F
                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-604-965E-9
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                      US-08-604-965E-9
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Pred. No. 42;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                             Length 67;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ele PC Compatible
COMPUTER: Ele PC Compatible
CORRANG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR.1991
ATTORNEY/AGENT INFORMATION:
NAME: 18 TREALS.
REGISTRATION NUMBER: 29,655
REFRENCE/DOCKET NUMBER: NHI01.001DV1
TELECOMMUTCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Knobbe, Martens, olson and Bear
620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                               Score 35; DB 4;
Pred. No. 30;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                          TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08194338
Patent No. 5474898
GENERAL INFORMATION:
                  PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60,
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4216
LENGTH: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.4%;
60.0%;
                                                                                                                                                                                                                                                                               38.5%;
                                                                                                                                                                                                                                                                                                                                                                                     4 VYDALNVLMAMNIIS 18
                                                                                                                                                                                                                                                                                                                                                                                                                  11 LYSKLNILMSIIILN 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.0%
Matches '6; Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 amino acida
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 NVLMAMNIIS 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-08-194-338-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION WUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION WUMBER: 60/048,997
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER APPLICATION NUMBER: 60/048,997
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER PELLING DATE: 1997-06-06
EARLIER PELLING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,977
EARLIER APPLICATION NUMBER: 60/048,977
EARLIER APPLICATION NUMBER: 60/048,977
EARLIER PELLING DATE: 1997-06-06
EARLIER PELLING DATE: 1997-06-06
EARLIER FILING DATE: 1997-01-18
EARLIER FILING DATE: 1997-01-18
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-130
NUMBER OF SEQ ID NOS: 1227
                                     EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER APPLICATION NUMBER: 60/048,916
                     APPLICATION NUMBER: 60/048,892
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,915
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/048,916
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                  LING DATE: 1997-06-06
PPLICATION NUMBER: 60/049,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILING DATE: 1997-06-06
PPLICATION NUMBER: 60/048,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILING DATE: 1997-06-06
PPLICATION NUMBER: 60/048,949
                                                                                                                                                                                                                                                                                                                                                                                  PLICATION NUMBER: 60/048,875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RVYDALNVLMAMNIISK 19
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Best Local Similarity 41...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-205-258-455
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US-09-134-001C-4216
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EARLIER I
EARLIER I
EARLIER I
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APPLICANT: Hodgen, John
APPLICANT: Knowles, David
APPLICANT: Lonetco, Michael
APPLICANT: Lonetco, Michael
APPLICANT: Pratt, Julie
APPLICANT: Reichard, Richard
APPLICANT: Rescherd, Martin
APPLICANT: Ward, Judith
TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
TITLE OF INVENTION: No. 6348582el Richard
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CONTY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 56.2%; Pred. No. 62;
Matches 9; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTRY: FA

COMPUTRY: USA

ZIP: 19406-0939

COMPUTRY: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-196
ATTORNEY/AGENT INFORMATION:
NAME: GIOMAT. EAWART
REGERRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELLEPHONE: 610-270-4478
TELLEPHONE: 610-270-4478
TELLEPHONE: 610-270-4978
TELLEPHONE: 610-270-690
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; Sequence 30, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
RESULT 34
8.08-936-165A-513
; Sequence 513, Application US/08936165A
; Patent No. 6348582
                                                                                                                                   Burnham, Martin
Hodgson, John
Knowles, David
Lonetto, Michael
Nicholas, Richard
Pratt, Julie
Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||| |||::|||
48 MYDAKMDNVLVPINII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 UYDAL--NVLMAMNII 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                               Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: siz
                                                                               GENERAL INFORMATION:
APPLICANT: Black.
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                                                                                                                                          APPLICANT
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RIBOSOME-INACTIVATING PROTEINS, INACTIVE PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF USING
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC comparitible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.2%; Score 32; DB 55.6%; Pred. No. 31; tive 3; Mismatches
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Sequence 30, Application US/08485.

Patent No. 5646026

Patent No. 5646026

APPLICANT: WALSH, TERENCE A APPLICANT: HEY, TIMOTHY D APPLICANT: HEY, TIMOTHY D APPLICANT: MORGAN, ALICE ER TITLE OF INVENTION: PRECURSOR FOITTLE OF INVENTION: DELMORANCE ADDRESSE: ADDRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSILLATION: 13-15
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGIGSTRATION NUMBER: 38-21
REFERENCE/DOCKET NUMBER: 38-7
RELEGOMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ||:||:
11 KTYDSLNVI 19
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R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,020
RR FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
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R FILING DATE: 1997-06-06
R R PLLING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,884
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,894
R FILING DATE: 1997-06-06
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ER APPLICATION NUMBER: 60/048,893
ER APPLICATION NUMBER: 60/048,900
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,901
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,901
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,915
ER FILING DATE: 1997-06-06
ER PELING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,962
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,963
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,916
FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-06-06
APPLICATION WOMBER: 60/048,882
ELING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/049,373
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APPLICATION NUMBER: 60/048,883
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APPLICATION NUMBER: 60/048,897
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EARLIER APPLICATION NUMBER: 60/048,898
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
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EARLIER 1
EARLIER 1
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EARLIER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.2%; Score 32; DB 1; Length 25; 55.6%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
NUMBER OF SEQUENCES: 49
CURRENT APPLICATION ADJAN:
APPLICATION NUMBER: US/07/535,636
FILING DATE: 11-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5248606
; APPLICANT: WALSH, TERENCE A.;HEY, TIMOTHY D.;MORGAN,
;ALICE B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPPLICATT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REPERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205, 258
CURRENT FILING DATE: 1998-12-04
EARLIER PILING DATE: 1998-06-04
EARLIER PILING DATE: 1998-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
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3; Mismatches
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                  NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33621
REFERENCE/DOCKET NUMBER: 3827;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 55.6
Matches 5; Conservative
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11 KTYDSLNVI 19
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11 KTYDSLNVI 19
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Best Local Similarity
Matches 5; Conservat
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US-09-205-258-812
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Sequence 8, Application US/09217293

Sequence 8, Application US/09217293

Sequence 8, Application US/09217293

GENERAL INFORMATION:
APPLICANT Stewart, Jeffrey J
TITLE OF INVENTION: QUASISPECIES
TITLE OF INVENTION: QUASISPECIES
FILE REFERENCE: Stewart 1
CURRENT APPLICATION NUMBER: US/09/217,293

CURRENT FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LINGTH: 43
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CTHER INFORMATION: Xaa5 is SN
CTHER INFORMATION: Capital letters indicate advantageous variants and
CTHER INFORMATION: Lowercase letters indicate possibly advantageous;
CTHER INFORMATION: variants (see detailed description)
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34.1%; Score 31; DB 4; Length 43;
Best Local Similarity 63.6%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 3; Length 22;
Pred. No. 40;
3; Mismatches 4; Indel8
CORRESPONDENCE ADDRESS:
ADDRESSER: Burgess, Ryan and Wayne
STREET: 370 Lexington Avenue, Suite 2105
CITY: NEW YORK
                                                                                CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.1%;
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 DALNVLMAMNIIS 18
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22
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Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 41
US-09-217-293-8
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                                                      LOCATION: (16)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
                                                                                                                                         ; LOCATION: (38)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-812
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                           Gaps
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APPLICANT: Washida, Nachiro
APPLICANT: Sataka, Toshiko
APPLICANT: Gataka, Toshiko
APPLICANT: Ocda, Masatsugu
APPLICANT: Ucda, Masatsugu
APPLICANT: Higashio, Kanji
TITLE OF INVENTION: 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.1%; Score 31; DB 3; Length 7; 100.0%; Pred. No. 2.5e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                         Score 32; DB 4; Length 97;
Pred. No. 1.6e+02;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08604965E
Patent No. 6046033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goto, Masaaki
Tsuda, Eisuke
Yano, Kazuki
Kobasehi, Fumie
Yamaguchi, Kyoji
Washida, Nachiro
Satake, Toshiko
Morinaga, Tomonori
Ueda, Masatsugu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                 Query Match 35.2%;
Best Local Similarity 38.5%;
Matches 5; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
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66 YDAIAVFLCIHIV 78
                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ALNVLMA 13
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APPLICANT: Goto, 1
                                               FEATURE:
NAME/KEY: SITE
LOCATION: (16)
                                                                                                                          NAME/KEY: SITE
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US-08-604-965E-7
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R APPLICATION NUMBER: 60/048,881
R FILING DATE: 1997-06-06
R R FILING DATE: 1997-06-06
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R R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
PILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,875
FILING DATE: 1997-06-06
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APPLICATION WUMBER: 60/048,974
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,883
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/048,895
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
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APPLICATION NUMBER: 60/048,882
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,972
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APPLICATION NUMBER: 60/048,916
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,917
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APPLICATION NUMBER: 60/048,949
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APPLICATION NUMBER: 60/048,962
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EARLIER FILING DATE: 1997-12-18
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APPLICATION NUMBER: 60/048,893
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APPLICATION NUMBER: 60/048,901
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APPLICATION NUMBER: 60/
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FILING DATE: 1997-06-06
                         PLICATION NUMBER: 60/
LING DATE: 1997-06-06
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                                                                                                                                                                                                                                        Sequence 7, Application US/08740644
Patent No. 6033877
BARENT NO. 6033877
APPLICANT: Timothy F. Murphy
APPLICANT: Kyungcheol Yi
TITLE OF INVENTION: Peptide Expression And Delivery System
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOGGRON, Russ, Andrews, Woods & Goodyear
STREET: 1800 One MET Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: BUFFED: CITY: BLIFED: STATE: New York
COUNTRY: United States
ZIP: 14.003-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM Compatible
COMPUTER: IBM COMP
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REPERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,644
FILING DATE: October 31, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,168
FILING DATE: No. 6033877ember 2, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REGISTRATION NUMBER: 11520.0065
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (116, 856-4000
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; Sequence 525, Application US/09205258
; Datent No. 6525174
; GENERAL INFORMATION:
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50.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                             YDALNVLMAMN 15
                                                                                       8 YPALNVTMPNN 18
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7 YDANNIIVAI 16
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Best Local Similarity
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US-08-740-644-7
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60/048,900

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Sequence 903, Application US/09732210

Patent No. 6573361

GENERAL INFORMATION:

APPLICANT: Bunkers, Greg J.

APPLICANT: Liang, Jihong

APPLICANT: Mittanck, Cindy A.

APPLICANT: Mittanck, Cindy A.

APPLICANT: Wit Younie S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use

FILE REPRENCE: 38-21(15036) B.

FILE REPRENCE: 38-21(15036) B.

CURRENT FILING DATE: 1999-12-07

PRIOR PPLICATION NUMBER: US 60/169,513

PRIOR FILING DATE: 1999-12-07

PRIOR APPLICATION NUMBER: US 60/169,340

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 1753

SEQ ID NO 903

LENGTH: 56

TURNERS DATE: 1999-12-07

SEQ ID NO 903
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                                                                                                                                                                                                                           Query Match

34.1%; Score 31; DB 4; Length 49;
Best Local Similarity 37.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 8; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 525
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                                                                                                                                                                                                                                                                                                             4 VYDALNVLMAMNIISK 19
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15 RRSHDALTAVTSLSV 29
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; ORGANISM: Escherichia coli
US-09-732-210-903
                                                                                                                                         LENGTH: 49
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                 US-09-205-258-525
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COMPUTER: PC
COMPUTER: PC
CORPATING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
PLICATION NUMBER: 60/085,598
FILING DATE: 10 Joun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 10 July 2, 1997
ATTORING DATE: 11 July 2, 1997
ATTORING DATE: 10 July 2, 1997
ATTORING DATE: 10 July 2, 1997
ATTORING DATE: 14 MNY 1998
REFERENCE/DOCKET NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 60/012
TELEPHONE (781) 893-807
TELEPHONE (781) 897-807
TELEPHONE (781) 897-8
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RESULT 34 AAR87181

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Mammalian, reproductive-specific protein; male infertility;
spermatogenesis; sperm count disorder; anti infertility; reproduction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel 15 kD protein with osteoblast proliferating activity - useful in treatment and diagnosis of bone reducing diseases such as
                                                                                                                                                           Osteoblast proliferating protein; human; foetal fibroblast; cell line IMR-90; ATCC-CCL186; treatment; bone reducing disease; osteoporosis; antigen; immunological diagnosis.
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Ueda M, Washida N, Yamaguchi K, Yano K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.0%; Score 40;
44.4%; Pred. No.
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                    AAR87182 standard; Protein; 85 AA.
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                                                                                                                           Osteoblast proliferating protein.
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis
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                                                                                          23-AUG-1996
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Tsuda E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                     AAR87182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 36
AAU07882
   AAR87182
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                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is an N-terminal fragment from a protein which has a mol. wt. of 15 kD by SDS-PAGE under reducing conditions, strong affinity to cation exchanger and heparin and osteoblast proliferating activity which is reduced after 10 mins. at 70 degrees C, and is lost after after 10 mins. at 90 degrees C. The protein, which was obtd. from the human foetal fibroblast cell line IMR-90 (ATCC-CCL186), can be used to treat bone reducing diseases, e.g. osteoporosis, and as an antigen for the immunological diagnosis of such diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful
                                                                                                                                                                                                                                                                                                                      Osteoblast proliferating protein; human; foetal fibroblast; cell line IMR-90; ATCC-CCL186; treatment; bone reducing disease; osteoporosis; antigen; immunological diagnosis; N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel 15 kD protein with osteoblast proliferating activity - in treatment and diagnosis of bone reducing diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Satake T;
K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.0%; Score 40; DB 17; Length 40; 44.4%; Pred. No. 3.3;
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                    6; Indels
                                                                                                                                                                                                                                                                                       Osteoblast proliferating protein N-terminal fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Higashio K, Kobayashi F, Morinaga T,
Ueda M, Washida N, Yamaguchi K, Yano
   Pred. No. 1.8;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "undefined"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "undefined"
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                                                                                                                                                                                 AAR87181 standard; Peptide; 40
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RREMEDTLNHLKFLNVLS 25
                                                       18
 44.48;
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RREMEDTLNHLKFLNVLS
                                                       1 RRRVYDALNVLMAMNIIS
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                                                                                                                                                                                                                                                    (first entry)
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                    Conservative
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les 8; Conserv
Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoporosis
                                                                                                                                                                                                                                                    23-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9600240-A1
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Tsuda E,
                                                                                                                                                                                                                  AAR87181;
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Best Loc Matches

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20-NOV-2001; 2001WO-US45177.

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The present invention relates to the isolation of novel mammalian and human reproductive-specific proteins (AAU07859-AAU07899), and the nucleic acids encoding them. The nucleic acids encoding infertility required encoding them. The nucleic acids encoding infertility which is a result of reduced sperm count, reduced sperm motility, which is a result of reduced sperm count, reduced sperm motility, which is a result of reduced sperm count, reduced sperm motility, and for capermaces of the invention are useful as markers for spermatcognial cells, for identifying genes or proteins characteristic of male infertility, diagnosing or aiding in proteins of infertility in men, and for contraception in which the diagnosis of infertility in men, and for contraception in which sperm the production or sperm count is reduced or defective sperm is contracted. Antibodies to reproductive-specific proteins are useful for dense in particular cell type or particular developmental stage, for setulates of spermatogenesis, and for immunofluorescence of germ cells or in Western blots for assessing the presence of the protein the antibody binds. The sequences of the invention are also useful in gene therapy. AAU07889 Tepresent the mammalian reproduction-specific proteins of the present invention.
                                                                                                                                                                                                                                                   Novel reproduction-specific protein, useful for treating disorders of reduced sperm count, enhancing/increasing sperm count and/or sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; prostate specific protein; cytostatic; PSP; prostate cancer; gene therapy; vaccine; non-cancerous prostatic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate specific protein DEX0283_180.
                                                                                                                                  (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG66872 standard; Protein; 48 AA.
                                                                                                                                                                                                                                                                                                                           claim 22; Fig 48; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RRVYDALNVLMAMNI 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 RKYYSVLNVAFACNI 44
                                              07-MAR-2001; 2001WO-US07371
                                                                                 07-MAR-2000; 2000US-0187518.
12-JAN-2001; 2001US-0261557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 53.3
Matches 8, Conservative
                                                                                                                                                                                                      WPI; 2001-570774/64.
N-PSDB; AAS13646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 AA;
                                                                                                                                                                         Wang PJ, Page DC;
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              13-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                 reduced s
activity
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The invention relates to an isolated polypeptide that comprises a sequence with 60 % sequences identity to one of 103 prostate specific corporates properly one of 104 prostate specific concoded by a mucleic acid comprising one of 114 prostate specific nucleic corcoded by a mucleic acid comprising one of 114 prostate specific nucleic acid (PSNA) sequences (S2), given in specification. Also included are a vector comprising the PSNA, a host cell comprising the vector.

The sequences of sequences (S2), given in specification. Also included are a vector comprising the PSNA, a host cell comprising a with vector of the PSP or the PSNA, in a sample of a patient cancer or presence of cancer in a patient, comprising a with for an avaccine comprising the PSP or the PSNA, The PSNA is useful for an avaccine comprising the PSP or the PSNA, The PSNA is useful for determining the presence of a prostate specific nucleic acid (PSNA) in a sample. The antibody to the PSP or the PSNA, The PSNA is also useful for a prostate specific protein in a sample. The antibody is also useful for arbibody induces an immune response against the prostate cancer cell antibody induces an immune response against the prostate cancer cell cut and onlecule or polypeptide. The PSP or the PSNA is useful for expressing the nucleic acid monicoring the presence and metastases of prostate cancer in a patient. The PSP is useful as a vaccine component of a liciting a humoral and entagnist. The PSNA is useful for cellular immune response, and for producing transgenic animals and cells, and for producing engineered producing transgenic animals and cells, and for producing prostate cancer by detecting generic lessues of prostate cancer. By detecting generic lessues of the PSNA are useful for detecting of identifying prostate tissue, and thus is useful in for identifying. Event and the antibody are useful for identifying prostate tissue, and the space of the PSNA are also useful in tenser cancer. The PSNA is useful in for identifying prostate cancer in a patient a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing, monitoring, staging, imaging and treating prostate cancer and non-cancerous disease states in prostate tissue. The present sequence is a prostate specific protein (PSP) sequence.
                                                                                                                                                                                                         New prostate specific polypeptides useful for identifying, diagnosing, monitoring, staging, imaging and treating prostate cancer and non-cancerous disease states in prostate
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                                                                                                                            Liu C;
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                                                                                                                            Sun Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38;
Pred. No.
                                                                                                                            Recipon H,
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                                                                                                                                                                                                                                                                                                               Claim 11; Page 233; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RRVYDALNVLMAMNIISK 19
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15 RRIYSALSLYISVVLSSK 32
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                                      21-NOV-2000; 2000US-252189P
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                                                                                                                                 Salceda S, Macina RA,
                                                                                      (DIAD-) DIADEXUS INC
                                                                                                                                                                            WPI; 2002-500278/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 AA;
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42.9%; Score 39; DB 22; Length 80; 53.3%; Pred. No. 12; cive 1; Mismatches 6; Indels

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29-58P-2000;
29-58P-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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                sigmoid disease; antibacterial; antiviral; antiinflammatory;
cytostatic.
                                                                                                                                                                       17-JAN-2001; 2001WO-US01240
                                                                                                   WO200155302-A2
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02-MAR-2000; 2
16-MAR-2000; 2
17-MAR-2000; 2
18-APR-2000; 2
19-MAY-2000; 2
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
                                                                Homo sapiens
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21-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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22-AUG-2000;
23-AUG-2000;
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07-JUN-2000; 2000US-0209467.
28-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-021647.
07-JUL-2000; 2000US-0216647.
11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217487.
26-JUL-2000; 2000US-0220963.
26-JUL-2000; 2000US-0220964.
14-AUG-2000; 2000US-0220964.
14-AUG-2000; 2000US-0220964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             000US-0229345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                     30-AUG-2000;
    The present invention relates to the isolation of novel human colon associated polypeptides, and the cDNA (AAS19348-AAS19581) and genomic sequences encoding for them. The sequences of the invention are useful in the diagnosis. Colon cancer, congenital abnormalities of the colon including colon cancer, congenital abnormalities of the colon including colon cancer, congenital abnormalities of the colon including colon cancer, congenital abnormalities inflammatory bowel disease (IBD), neoplastic cell disorders inflammatory bowel disease (IBD), neoplastic cell disorders, colonic inflammation, diarrhoes and dysentery, malabsorption syndromes colonic inflammation, diarrhoes and dysentery, malabsorption syndromes colonic inflammation, diarrhoes and dysentery, malabsorption syndromes colonic inflammation, represent the invention can also be used in gene the polymucleocides sequences of the invention can also be used in gene therapy. AAU22468-AAU22701 represent the novel human colon associated color properties of the invention. The sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not form part of the printed Security from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; digestive system antigen; gene therapy; cancer; appendicitis;
ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
digestive system disorder; Meckel's diverticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                      Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon including colon cancers and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.8%; Score 38; DB 22; Length 63; 56.2%; Pred. No. 14; tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human digestive system antigen SEQ ID NO: 1879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                    Claim 11; SEQ ID No 344; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM92530 standard; Protein; 63 AA.
                                                                      Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0186350.
2000US-0189874...
2000US-0190076.
2000US-0198123.
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2000US-0184664.
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                                           (HUMA-) HUMAN GENOME SCI INC.
              05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001 (first entry)
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Best Local Similarity 56.2
Matches 9; Conservative
                                                                      Barash SC,
                                                                                                     WPI; 2001-465567/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AA;
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                                                                                                                   N-PSDB; AAS39447
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18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM92530;
                                                                           Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 39
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infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a digestive system antigen of the invention.

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Gaps

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6; Indels

1; Mismatches

4 VYDALNVLMAMNIISK 19

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9; Conservative

Query Match Best Local Similarity Matches 9; Conserv

63 AA;

Sequence

8 X C/C C

8 VYFLLNFLMLKNLIFK

AAR56646 standard; peptide; 24 AA.

RESULT 40 AAR56646

41.8%; Score 38; 56.2%; Pred. No.

DB 22; Length 63 14;

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Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                     20-OCT-2000; 2000US-02411787.
20-OCT-2000; 2000US-0241808.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
01-NOV-2000; 2000US-0244617.
08-NOV-2000; 2000US-0246474.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246527.
                                                                                                                                                                                                                                                08-NOY-2000; 2000US-0246610.
08-NOY-2000; 2000US-0246611.
08-NOY-2000; 2000US-0246611.
17-NOY-2000; 2000US-0249207.
17-NOY-2000; 2000US-0249209.
17-NOY-2000; 2000US-0249210.
17-NOY-2000; 2000US-0249211.
17-NOY-2000; 2000US-024924.
17-NOY-2000; 2000US-024924.
17-NOY-2000; 2000US-024924.
17-NOY-2000; 2000US-0249265.
17-NOY-2000; 2000US-0249297.
17-NOY-2000; 2000US-0249297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2000; 2000US-0251479
08-DEC-2000; 2000US-0251856
08-DEC-2000; 2000US-0251868
08-DEC-2000; 2000US-0251869
08-DEC-2000; 2000US-0251969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-502630/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAK88303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-DEC-2000;
05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          This TAM mimic may be used to treat or prevent conditions associated with immune responses and inflammation, e.g. arthritis, systemic lupus erthyematosus, asthma, inflammatory bowel disease, allergies, allografic rejection, etc. This peptide probably prevents natural activation of target proteins so inhibit signal transduction. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                Sundaramoorthi R, Dalgarno DC, Zydowsky LD;
                                                                                                                                                                                                                                                                                                                                                                                New tyrosine activation motif analogues - for treating and preventing immune and inflammatory disorders, e.g. allergies, by inhibiting activation of mast cells, lymphocytes, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                        Tyrosine activation motif mimic; arthritis; asthma; allergy; systemic lupus erythematosus; inflammatory bowe; disease; allograft rejection; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                  Tyrosine activation motif mimic Fc-epsilon-RI-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 75; 94pp; English.
                                                                                                                                                                                                                                 94WO-US01025.
                                                                                                                                                                                                                                                           93US-0013414.
                                       (first entry)
                                                                                                                                                                                                                                                                                       (ARIA-) ARIAD PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 RVYDALNVLMA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [||: ||: | |
RVYEELNILSA 13
                          (updated)
                                                                                                                                                                                                                                                                                                                Weigele M, Tao G,
Green J, Green OM;
                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-264027/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 AA;
                                                                                                                                                                             WO9417095-A1.
                                                                                                                                                                                                                                28-JAN-1994;
                                                                                                                                                                                                                                                           29-JAN-1993;
                       25-MAR-2003
23-MAR-1995
                                                                                                                                                                                                        04-AUG-1994.
                                                                                                                                                  Synthetic.
AAR56646;
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Matches
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RESULT 41

The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic

Claim 11; SEQ ID NO 1879; 986pp; English.

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2000US-0246524.
2000US-0246525.
2000US-0246526.
2000US-0246528.
2000US-0246528.
2000US-0246610.
2000US-0246610.
2000US-0246610.
2000US-0246610.
2000US-0249209.
2000US-0249209.
2000US-0249209.
2000US-0249210.
2000US-0249211.
2000US-0249212.
2000US-0249212.
2000US-0249213.
2000US-0249214.
2000US-0249214.
2000US-0249216.
2000US-0249216.
2000US-0249216.
2000US-0249216.
2000US-0249218.
2000US-0249218.
2000US-0249218.
2000US-0249218.
2000US-0249218.
2000US-0249218.
2000US-0249218.
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2000US-0246478.
2000US-0246523.
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2000US-0251030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0241221.
2000US-0241785.
2000US-0241786.
2000US-0241786.
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
                                                                                                                                                                                        Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                          Human immune/haematopoietic antigen SEQ ID NO:16955
AAM89362

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AAM89362;

XX

AAM89362;

XX

XX

AHUMAN immune/haematopoietic antigen by the man immune/haematopoietic; immun cytostatic; gene therapy; vaccine; max cytostatic; gene therapy; vaccine; gene therapy; gene therapy; vaccine; gene therapy; gene therapy; gene therapy; gene therapy; vaccine; gene therapy; gene therapy; gene therapy; gene therapy; gene therapy; gene therapy; gene therapy; gene therapy; gene thera
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Penn SG, Hanzel DK,
                                                                                                                                                                                                      and arteriosclerosis
                                                                                                                                                               WPI; 1998-240020/21
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
               WO9814474-A1.
                                                               26-SEP-1997;
                                                                                        30-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000;
                                                                                                                                       Mizukami T,
                                  09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG56095;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 43
     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                            amino acid sequences given in AAM819217 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting polynucleotides may be used to produce the secreted (I), by inserting colorin. (I) proteins and polynucleotides may be used to produce the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metasteses of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK349421 to AAK87690 and AAM82169 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK349421 to AAK87690 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                    AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 16955; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E2F activity; inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 22; Length 87; Pred. No. 33; 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2F activity inhibiting compound Ia-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ż
                                                                                                                                                                Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW57050 standard; peptide; 15
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0256719.
06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
11-DEC-2000; 2000US-0251990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.7%;
53.3%;
                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                              2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                Barash SC,
                                                                                                                                                                                       2001-483426/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 AA;
                                                                                                                                                                                      WPI; 2001-483426/
N-PSDB; AAK62143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                              05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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  a
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This represents a compound that can inhibit E2F activity. The compound alkanoyl, aloyl, hetero-arylcarbonyl, alkoycarbonyl, aryloxycarbonyl, hetero-arylcarbonyl, alkoycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2P activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                          E2F activity inhibitors - for treatment and prevention of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, liver, cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.6%; Score 36; DB 19; Length 15; 60.0%; Pred. No. 5.4; ive 2; Mismatches 2; Indels
                                                                                                                                                                                 Yoshida T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                                                                                                                                 Yamasaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human liver peptide, SEQ ID No 34743.
                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 26; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG56095 standard; Peptide; 41 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK
97WO-JP03442.
                                                            96JP-0259432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-2003 (first entry)
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                                                                                                                                                                                 Shibata K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||:|| ||
KRRIYDITNV 15
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ABB24904
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                                                                                                                                                                                                                                                                  Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
             Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver
                                                                                                                                                             ö
                                                                                                                                                                                                                                                      Peptide #8153 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID NO 33282; 639pp + sequence listing; English.
                                                                                                                                                39.6%; Score 36; DB 22; Length 41; 53.3%; Pred. No. 19;
                                                                                                                                                             Indels
                                                                                                                                                              5.
                                                                                                                                                              2; Mismatches
                                Claim 27; SEQ ID No 34743; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                            Rank DR
                                                                                                                                                                                                                      ABB40647 standard; Peptide; 41 AA.
                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                                  2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00669
                                                                                                                                                                          2 RRVYDALNVLMAMNI 16
                                                                                                                                                                                      22 REYQDLLNVKMALDI 36
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                              Query Match
Best Local Similarity 53.3.
Best Local 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483447/52
   WPI; 2001-488898/53
                                                                                                                                       41 AA;
                                                                                                                                                                                                                                                                                              WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                              04-FEB-2002
                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                                   ABB40647;
                                                                                                                                         Sequence
                                                                                                                                                                                                           RESULT 44
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA1155-ABA41305). The present sequence is a protesin encoded by one such probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, human heart sate useful for predicting, human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein #6903 encoded by probe for measuring heart cell gene expression.
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measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                     Score 36; DB 22; Length 41;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W, Rank DR;
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0532366.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                         39.6%;
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Query Match
Best Local Similarity 53.3
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                          41 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB24904;
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Query Match 39.6%; Score 36; DB 22; Length 41; Best Local Similarity 53.3%; Pred. No. 19; Matches 8; Conservative 2; Mismatches 5; Indels
                     Sequence 41 AA;
X S
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0; Gaps

Search completed: February 17, 2004, 10:53:41 Job time : 37.1188 secs

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February 17, 2004, 10:53:48; Search time 27.8416 Seconds (without alignments) 142.889 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.ppp:*
(cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.ppp:*
(cgn2_6/ptodata/1/pubpaa/PCTUBW_PUB.ppp:*
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(cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            801455 seqs, 209382283 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRRVYDALNVLMAMNIISK 19
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                               US-09-900-147-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 100
                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                      OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 3, Appli	Sequence 1, Appli	Sequence 10, Appl	Sequence 15, Appl	Sequence 17, Appl	Sequence 16, Appl	'n	Sequence 6, Appli	1	Sequence 45697, A	Sequence 9, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 7, Appli	Sequence 9, Appli
		ជា	US-09-900-147-3	US-09-900-147-1	US-10-214-188-10	US-09-900-147-15	US-09-900-147-17	US-09-900-147-16	US-09-900-147-5	US-09-900-147-6	US-09-900-147-11	US-09-864-761-45697	US-09-900-147-9	US-09-900-147-4	US-10-214-188-5	US-10-214-188-7	US-10-214-188-9
		DB	10	10	15	10	10	10	10	10	10	σ	10	10	15	15	12
		Match Length DB	19	37	74	19	19	19	16	30	14	96	11	20	74	74	75
æ	Query	Match	100.0	100.0	100.0	91.2	86.8	84.6	83.5	79.1	75.8	63.7	59.3	56.0	26.0	56.0	56.0
		Score	16	91	91	83	79	77	9/	72	69	28	54	51	51	51	51
	Result	No.	н	7	æ	4	ហ	9	7	80	đ	10	11	12	13	14	15

Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 8, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 180, Appli Sequence 180, Appli Sequence 180, Appli Sequence 180, Appli Sequence 455, Appli Sequence 455, Appli Sequence 455, Appli Sequence 455, Appli Sequence 886, Appli Sequence 2941, Appli	148 4326 513, 10, 197 197 197 2,
US-10-029-386-29071 US-09-932-581-5 US-10-165-614-2 US-10-165-614-2 US-10-214-188-8 US-10-38-294-6 US-10-38-294-6 US-10-38-294-6 US-10-214-188-6 US-10-214-188-6 US-10-214-188-6 US-10-001-870-180 US-09-900-147-2 US-09-901-147-2	
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1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 W W W 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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Sequence 3, Application US/09900147

Sequence 3, Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

CURRENT FILING DATE: 201-07-09

PRIOR PLILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR PLILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR PLILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTION NUMBER: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTIANG DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTIANG DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTIANG DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTIANG DATE: 1996-12-20

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SOFTWARE: PATENTIANG DATE: 1996-12-20

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SOFTWARE: PATENTIANG DATE: 1996-12-20

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NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTIANG DATE: 1996-12-20

SOFTWARE: PATENTIANG DATE: 1996-12-20

SOFTWARE: PATENTIANG DATE: PATENTIANG DATE: 1996-12-20

SOFTWARE: PATENTIANG DATE: PATENTIANG DATE: 1999-05-27

SOFTWARE: PATENTIANG DATE: PATENTIANG DATE: 1996-12-20

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RESULT 2 US-09-900-147-1 'Sequence 1, Application US/09900147 'Patent No. US20020103121A1 ô

Gaps

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Indels

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Score 91; DB 15;
Pred. No. 2.8e-08;
                                                                 Query Match 100.0%; Score 91; DB Best Local Similarity 100.0%; Pred. No. 2.8 Matches 19; Conservative 0; Mismatches
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRRVYDALNVLMAMNIISK 19
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                                                                                                                                                                  1 RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                               46 RRRVYDALNVLMAMNIISK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
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ORGANISM: Artificial Sequence
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US-10-214-188-10
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                 APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Lasantha R
TITLE OF INVENTION Peptide antagonists of DP transcription factors
TITLE OF INVENTION PRESSERVE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR APPLICATION NUMBER: EARLIER PRILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: EARLIER PRILING DATE: 1996-12-20
WUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTING DATE: 1996-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-900-147-1
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPUTER: BATENTIN Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-AMG-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INPERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-10-214-188-10
US-10-214-188-10
Sequence 10. Application US/10214188
Sequence 10. Application No. US20030022260A1
GENERAL INFORMATION:
HITMORY THANGE, NICHOLAS B.
HITMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 91, DB 10; Best Local Similarity 100.0%; Pred. No. 1.3e-08; Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WILSON, MARY J.
REGIGERATION UNDBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703) 816-4100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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LENGTH: 37
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US-09-900-147-17

Sequence 17. Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:
APPLICANT: La Thanque, Nicholas B
APPLICANT: La Thanque, Nicholas B
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: BARLIER FILING DATE: 1999-05-27

PRIOR APPLICATION NUMBER: EARLIER PLICATION NUMBER: GB 9626589.7

PRIOR SPURG FILING DATE: BARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTIN VEY: 2.1

SEQ ID NO 17

FENNOW: 10 PRIOR PLING DATE: 1096-12-20
Sequence 15, Application US/09900147
; Sequence 15, Application US/09900147
; Parent No. US20020103121A1
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas B
; APPLICANT: La Thangue, Nicholas B
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; CURRENT APPLICATION NUMBER: US/09/900,147
; CURRENT FILING DATE: ARLIER APPLICATION NUMBER: 09/308,935
; PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: FALLIER PILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 15
; LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide
US-09-900-147-15
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Pred. No. 1.5e-07;
0; Mismatches 2; Indels
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Pred. No. 7.1e-07;
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Best Local Similarity
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; Sequence 45697, Application US/09864761
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                                                                       IS-09-900-147-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT PILING DATE: 2001-07-09
FRIOR PRILING DATE: EARLIER PELING DATE: 1999-05-27
FRIOR PELING DATE: EARLIER FILING DATE: 1999-05-27
FRIOR PILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 16
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       Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide
US-09-900-147-16
                                                                                                                                                                                                                                                                                          APPLICANT: Bandara, Lesantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENT FILING DATE: 1996-12-20
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Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 84.6%; Score 77; DB 10; Length 19; Best Local Similarity 89.5%; Pred. No. 1.6e-06; Matches 17; Conservative 0; Mismatches 2; Indels
    2; Indels
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  0; Mismatches
                                                                                                                                                                                                  Sequence 16, Application US/09900147; Patent No. US20020103121A1; GENERAL INFORMATION:
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Patent No. US20020103121A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         APPLICANT: La Thangue, Nicholas B
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                                               1 RRRVYDALNVLMAMNIISK 19
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
17; Conservative
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US-09-900-147-16
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US-09-900-147-5
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                                                                         APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
ITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09
FRIOR PELICATION NUMBER: RARLIER APPLICATION NUMBER: 09/308,935
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LINGUIL SEQ ID NOS: 18
SEQ ID NO 6
LENGTH: 30
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APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
ITILE OF INVENTION: Peptide antagonists of DP transcription factors
TILE OF TOWERN PROPERTION OF THE TOWNER: US/09/900,147
CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/308,935
PRIOR PLING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 11
LENGTH: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09900147 Patent No. US20020103121A1
Sequence 6, Application US/09900147
Patent No. US20020103121A1
GENERAL INFORMATION:
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Sequence 4, Application US/09900147

Sequence 1, Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: La Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FITE REPRESENCE: 200-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 4

LENGTH: 20

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
TITLE OF INVENTION: Poptide antagonists of DP transcription factors
TITLE PERBENCE: 620-67-67
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
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56.0%; Score 51; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0075;
iive 0; Mismatches 0
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Patent No. US20020103121A1
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Best Local Similarity 100.
Matches 11, Conservative
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"AND MAN GROWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CONTINUED NUMBER: 105/09/864,761

"ONLY HUMAN GROWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CONTINUE NUMBER: 105/09/864,761

"CONTINUE NUMBER: 105/09/864,761

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"AND PAPLICATION NUMBER: 105/09/864,761

PRIOR PAPLICATION NUMBER: 105/09/864

PRIOR PAPLICATION NUMBER: 105/09/864

PRIOR PAPLICATION NUMBER: 105/09/864

PRIOR PAPLICATION NUMBER: 105/09/964

PRIOR PAP
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.99

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.9

OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 0.92

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.75

OTHER INFORMATION: EST HUMAN HIT: BE880658.1, EVALUE 2.00e-51

OTHER INFORMATION: SWISSPROT HIT: Q61501, EVALUE 5.00e-06
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 45697
LENGTH: 96
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserv
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US-10-214-188-5; Sequence 5, Application US/10214188; Publication No. US20030022260A1

RESULT 13

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Gaps ö

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COMPUTER: IBM PC Compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/10214188;
Publication No. US20030022260A1
GENERAL INPORMATION:
HANGUR, NICHOLAS B.
HIJMANS, RENE
HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F;
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
             PRIOR APPLICATION NUMBER: US/10/214,188

FILING DATE: 08-Aug-2002

CLASSIFICATION: «Unknown»

PRIOR APPLICATION NUMBER: US/08/894,139

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REGISTRATION NUMBER: 620-22

TELECOMUNICATION:

TELECOMUNICATION:

TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,186
FILING DATE: 08-Aug-2002
FILING DATE: 08-Aug-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, WARY J
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: ......
COUNTRY: U.S.A.
ZIP: Z2201-4714
COMPUTER READABLE FORM: .....TIM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 KRRIYDITNVLEGIHLIKK 63
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.44

Sest Local 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-214-188-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
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Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
BERNARDS, RENE
HIJMANS, BLEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                      BERNARDS, RENE
HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: .25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON CITY: ARLINGTON COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                               ADDRESSEE: NIXON & VANDERHYB P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,186
FILING DATE: 08-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/M9-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                      NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                  APPLICANT: LA THANGUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 47.4
Matches 9; Conservative
GENERAL INFORMATION:
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US-10-214-188-7
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Sequence 2. Application US/10165614

Publication No. US20020193289A1

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION

TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION

TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION

FILE REPREBENCE: SIER-Ols

CURRENT APPLICATION NUMBER: US/10/165,614

CURRENT APPLICATION NUMBER: 60/296,992

PRIOR FILING DATE: 2001-06-07

NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                                                             DB 11; Length 85;
                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 47.4%; Pred. No. 0.24
Matches 9; Conservative 5; Mismatches
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/238,345
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRRVYDALNVLMAMNIISK 19
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                                                                                                                                                                                                                                                                                                                                           1 RRRVYDALNVLMAMNIISK 19
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55 KRRIYDITNVLEGIQLIAK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: human
                                                                                                                                                             ; TYPE: PRT
; ORGANISM: human
US-09-932-581-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-338-294-5
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Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: 34288

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 29071

LENGTH: 76

TENTION: ANALYSIS TWO
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Sequence 5. Application WS 00000264A1

GENERAL INFORMATION

APPLICANT: Andrews, William H.

APPLICANT: Praser, Stephanie

APPLICANT: Hamid

TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR MODULATING

TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION

TITLE OF INVENTION: TELOMERASE REVERSE (TERT) EXPRESSION

TITLE OF INVENTION UNMER: US/09/932,581

CURRENT APPLICATION NUMBER: 60/227,865

PRIOR APPLICATION NUMBER: 60/227,865

PRIOR APPLICATION NUMBER: 60/227,865
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47.4%; Pred. No. 0.22;
tive 5; Mismatches 5; Indels
                                                                                                                                          Query Match
Best Local Similarity 47.4%; Pred. No. 0.21;
Matches 9; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MAP TO CHR20.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4

OTHER INFORMATION: SWISSPROT HIT: Q01094, EVALUE 1.00e-36

US-10-029-386-29071
                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRRVYDALNVLMAMNIISK 19
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                                                                                                                                                                                                                                          1 RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                  46 KRRIYDITNVLEGIDLIEK 64
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Best Local Similarity 47...
Best Local Similarity 47...
Secondary 47...
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ORGANISM: Homo sapiens
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US-09-932-581-5
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APPLICANT: Foster, Christopher A.
APPLICANT: Foster, Christopher A.
APPLICANT: Foster, Christopher A.
APPLICANT: Fraser, Stephanie
APPLICANT: Mchammadpour, Hamid
TITLE OF INVENTION: METHODS AND CCMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELLOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER-005
CURRENT APPLICATION NUMBER: US/10/338,294
CURRENT FILING DATE: 2003-01-07
PRIOR PLLING DATE: 2001-08-17
PRIOR PLLING DATE: 2000-08-24
PRIOR PPLICATION NUMBER: 60/227,865
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR PLLING DATE: 2000-09-01
PRIOR PLLING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 76
                     Publication No. US20030050264A1
GENERAL INFORMATION:
APPLICANT: Foster, Christopher A.
APPLICANT: Fraser, Stephanie
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILER REPRENSOR: SIER-005
CURRENT APPLICATION NUMBER: US/09/932,581
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR PLILNG DATE: 2000-09-01
PRIOR PLING DATE: 2000-09-01
PRIOR PLING DATE: 2000-09-01
PRIOR PLING DATE: 2000-09-05
SSOITHARE: PRESENG for Windows Version 4.0
SSOITHARE: PRESENG for Windows Version 4.0
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Pred. No. 0.32;
4; Mismatches 6; Indel8
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Publication No. US20030171326A1
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
       Sequence 6, Application US/09932581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *||:|| ||| ::| |
45 KRRIYDITNVLEGIGLIEK 63
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45 KRRIYDITNVLEGIGLIEK 63
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milarity 47.4%;
Conservative 4
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Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: human
US-09-932-581-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: human
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/10214188
Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
HIGHARDS, RENE
HIGHANS, BLEANORE M.
TITLE OF INVENTION TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLGGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-214-188-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *||:|| ||| ::| |
40 KRRIYDITNVLEGIGLIEK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                    1 RRRVYDALNVLMAMNIISK 19
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55 KRRIYDITNVLEGIQLIAK 73
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                         ; ORGANISM: homo sapiens
US-10-165-614-2
                                                                                                                                                                                                                                                                                                                                                                   RESULT 20
US-10-214-188-8
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US-09-932-581-6
                                                                      TYPE: PRT
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Gaps

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Gaps

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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-214-188-6
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US-09-900-147-2
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                                                                   Sequence 3, Application US/10165614
; Sequence 3, Application US/10165614
; Publication No. US2002019328941
; GENERAL INFORMATION:
    APPLICANT: AAdrews, William H.
    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
    TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
    FILLE REPRESSION TELOMERASE US/10/165,614
    CURRENT APPLICATION NUMBER: US/10/165,614
    CURRENT FILING DATE: 2002-06-25
    FRIOR FILING DATE: 2001-06-07
    NUMBER OF SEQ ID NOS: 4
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 3
    LENGTH: 76
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Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIJMANS, KENE
BERNARDS, KENE
HIJMANS, ELEANORE M.
HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10214188
; Publication No. US20030022260A1
; GENERAL INPORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRRVYDALNVLMAMNIISK 19
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 54.9%;
Best Local Similarity 47.4%;
Matches 9; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: homo sapiens US-10-165-614-3
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                                                  RESULT 23
US-10-165-614-3
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| Sequence 2. Application US/09900147
| Patent No. US20020103121A1
| GENERAL INFORMATION:
| APPLICANT: La Thangue, Nicholas B
| APPLICANT: Bandara, Lasantha R
| TITLE OF INVENTION: Peptide antagonists of DP transcription factors
| TITLE OF INVENTION: Peptide antagonists of DP transcription factors
| TITLE OF INVENTION: Peptide antagonists of DP transcription factors
| TITLE OF INVENTION: Peptide antagonists of DP transcription factors
| TITLE OF INVENTION NUMBER: US/09/900,147 |
| CURRENT FILING DATE: EARLIER FILING DATE: 1999-05-27 |
| PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20 |
| NUMBER OF SEQ ID NOS: 18 |
| SEQ ID NO 2 |
| LINGAR |
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| SEQ ID NO 2 |
| LINGAR |
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                                                                                             Gaps
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Score 49; DB 15; Length 74;
Pred. No. 0.46;
4; Mismatches 6; Indels
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patent No. US2002081592A1

GENERAL INFORMATION:

APPLICANT: Wang, Peijing Jeremy
APPLICANT: Page, David C.

TITLE OF INVENTION: Reproduction-Specific Genes
FILE REFERENCE: 0399.2007-002

CURRENT APPLICATION NUMBER: US/09/801,574

CURRENT FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: 60/187,518

PRIOR APPLICATION NUMBER: 60/187,518

PRIOR PILING DATE: 2001-01-01

NUMBER OF SEQ ID NOS: 90

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 48

LENGTH: 80

TYPE: PRI
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46.2%; Score 42; DB 10;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 9; Conservative 0; Mismatches 0
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42.9%; Score 39; DB 9;
Best Local Similarity 53.3%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 6
                                                                                                                                                                                           1 RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                            45 KRRIYDITNVLEGIQLIRK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                 Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus US-09-801-574-48
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Aconica-X.
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR PELING DATE: 2000-05-26
PRIOR PALICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PAPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIT: AV724222.1, EVALUE 9.00e-17
HIT: P54938, EVALUE 7.00e-18
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D IN PLACENTA, SIGNAL = 1.4
D IN PRART, SIGNAL = 1.7
SD IN BRAIN, SIGNAL = 5.2
SD IN FETAL LIVER, SIGNAL = 1.8
ED IN ADULT LIVER, SIGNAL = 1.8
ED IN HELA, SIGNAL = 2.6
ED IN BOWE MARROW, SIGNAL = 1.8
ED IN BOWE MARROW, SIGNAL = 1.6
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Pred. No. 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-29
           Patent No. US2002064761
GENERAL INFORMATION:
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53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-01-30
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SOFTWARE: Annomax Sequence
SEQ ID NO 40202
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER
OTHER
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OTHER
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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Sun, Yongming
APPLICANT: Sun, Lo, Chengina
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and FILE REPERENCE: DEX-0283
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-872-344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (3)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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US-09-764-872-344
US-09-764-872-344
Sequence 344, Application US/09764872
Publication No. US2003005231A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA125
CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.8%; Score 38; DB 11; Length 63; ilarity 56.2%; Pred. No. 30; Conservative 1; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION UNDER: US/10/001,870
CURRENT FILING DATE: 2001-11-20
PRIOR PILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin version 3.1
LENGTH: 48
                                                                                                                                                Sequence 180, Application US/10001870 Publication No. US20020150924A1 GENERAL INFORMATION:
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15 RRIYSALSLYISVVLSSK 32
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38.9%;
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RRVYDALNVLMAMNI 16
                       30 RKYYSVLNVAFACNI 44
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Best Local Similarity 38.9
Matches 7; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserva
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                                                                                                        RESULT 27
US-10-001-870-180
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Pred. No. 55;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/048, 883
PRIOR APPLICATION NUMBER: 60/048, 893
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR PRILING DATE: 1997-06-06
PRIOR PELICATION NUMBER: 60/048, 963
PRIOR PELICATION NUMBER: 60/048, 963
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR PELING DATE: 1997-12-18
PRIOR PELING DATE: 1998-01-30
                    R FILING DATE: 1997-06-06
R PAPLICATION NUMBER: 60/048,875
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,374
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,917
R APPLICATION NUMBER: 60/048,949
R APPLICATION NUMBER: 60/048,949
R PILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/048,974
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,883
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ilarity 41.2%;
Conservative
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RVYPAMHFTLCVHIYSK
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CRGANISM: Homo sapiens
US-09-933-767-455
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Best Local Similarity
Matches 7; Conserva
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US-10-023-282-455
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   Gaps
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   Indels
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      Mismatches
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APPLICATION NUMBER: 60/048,970
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APPLICATION NUMBER: 60/048,901
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                                                                                                                                                                                                                                                                                     Sequence 455, Application US/09933767
Publication No. US20030181692A1
GENERAL INFORMATION:
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                                                                                                           22 REYQDLLNVKMALDI 36
                                                               2 RRVYDALNVLMAMNI 16
      8; Conservative
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US-09-933-767-455
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          Matches
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Gaps

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equence 455, Application.

ublication No. US2003005893A1

BENERAL INPROMATION: 207 Human Secreted Proteins FILE OF PREFIXERS.

FILE SPERBACE: P2007P1

CURRENT PILING DATE: 1990-12-20

GURRENT FILING DATE: 2001-12-20

GURRENT FILING DATE: 1998-12-04

EAULIRR FILING DATE: 1998-06-04

EAULIRR FILING DATE: 1997-06-06

EAULIRR FILING
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-20
PRIOR FILING DATE: 2000-05-30
PRIOR FILING DATE: 2000-06-04
PRIOR FILING DATE: 2000-00-04
PRIOR FILING DATE: 2000-00-04
PRIOR PRILING DATE: 2000-00-04
PRIOR PRILING DATE: 2000-00-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PRILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: PCT/US01/00666
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Pred. No. 55;
5; Mismatches 5; Indels
                                                                       EARLIER APPLICATION NUMBER: 60/048, 962
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PRING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 878
EARLIER APPLICATION NUMBER: 60/048, 878
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092, 921
EARLIER APPLICATION NUMBER: 60/092, 921
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SEQ ID NO 455

LENGTH: 54
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
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APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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FILING DATE: 2001-01-30
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Patent No. US20020048763A1
GENERAL INFORMATION:
                              60/048,898
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FILING DATE: 1997-06-06
                              APPLICATION NUMBER: 60/
FILING DATE: 1997-06-06
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Best Local Similarity 41.2%;
Matches 7; Conservative
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US-10-023-282-455
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Sequence 29941, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 38.9°
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRE
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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42 FDALNILM 49
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US-09-925-299-824
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN BARN, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN PLACETYA, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HILL, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN HILL, SIGNAL = 5.6
OTHER INFORMATION: SYLENGEN HILT: POB670, EVALUE 6.00e-36
US-09-864-761-41902
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APPLICANT: ROSE et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302; CURRENT FILING DATE: 2001-08-10; PRIOR APPLICATION NUMBER: PCT/US00/05918; PRIOR FILING DATE: 1999-03-12; NUMBER OF SEQ ID NOS: 896.
SEQ ID NO 886
LENGTH: 91
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Pred. No. 99;
9; Mismatches 4; Indels
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Pred. No. 77;
           PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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67 RQIYPPINVLPSLSTVNE 84
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Best Local Similarity 27.8%;
Matches 5; Conservative
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Best Local Similarity 53.3%;
Matches 8; Conservative 5
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CRGANISM: Homo sapiens
US-09-925-302-886
                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 33
US-09-925-302-886
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LENGTH: 73
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RESULT 36

RESULT 34 US-10-029-386-29941

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US-10-036-542-148
i Sequence 148 Application US/10036542
i Publication No. US20030083481A1
i Sequence 148 Application No. US20030083481A1
i GENERAL INFORMATION:
i APPLICANTO BISE et al.
i TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
FILE REFERENCE: PA002P1
CURRENT PFLICATION NUMBER: US/10/036,542
CURRENT FILING DATE: 2002-01-07
PRIOR PPLICATION NUMBER: 60/144,972
PRIOR PELING DATE: 1999-07-21
PRIOR PPLICATION NUMBER: 60/144,972
PRIOR PPLICATION NUMBER: 60/149,173
PRIOR PPLICATION NUMBER: 60/149,173
PRIOR PLING DATE: 1999-08-17
PRIOR PLING DATE: 1999-10-06
PRIOR PLING DATE: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . LOCATION: (36)
. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                 Sequence 824, Application US/09925299;
Sequence 824, Application US/09925299;
Publication No. US20030040617A9;
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REPERENCE: PALO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR SEC ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
; LENGTH: 90

TYPE: PRT
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Pred. No. 1.3e+02;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 38.5%; Score 35; DB 11; Length 90; Best Local Similarity 75.0%; Pred. No. 1.5e+02; Matches 6; Conservative 2; Mismatches 0; Indels
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Best Local Similarity 50.0
Matches 6; Conservative
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ORGANISM: Homo sapiens
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42 FDALNILM 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-036-542-148
US-09-925-299-824
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SEQ ID NO 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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| PRICANT | REAL AND | LOUGH |
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Gaps

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; LOCATION: (88)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-846-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence 197, Application US/09764846
| Patent No. US20020102638A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| CURRENT APPLICATION NUMBER: US/09/764,846
| CURRENT APPLICATION NUMBER: US/09/764,846
| CURRENT APPLICATION NUMBER: US/09/764,846
| Prior application data removed - consult PALM or file wrapper
| NUMBER OF SEQ ID NOS: 348
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 197
| LENGTH: 92
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; Sequence 197, Application US/10091483
; Publication No. US20030049650A1
; GENERAL INFORMATION:
; APPLICATY: Rosen et al.;
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION: Nucleic 2002-03-07
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 348
; FAIOR Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 197
; LENGTH: 92
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Pred. No. 3.3e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                          Score 33; DB 14; Length 59;
Pred. No. 2e+02;
6; Mismatches 4; Indels
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR FILING DATE: 2000-06-22
PRIOR PELING DATE: 1999-06-22
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 59
TYPE: PRT
ORGANISM: Hottentotta judaica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.3%;
Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local Similarity 33.3%;
Matches 5; Conservative
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5 RLYAIILIVLVMNVI 19
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (88)
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NAME/KEY: SITE
LOCATION: (88)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-764-846-197
                                                                                                                                                                                                                                      US-10-044-359-10
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                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. US20020082234Alel Prokaryotic Polynucleotides, Polypeptides and Their Uses NUMBER OF SEQUENCES: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gabe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM ITES: LBM Compatible
COMBUTER: IBM Compatible
CORRENTING SYSTEM: DOS
SOFTWARE: FBSEEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION NUMBER: 08/936,165
APPLICATION NUMBER: 08/936,165
APPLICATION NUMBER: 08/936,165
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
RECISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 950549
TELECHOMONICATION INFORMATION:
TELECHOMONICATION INFORMATION:
TELECHOMONICATION INFORMATION:
TELECHOMONICATION INFORMATION:
TELECHOMONICATION INFORMATION:
TELECHOMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSES: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.4%; Score 34; DB 9; 156.2%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 40
US-10-044-359-10
Sequence 10, Application US/10044359
Sequence 10, Application US/10044359
PUDIcation No. US20020160454A1
GENERAL INFORMATION:
APPLICANT: Herrman, Rafael
APPLICANT: Wong, James F.
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2002-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDENES: single TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 513: US-09-939-980-513
                                                                                                    Hodgson, John
Knowles, David
Lonetto, Michael
Nicholas, Richard
Pratt, Julie
Reichard, Richard
Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 513:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                Patent No. US20020082234A1
GENERAL INFORMATION:
APPLICANT: Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VYDAL -- NVLMAMNII 17
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48 MYDAKMDNVLVPINII 63
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Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19406-0939
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Score 32; DB 15; Length 60;
Pred. No. 3e+02;
5; Mismatches 2; Indels
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Best Local Similarity 46.27
Conservative
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38 RDVYEYLNLLISV 50
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US-10-036-542-101
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                                                                                                                                                                                                                                                                           APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US2004009474Alel Human Polynucleotides and Polypeptides Enco FITLE OF INVENTION: No. US2004009474Alel Human Polynucleotides and Polypeptides Enco FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR PILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8870
LENGTH: 50
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-091-483-197
                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 14; Length 58;
Pred. No. 2.9e+02;
6; Mismatches 4; Indels
                                              Score 33; DB 15; Length 92;
Pred. No. 3.3e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFOGRATION:
GENERAL INFOGRATION:
APPLICANT: Wong, James F.
APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
FILE REFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT APPLICATION NUMBER: 09/599,416
PRIOR PILING DATE: 2000-06-22
PRIOR PILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
SENGTH: 58
                                                                                                                                                                                                                              Sequence 8870, Application US/09864408A, Publication No. US20040009474A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/10044359; Publication No. US20020160454A1; GENERAL INFORMATION:
                                                36.3%;
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ORGANISM: Hottentotta judaica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 33.3%;
Matches 5; Conservative
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3 RIFTIILIVFALNII 17
                                                Query Match 36.3
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                  8 LNVLMAMNIISK 19
                                                                                                                                     |:||: |:|:|
72 LSVLLCKNVITK 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-09-864-408A-8870
                                                                                                                                                                                                 RESULT 43
US-09-864-408A-8870
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US-10-044-359-2
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

February 17, 2004, 10:50:13; Search time 11.4752 Seconds (without alignments) 159.230 Million cell updates/sec Run on:

US-09-900-147-3

1 RRRVYDALNVLMAMNIISK 19 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

37673

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d¥			SUMMARIES	
Result No.	Score	Query Match	Query Match Length.DB	DB	ID	Description
	37	40.7	71	2	B86477	protein F1504.31
8		39.6	57	~	PN0624	c
m		38.5	34	~	E49410	t-complex polypept
4	35	38.5	9	7	JC1386	homeotic protein E
2		37.4	74	~	D89831	hypothetical prote
9	34	37.4	77	-	C69425	transcription requ
7	34	37.4	82	~	T42312	
80		36.3		~	F84283	
6		35.2	53	71	D91064	
10		35.2	9	~	G69115	Н
11	32	35.2	99	~	A99954	_
12	32	35.2	67	~	T27124	Н
13	32	35.2	83	~	H84088	
14	32	35.2	89	7	863609	н
15	32	35.2	93	7	G70401	flagellar hook-bas
16	32	35.2	94	~	H84227	hypothetical prote
17	32	35.2	96	~	E69550	conserved hypothet
18	31.5	34.6	40	7	801102	hypothetical prote
	31	34.1	35	7	D83924	hypothetical prote
	31	34.1	4	~	A42766	jararafibrase II (
21		34.1	57	ч	R5EC32	ribosomal protein
22	31	34.1	57	7	C90812	50S ribosomal subu
23	31	34.1	57	7	G85671	
	31	34.1	57	~	AH0641	50S ribosomal prot
	31	34.1	68	N	AI2346	hypothetical prote
26	31	34.1	70	~	183374	Œ
27	31	34.1	84	~	T10345	hypothetical prote
28	31	34.1	95	~	S74489	ia]
	31	34.1	98	~	H89910	conserved hypothet

transposase, pseud acyl carrier prote	heat shock protein hypothetical prote	H+-transporting tw hypothetical prote	hypothetical prote hypothetical prote	hypothetical prote hypothetical prote		hypothetical prote regA protein - Ser PhiHl repressor -
B75624 G82881	PA0105 E89904	PWCK8P E95849	D82422 AC0657	D83797 A84215	H81811 B82699	T30649 JC6046 A38167
2 2	000	7 7 7	0 0	0 0	0 0	0 0 0
99	15 29	54 51	53	59 60	64 72	88 88 89
33.5	33.0	33.0	33.0	33.0	33.0	33.0 33.0
30.5	000	000	300	0 0 3 0 8 0	88	000
30 31	332	323	37 38	39 40	41	43 45 5

ALIGNMENTS

		d) - Arabidopsis thaliana
		n F1504.31 [imported]
SULT 1	16477	otein F1

Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thalian: Constant of the cispecial of chromosome of the cispecial of chromosome of the cispecial of the cispecial of cispecial of cispecial of the cispecial of cispecial

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-71 <STO>

A;Cross-references: GB:AE005172; NID:g8778365; PIDN:AAF79373.1; GSPDB:GN00141 C;Genetics:

A; Gene: F1504.31 A; Map position: 1

Gaps ; 0 40.7%; Score 37; DB 2; Length 71; 37.5%; Pred. No. 25; 5; Indels tive 5; Mismatches 5; Indels Query Match
Best Local Similarity 37.5
Matches 6; Conservative

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alpha-internexin - pig (fragments) C;Species: Sus scrofa domestica (domestic pig) C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999 C;Accession: PN0624

R.Tanaka, J.; Ogawara, M.; Ando, S.; Shibata, M.; Yatani, R.; Kusagawa, M.; Inagaki, M. Biochem. Biophys. Res. Commun. 196, 115-123, 1993
A;Title: Phosphorylation of a 62kD porcine alpha-internexin, a newly identified intermed A;Reference number: PN0624; WUID:94029981; PMID:8216281

A; Accession: PN0624

A, Molecule type: protein

A,Residues: 1-18,19-28,29-45,46-57 <TAN>
C,Comment: This intermediate filament protein polymerizes to form filament itself, in vi C,Superfamily: cytoskeletal keratin
C,Keywords: brain, intermediate filament

Gaps

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2; Length 74 2; Indels

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transcription regulator asnC - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: C69425,
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.Klenk, H.P.; Clayton, L.; Overbeek, R.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F., Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Aitle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeoring A;Reference number: A69200, MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gross-references: GB:AE001007; GB:AE000782; NID:g2689330; PIDN:AAB89844.1; PID:g2649171
C;Superfamily: Archaeoglobus fulgidus transcription regulator asnC
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R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of Bacillus subtil
A;Reference number: Z22137; WUID:98094274; PMID:9434185
A;Accession: T42312
                                                                                                                                                  A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-74 < KURA
A; Cross-references: GB:BA000018; PID:g13700510; PIDN:BAB41807.1; GSPDB:GN00149
A; Experimental source: strain N315
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-77 <KLE>
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.4%; Score 34; DB 2; Length 82;
46.2%; Pred. No. 95;
tive 5; Mismatches 2; Indel8
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A;Molecule type: DNA
A;Residues: 1-82 <ALO>
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                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB
Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          37.4%;
50.0%;
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Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 DALNVLMAMNII 17
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                A; Accession: D89831
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hypothetical protein [imported] - Staphylococcus aureus (strain N315)

hypothetical protein [imported] - Staphylococcus aureus

c;Species 22-Oct-2001

#sequence_revision 10-May-2001 #text_change 22-Oct-2001

C;Accession: D89831

R;Kuroda, M.; Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
                                                                                                                                                                                                                                                                                                                                                         NyAlternate names: chaperonin homolog (peak 2)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998
C;Accession: E49410
R;Rommelaere, H.; Van Troys, M.; Gao, Y.; Melki, R.; Cowan, N.J.; Vandekerckhove, J.; An Proc. Natl. Acad. Sci. U.S.A. 90, 11975-11979, 1993
A;Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven rela A;Reference number: A49410; MUID:94089752; PMID:7903455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homeocic protein EgHbx1 - tapeworm (Echinococcus granulosus) (fragment)
C;Species: Echinococcus granulosus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Oct-1997
C;Accession: JC1386
R;Oliver, G; Vispo, M; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlic Gene 121, 337-342, 1992
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>
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                       Length 57;
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A,Note: sequence modified after extraction from NCBI backbone
A,Note: sequence extracted from NCBI backbone (NCBIP:141043)
C,Superfamily: molecular chaperone t-complex-type
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A,Reference number: JC1386; MUID:93077050; PMID:1359988
A,Accession: JC1386
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              Score 36; DB 2;
Pred. No. 29;
2; Mismatches
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Pred. No. 24;
7; Mismatches
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Pred. No. 45;
6; Mismatches
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1 RSLHDAIMIVRALEIIPR 18
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33.3%;
                       39.64;
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Best Local Similarity 38.5%;
Matches 5; Conservative
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VYERLNLALSINL 40
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Best Local Similarity 33.34
Best Local Similarity
For Conservative
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                                                  Best Local Similarity 53.3
Matches 8; Conservative
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A Molecule type: protein
A Residues: 1-34 < ROM>
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A, Residues: 1-60 <OLI>
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                          Query Match
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Gaps

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A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct; A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession; G69115
A;Status; preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                             A,Cross-references: GB:AE000806, GB:AE000666; NID:g2621222, PIDN:AAB84692.1; PID:g262123(
A,Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: A99954
R; Kuroda, M; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch R; Kuroda, M; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzama, R.; Kaito, C.; Sekimizu, K.; F. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1228-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Molecule type: DNA
A;Residues: 1-66 xURA
A;Cross-references: GB:BA000018; PID:gl3702454; PIDN:BAB43595.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SA2292 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 
C;Accession: T27124
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A;Experimental source: clone Y53C10A
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C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 2; Length 60;
Pred. No. 1.5e+02;
4; Mismatches 3; Indels
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A;Molecule type: DNA
A;Residues: 1-67 <WIL>
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A;Reference number: Z20314
A;Accession: T27124
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46.2%;
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20 AINISIFLNIICK 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A,Introns: 59/3
                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-60 <MTH>
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                                                                                                                                                                                                                                                                                                                                        A;Start codon: GTG
                                                                                                                                                                                                                                                                                               A, Gene: MTH186
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Matches
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101064
hypothetical protein EC83484 [imported] - Escherichia coli (strain O157:H7, substrain RI
hypothetical protein EC83484 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: D91064
B;Haysahi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MuID:21156231; PMID:11258796
A;Status: preliminary
A;Residues: 1-53 <HAY>
A;Residues: 1-53 <HAY>
                                                                                                                                                                                          hypothetical protein Vng1283h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84283
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Reference number: A84160; MUID:20504483; PMID:11016950
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hypothetical protein MTH186 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species Methanobacterium thermoautotrophicum
C;Species Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: 669115
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Aju, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
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C;Genetics:
A;Gene: VNG1283H
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC83484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.3%; Score 33; DB 2; Length 66; 50.0%; Pred. No. 1.1e+02; ive 4; Mismatches 4; Indels
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RTTQTSQNIVAAMNLYNK 53
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20 RVFDALLVLGPVVIVA 35
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Best Local Similarity 50.0
Matches 8; Conservative
   ::||||::|| :
39 QQVYDAVSVLFTI
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Query Match
35.2%; Score 32; DB 2; I
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 4;
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Best Local Similarity 36.8%;
Matches 7; Conservative
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Matches 6; Conserva
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A,Status: preliminary
A,Getus: preliminary
A,Rolecule type: DNA
A,Residues: 1-83 <STO>
A,Crose-references: GB.AP001519, GB.BA000004; NID:g10176109; PIDN:BAB07231.1; GSPDB:GNOG C;Genetics:
A,Reperimental source: strain C-125
A;Gene: BH3512
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Ligaellar hook-basal body protein - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000
C;Accession: G70401
R;Deckert, G.; Marren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
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CiSpecies: Serratia marcescens
CiSpecies: Serratia marcescens
CiSpecies: Serratia marcescens
CiDate: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
CiAccession: 563609
Rijin, S.; Chen, Y.; Christie, G.E.; Benedik, M.J.
Mol. Biol. 256, 264-278, 1996
A;Title: Regulation of the Serratia marcescens extracellular nuclease: positive control A;Reference number: 563609; MuID:96174474; PMID:8594195
                                                                                                                                                                               C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: H84088
F;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
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A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300; MUID:98196666; PMID:9537320
A,Accession: G70401
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                                                                                                                 RESULT 13
H84088
hypothetical protein BH3512 [imported] - Bacillus halodurans (strain C-125)
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A;Molecule type: DNA
A;Residues: 1-89 <1IN>
A;Residues: 1-89 <1IN>
Cross-references: EMBL:Ul1698; NID:g509550; PIDN:AAA98439.1; PID:g509551
A;Gene: nucE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 83;
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Pred. No. 2.3e+02;
2; Mismatches 2;
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55.6%;
RVYDALNVLMAMNIIS 18
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RIYRAFEMSMEKDIIS 17
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RRKIYDECN 88
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Matches 5; Conserv
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Best Local Similarity
Matches 6; Conserv
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Conserved hypothetical protein AF2404 - Archaeoglobus fulgidus
Cyspecies: Archaeoglobus fulgidus
Cyspecies: Archaeoglobus fulgidus
Cyspecies: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999
Cyspecies: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999
Cyspecies: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999
Cyspecies: O5-Dec-1997
Cystenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, S.Kirlenk, H.O.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Reference number: A69250, MUID:98049343; PMID:9389475
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                                                                                                                                                                 A;Cross-references: GB:AE000727; NID:g2983623; PIDN:AAC07208.1; PID:g2983640; GB:AE00065; A;Cross-references: GB:AE00065; C;Genetics: A;Gene: fliE C;Superfamily: flagellar hook-basal body protein fliE
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1.94 <270>
A; Cross-references: GB: AE004437; NID: 910580284; PIDN: AAG19188.1; GSPDB: GN00138
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-93 <AQF>
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C.Species: Halobacterium sp. NRC-1
C.Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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Pred. No. 2.5e+02;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.2%; Score 32; DB 2; 1
ilarity 37.5%; Pred. No. 2.4e+02;
Conservative 4; Mismatches 6;
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Gaps

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ribosomal protein L32 [validated] - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Achar-1984 #sequence_revision 30-Jun-1991 #text_change 01-Mar-2002
C;Accession: JV0048; A02832; A30419; F64852
R;Tanaka, Y.; Tsujimura, A.; Fujita, N.; Isono, S.; Isono, K.
A;Talaka, Y.; Tsujimura, A.; Fujita, N.; Isono, S.; Isono, A.; A;Title: Cloning and analysis of an Escherichia coli operon containing the rpmF gene for A;Reference number: JV0048; MUID:90008815; PMID:2477362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M29698; NID:g147710; PIDN:AAA24575.1; PID:g147712
A;Experimental source: strain K-12
R;Wittmann-Liebold, B.; Greuer, B.; Pannenbecker, R.
Hoppe-Seyler's Z. Physiol. Chem. 356, 1977-1979; 1975
A;Title: The primary structure of protein L32 from the 50S subunit of Escherichia coli r3
A;Reference number: A02832; MUID:76119562; PMID:765258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 2-57 < VIN>
A; Residues: 2-57 < VIN>
A; Experimental source: strain MRE-600
B; Experimental source: strain MRE-600
A; Experimental source: strain MRE-600
A; Rose, D.7; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Recession: F64852
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Complex: the ribosome is composed of the large (508) and small (308) subunit; the large S RRNA and 22 distinct protesins C.Complex: large subunit ribosomal protesins: L1 (PIR:REBC1), L3 (PIR:REBC3), L2 (PIR:REBC3) (PIR:REBC13), L13 (PIR:REBC13), L14 (PIR:REBC14), L15 (PIR:REBC15), L16 (PIR:REBC16), L17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: strain K
R;Vinokurov, L.M.; Alakhov, Y.B.; Golov, E.A.; Ovchinnikov, Y.A.
Bioorg. Khim. 2, 1013-1017, 1976
                       A, Residues: 1-49 <MAR>
A, Experimental source: venom
A, Force: sequence extracted from NCBI backbone (NCBIP:113117)
C, Superfamily: atrolysin C
C, Superfamily: atrolysin C
C, Keywords: hydrolase; metalloproteinase; zinc
                                                                                                                                                                                      h 34.1%; Score 31; DB 2; Le Similarity 36.4%; Pred. No. 1.8e+02; 4; Conservative 5; Mismatches 2;
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C; Superfamily: Escherichia coli ribosomal protein L32
                                                                                                                                                                                                                                                                                                           1 RRRVYDALNVL 11
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A;Accession: A30419
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A, Molecule type: protein
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A; Residues: 1-57 <TAN>
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Matches
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                                                                                                                                                                                   hypothetical protein 1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jul-2000
C;Accession: 501102
K;Eveleth, D.D.; Marsh, J.L.
Mol. Gen. Genet. 209, 290-298, 1987
A;Title: Overlapping transcription units in Drosophila: sequence and structure of the Cs A;Reference number: 501102; MuID:88038375; PMID:3478553
A;Accession: 501102
A;Molecule type: DNA
A;Residues: 1-40 eEWB.
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D83924
Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
A;Fitle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83924
A;Statuus: preliminary
A;Acleule type: DNA
A;Residues: 1-35 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05915.1; GSPDB:GN00
A;Experimental source: strain C-125
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C;Species: Bothrops jararaca (jararaca)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 25-Mar-1998
C;Accession: A42766
B;Maruyama, M.; Sugiki, M.; Yoshida, E.; Mihara, H.; Nakajima, N.
Toxicon 30, 853-864, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein BH2196 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X05991; NID:g7759; PIDN:CAA29405.1; PID:g2598388
C;Genetics:
A;Gene: Cs
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Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
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A;Introns: 3/2
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                                60 LKALMQLNIVEK 71
8 LNVLMAMNIISK 19
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A,Gene: BH2196
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C; Superfamily: Escherichia coli ribosomal protein L32
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34.1%; Score 31; DB 2; I

Best Local Similarity 33.3%; Pred. No. 2.1e+02;

Matches 5; Conservative 6; Mismatches 4;
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Pred. No. 2.6e+02;
2; Mismatches 1;
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Best Local Similarity 66.7%;
Matches 6; Conservative 5
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16 RRSHDALTAVTSLSV 30
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A;Residues: 1-68 <KUR>
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C90812
C90812
C90812
CSOS ribosomal subunit protein L32 [imported] - Escherichia coli (strain O157:H7, substra C; Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C;Accession: C90812
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B, 11-22, 2001
A;Pitle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Accession: C90812
A;Accession: C90812
A;Status: preliminary
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A;Readdues: 1-57 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34890.1; PID:g13360931; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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C;Keywords: protein biosynthesis; ribosome
F;2-57/Product: ribosomal protein L32 #status experimental <MAT>
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Best Local Similarity 33.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 6; Mismatches 4; Indels
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Pred. No. 2.1e+02;
6; Mismatches 4; Indels
                                                                                     Score 31; DB 1; Length 57; Pred. No. 2.1e+02; 6; Mismatches 4; Indels
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A;Gene: ECG1467
C;Superfamily: Escherichia coli ribosomal protein L32
                                                                                        34.1%;
33.3%;
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33.3%;
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RRSHDALTAVTSLSV 30
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16 RRSHDALTAVTSLSV 30
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RRSHDALTAVTSLSV 30
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Matches 5; Conservative
                                                                                                   Query Match
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RESULT 24

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hypothetical protein as14328 [imported] - Nostoc sp. (strain PCC 7120)
hypothetical protein as14328 [imported] - Nostoc sp. (strain PCC 7120)
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AI2346
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. NNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anaklakierence number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: 183374
R;Hebbert, B.; Bargeron, J.; Tijssen, P.; Potworowski, E.F.
Gene 143, 257-260, 1994
A;Title: Protein tyrosine kinases transcribed in a murine thymic medullary epithelial ce
A;Reference number: 160294; MUID:94266162; PMID:8206383
GS ribosomal protein L32 [imported] - Salmonella enterica subsp. enterica serovar Typhi C; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: this species has also been called Salmonella typhi C;Date: this species has also been called Salmonella typhi C;Date: this species now-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0641
R;Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Ateference number: AB0502; MUID:21534947; PMID:11677608
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A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: AH0641
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-57 < PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08315.1; PID:g1650236j; GSPDB:GN00176
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C;Species: Mus musculus (house mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
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Rikuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
M. A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; F.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: B75624
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F.S.; Smith, H.O.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mals.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-66 -MIL>
A;Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12601.1; PID:g6460897; TIGR:DRB009
A;Experimental source: strain R1
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C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: 682881
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
R;bescription: The complete sequence of Ureaplasma urealyticum: Alternate views of a minn
A;Reference number: A82870
          conserved hypothetical protein SA1186 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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A;Experimental source: strain N315
                                                                                                                                                                                                                                                                 A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146
A,Accession: H89910
                                               C,Species: Staphylococcus aureus
C,Dàte: 10-May<sub>-2</sub>2001 #sequence_revision 10-May-2001 #text_change 09-Dec-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.1%; Score 31; DB 2; Length 98; 66.7%; Pred. No. 3.8e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transposase, pseudogene - Deinococcus radiodurans (strain R1)
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Best Local Similarity 44.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 YDALNVLMA 13
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62 YDDLNVVVA 70
                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <KUR>
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                                                                                                         C; Accession: H89910
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110345

Hydothetical protein 76 - Orgyia pseudotsugata nuclear polyhedrosis virus
C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpfMPV
C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpfMPV
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C;Accession: T10345
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A;Reference number: Z17011; MUID:97271300; PMID:9126251
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3/4489
hypothetical protein ssr1853 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: 374489
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyajima, N.; O. K.; Owmura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA, Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A; Accession: S74489
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-95 < KAN>
A; Cross-references: EMEL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA16641.1; PID:d101737
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A;Molecule type: mRNA
A;Residues: 1-70 <RES>
A;Crose-references: GB:L25762; NID:g413748; PIDN:AAA40020.1; PID:g554265
C;Genetics:
A;Gene: PTK
C;Superfamily: protein kinase homology
F;1-70/Domain: protein kinase homology
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34.1%; Score 31; DB 2; Length 84;
Best Local Similarity 31.6%; Pred. No. 3.2e+02;
Matches 6; Conservative 7; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                        Length 70;
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A,Molecule type: DNA
A;Residues: 1-84 <AHR.>
A;Cross-references: EMBL:U75930; NID:g2934903; PID:g1911322
                                                                                                                                                                                                                                                                 Score 31; DB 2; I
Pred. No. 2.7e+02;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                 Query Match 34.1%;
Best Local Similarity 46.2%;
Matches 6; Conservative
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H89910
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C;Accession: A81346
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Riguelin, E.; Velours, J.; Guerin, M.
Nucleic Acids Res. 18, 4267, 1990
A;Title: Cloning and sequencing of a fragment of the linear mitochondrial DNA of the yeas
A;Reference number: S10465; MUID:90332440; PMID:2143015
A;Accession: S10465
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C.Keywords: ATP blosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
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R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endor A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:All39076; GB:All11168; NID:g6968128; PIDN:CAB73017.1; PID:g6968199:
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - yeast (Candida parapsilosis) C;Species: mitochondrion Candida parapsilosis C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 14-Dec-2001
                  hypothetical protein Cj0747 [imported] - Campylobacter jejuni (strain NCTC 11168)
                                                        C,Species: Campylobacter jejuni
C,Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-48 <GUE>
A;Cross-references: EMBL:X52115; NID:g12890; PIDN:CAA36361.1; PID:g829334
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30; DB 2;
Pred. No. 1.9e+02;
5; Mismatches 1
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Best Local Similarity 25.9%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Genome: mitochondrion A; Genetic code: SGC3
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-51 < KUR>
                                                                                                                                                                                                                                                                                               A; Accession: A81346
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-35 < PAR>
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Matches
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Moscale type: DNA
A;Essidaes GB:AE002149; GB:AF222894; NID:g6899503; PIDN:AAF30918.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics: acpp; UU506
A;Genetic acpp; UU506
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heat shock protein dnaJ type - fungus (Fusarium sporotrichioides) (fragment)
C; Species: Fusarium sporotrichioides
C; Species: Co-reb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C; Accession: PA0105
R; Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
B; Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
A; Description: Two dimensional polyacrylamide gel electropheresis of Fusarium sporotrich
A; Reference number: PA0051
A; Accession: PA0105
A; Accession: PA0105
A; Accession: Lype: Drotein
A; Residues: 1-15 < CHO>
C; Keywords: heat shock; stress-induced protein
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BB9904
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: B89904
R;Mccoda, M.; Obte. T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Experimental source: strain N315
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                                                                                                                                                                                                                                                                         33.5%; Score 30.5; DB 2; Length 77; 39.1%; Pred. No. 3.6e+02;
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Pred. No. 73;
2; Mismatches 1; Indels
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                           9; Conservative
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Matches 5; Conservative
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Matches 9; Conser
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A;Molecule type: DNA
A;Residues: 1-29 <KUR>
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A; Cross-references: GB: AL591985; PIDN: CAC48461.1; PID: g15139933; GSPDB: GN00167

RESULT 34

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14; Gaps

Length 35, 1; Indels σ

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RiTakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Mucleic Acids Res. 28, 4317-4331, 2000
Alitile: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and garerence number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: GB:AD001511, GB:BA000004; NID:g10173727; PIDN:BAB04899.1; GSPDB:GN001
A,Experimental source: strain C-125
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A,Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lish, Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: A64215
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                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein BH1180 (imported) - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Vng0568c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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                                                                                   Length 57;
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Pred. No. 3.3e+02;
2; Mismatches 4;
                                                                                   Score 30; DB 2; I
Pred. No. 3.2e+02;
2; Mismatches 4;
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                                                                                 33.0%;
Similarity 50.0%;
6; Conservative
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Best Local Similarity 31.2
Matches 5; Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
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23 RRFYKYCNILIA 34
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-60 <STO>
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        C,Genetics:
A,Gene: STY1359
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G;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
G;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
G;Accession: AC0657
R;Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.W.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Dela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE004403; GB:AE003853; NID:g9658159; PIDN:AAF96644.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein VCA0746 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: D82422
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Pred. No. 2.9e+02;
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58.3%; Pred. No. 2.8e+02;
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C;Genetics:
A;Gene: SMb20061
A;Genome: plasmid
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-53 <HEI>
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A Molecule type: DNA
A, Residues: 1-57 < PAR>
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33.0%;
35.3%;
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A.Gene: regA
C.Keywords: transmembrane protein
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55.6%;
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Matches 5; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-88 <FER>
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A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1.72 < SIM:
A; Cross references: GB: AE003963; GB: AE003849; NID: G9106285; PIDN: AAF84114.1; GSPDB: GN001
A; Experimental source: strain 9a5c
A; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M. R.S.; Bueno, M. R.P.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H Briones, M. R.S.; Bueno, M. R. Ferroira, V.C.A.; Ferro, J.B.A.; Franco, M.C.; Franco, M.C.; Fronco, M.C.; Fronco, M.C.; Fronco, M.D.; Jouqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, B.B.; Laign Chado, M.A.; Madelra, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Mateukuma, A.Y.; Monck, C.F.M.; Maracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Balmieri, D.A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.A.; Acherence number: A5928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein XF1305 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: B82699
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenter 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Peb-2001
C;Accession: H81811
K;Parkhill, J; Acthman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H81811
A;Accession: H81811
A;Residues: 1-64 < PAR>
                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85076.1; PID:g738049
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1853
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Pred. No. 4.1e+02;
---Ahen 3; Indels
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Pred. No. 3.6e+02;
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RiFerrer, S.; Viejo, M.B.; Guasch, J.F.; Enfedaque, J.; Regue, M.
R. Ferrer, S.; Viejo, M.B.; Guasch, J.F.; Enfedaque, J.; Regue, M.
Bacteriol. 178, 951-960, 1996
A; Title: Genetic evidence for an activator required for induction of colicin-like bacterio.
A; Reference number: JC6046; MUID:96165247; PMID:8576068
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J. Bacteriol. 173, 955-960, 1991
A;Title: Halobacterium halobium strains lysogenic for phage phiH contain a protein resem?
A;Reference number: A38167; MUID:91123222; PMID:1991733
A;Accession: A38167
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A;Molecule type: DNA
A;Residues: 1-89 «KENN»
A;Cross-references: GB:X52504; NID:g14814; PIDN:CAA16746.1; PID:g14816
A;Cross-references: GB:X52504; NID:g14814; PIDN:CAA16746.1; PID:g14816
A;Note: the source is designated as Halobacterium halobium phage PhiH1
A;Note: the authors translated the codon GCG for residue 14 as Arg, and CAA for residue
C;Keywords: DNA binding; transcription regulation
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C;Comment: This protein has two transmembrane helical domains and the charge-rich amino-
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
C;Accession: T30649
K;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host
A;Reference number: 220876; MUID:96325459; PMID:8670425
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C;Species: Halobacterium salinarium phage phi-H
C;Date: 28-Aug-1992 #sequence_revision 18-Sep-1992 #text_change 18-Jul-2001
C;Accession: A38167; S11641
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C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
C;Accession: JC6046
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Pred. No. 5.1e+02;
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Pred. No. 5.1e+02;
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Pred. No. 4.7e+02;
3; Mismatches 3;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-82 <SEN>
A;Cross-references: EMBL:U60315; PIDN:AAC55175.1 C;Genetics: A;Note: MC047L
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RRRVVDALNVLMAMNII 17

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 17, 2004, 10:50:13; Search time 6.0198 Seconds (without alignments) 148.428 Million cell updates/sec Run on:

US-09-900-147-3 91 1 RRRVYDALAVLAMAMNIISK 19

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

13973 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Query Match

44.0%; Score 40; DB 1; Length 38;
Best Local Similarity 63.6%; Pred. No. 1.6;
Matches 7; Conservative 2; Mismatches 2; Indels

34	27	29.7	72	н	HSLU BUCSC	069227 buchnera ap	
35	27	29.7	75	Н	Y420 TREPA	O83435 treponema p	
36	27	29.7	78	н	DLTC_STAXY	Q9x2n6 staphylococ	
37	27	29.7	82	Н	YNI1_FRAAL		
38	27	29.7	83	Н	RL31_THEAC	Q9hm17 thermoplasm	
39	27	29.7	90	н	BAF2 HUMAN	_	
40	27	29.7	16	н	ILG1 CAEEL	Q18060 caenorhabdi	
41	27	29.7	92	н	DBH BUCAI	P57144 buchnera ap	
42	27	29.7	95	н	RPCI BPP22	P03041 bacteriopha	
43	27	29.7	95	_	VAPD_ACTAC	Q52243 actinobacil	
44	27	29.7	96	-	C553 HELPJ	Q9zjz9 helicobacte	
45	27	29.7	98	н	NULM_BALMU	P41301 balaenopter	
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RESULT 1							

DEPENDENT STANDARD; PRT; 38 AA. 1D E2PT_ART 1D E2PT_ART 1D F2PT_ART 1D F2PT_ART
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Gaps

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Score 32; DB 1; Length 93; Pred. No. 1.1e+02; 4; Mismatches 6; Indels

35.2%;

4; Mismatches

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93 AA; 10764 MW; 6180AEA1C8FB9C39 CRC64;
or send an email to license@isb-sib.ch)
                                       EMBL, AE000727, AAC07208.1; -. PIR, G70401, G70401. InterPro, IPR001624; FliE.
                                                                                                             Pfam; PF02049; FliE; 1.
PRINTS; PR01006; FLGHOOKFLIE.
TIGREAMs; TIGR00205; fliE; 1.
Flagella; Complete proteome.
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                                                                                                                                                                                                                                                                     Similarity 37.5%;
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 79;
4; Mismatches 6; Indels
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30-MaY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last amnotation update)
Flagellar hook-basal body complex protein fils.
FLIS OR AQ 1182.1 OR AQ 1182A.
Aquifex acolicus.
Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
Hypothetical 8.1 kDa protein.
Thermoproteus tenax virus 1 (strain KRAI) (TTV1),
Viruses, deNNA viruses, no RNA stage; Lipothrixviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Neumann H.;
Submitted (MAR-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 70 AA; 8125 MW; F88F0A8E46323EDC CRC64;
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-!- SIMILARITY: BELONGS TO THE FLIE FAMILY.
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MEDLINE=98196666; PubMed=9537320;
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32 VYVAITVTLTENLARK 47
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nes 6; Conservative
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26 KRRIYDITNVL 36
    RRRVYDALNVL
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067242;
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ID YORA TTV1
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Tanaka Y., Tsujimura A., Fujita N., Isono S., Isono K., "Cloning and analysis of an Escherichia coli operon containing the rpmF gene for ribosomal protein L32 and the gene for a 30-kilodalton
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SPECIES=E.coli; STRAIN=K12;
MEDLINE=9762102; PubMed=8905232;
MEDLINE=9762102; PubMed=8905232;
MEDLINE=9762102; PubMed=8905232;
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Moril H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
50S ribosomal protein L32.
RPMF OR B1089 OR Z1728 OR ECS1467 OR STM1191 OR STY1230 OR T1729 OR
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SPECIESE=C.001; STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia col1 K-12.";
Science 277:1453-1474(1997)
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                                                                                                                                                                                                         56 AA.
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MEDLINE=90008815; PubMed=2477362;
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78 RNKLLEAYNELMKMQV 93
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Escherichia coli 0157:H7,
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Salmonella typhi, and
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SPECIES=E.coli; STRAIN=C157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21534947; PubMed=11677608;
MEDLINE-21534947; PubMed=11677608;
MEDLINE-21534947; PubMed=11677608;
MEDLINE-21534947; PubMed=11677608;
MIDLINE-21534947; PubMed=11677608;
Charcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIESE. Typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed=11677609; MCC1elland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Florae L., Miller W., Stoneking T., Nhan M., "Atcourten R., Wilson R.K.," Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=E.coli; STRAIN=MRE-600;
Vinokurov L.M., Alakhov Y.B., Golov E.A., Ovchinnikov Y.A.;
"The primary structure of ribosomal protein L32 from E. coli MRE-600
ribosomes.";
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SPECIES—S. typhimurium; STRAIN=LT2;
MEDLINE=98317265; PubMed=9642179;
MEDLINE=98317265; PubMed=9642179;
Zhang Y., Cronan J.E. Jr.;
"Transcriptional analysis of essential genes of the Escherichia coli fatty acid biosynthesis gene cluster by functional replacement with the analogous Salmonella typhimurium gene cluster.";
J. Bacteriol. 180:3295-3303(1998).
                                                                                                       "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
            Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                       SPECIES=E.coli; STRAIN=K; MEDLINE=76119562; PubMed=765258; Wittmann-Liebold B., Greuer B., Pannenbecker R.; The primary structure of protein L32 from the 50S subunit of Escherichia coli ribosomes."; Hoppe-Seyler's Z. Physiol. Chem. 356:1977-1979(1975).
 MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bioorg. Khim. 2:1013-1017(1976)
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SPECIES=S.typhi; STRAIN=TY2 / ATCC 700931; MEDLINE=22531367; PubMed=12644504; Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIESS.[Lexareri; STRAIN=301 / Serotype 2a;
SPECIESS.2.[Lexareri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang F., Zhang X., Zhang Y., Zhang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A. (Sao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-E.coli; STRAIN-K12 / ATCC 25404;
MEDLINE-99196679; Pubmed-10094780;
Arnold R.J., Reilly J.P., "Observation of Escherichia coli ribosomal proteins and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
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Pred. No. 93;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribosomal protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                             J. Bacteriol. 185:2330-2337(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000209; AAC74173.1; -.
EMBL; D90744; BAA35897.1; -.
EMBL; AE005319; AAG55835.1; -.
EMBL; AP04565; BAB34890.1; -.
EMBL; AF044668; AAC38646.1; -.
EMBL; AE008751; AAL20120.1; -.
EMBL; AL627269; CAD08115.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EcoGene; EC10890; rpmF.
StyGene; SG10689; rpmF.
HAMAP; MF 00340; -; InterPro; IPR005718; S32 bact or TIGRPAMS; TIGR01031; rpmF_bact;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL627269; CAD08315.1; --
EMBL; AE016839; AA069353.1; --
EMBL; AE015136; AAV42712.1; --
PIR; C90812; C90812.
PIR; G88571; G85671.
PIR; JV0048; R5EC32.
ECC2DBASE; I011.7; --
ECC2DBASE; I011.7; --
EMBL; EMBL; EMBLTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M29698; AAA24575.1; -.
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33.3%;
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RRSHDALTAVTSLSV 29
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MASS SPECTROMETRY
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ID ATP8_CAN
AC P17345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9PP¥4;
                                                                                                                                                                                                                                                                                                                                                                                                                                 UREPA
                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
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                                                                                                                                                                                                                                                                                                                                            WEDLINES.21060447; Pubmed=10749672;
Chen S.C.A., Wright L.C., Golding J.C., Sorrell T.C.;
Chen S.C.A., Wright L.C., Golding J.C., Sorrell T.C.;
Purification and characterization of secretory phospholipase B,
"Purification and lysophospholipase/transacylase from a virulent
strain of the pathogenic fungus Cryptococcus neoformans.";
Biochem. J. 347:431-439(2000)
-!- FUNCTION: A NOVEL FUNGAL PROTEIN THAT EXHIBITS PHOSPHOLIPASE B
-!- FUNCTION: LYSOPHOSPHOLIPASE (LPL) AND LYSOPHOSPHOLIPASE JAC.
-!- CATIVITIES. ACTIVE ONLY AT ACIDIC PH.
-!- CATIVITIES. ACTIVE AT A ACIDIC PH.
-!- CATIVITIES. ACTIVE A ACIDIC PH.
-!- GATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
-!- Glycerophosphocholine + a fatty acid anion.
-!- ENZYME REGULATION: INHIBITED BY FERRIC ION.
                                                    30-WAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Extracellular phospholipase (RC 3.1.1.5) (Fragments).
Cryptococcus neoformans (Filobasidiella neoformans)
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Akramann G.F.,
Rohrmann G.F.,
"The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 9.4 kDa protein (ORF76).
Orgyla pseudotaugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; daDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 1; Length 79;
Pred. No. 1.3e+02;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8637 MW; 685F80B144195AF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyhedrosis virus genome.";
Virology 229:381-399(1997).
-!- SIMILARITY: TO CORRESPONDING ORF IN ACMNEV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLUIAR LOCATION: INHIBITED BY PERRIC Hydrolase; Lipid degradation; Glycoprotein. NON CONS 40 22
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                                       Created)
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Best Local Similarity 40...
7; Conservative
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39 RRNVADAFNMEXYLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
66
74
79
                                       30-MAY-2000 (Rel. 39, 30-MAY-2000 (Rel. 39, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40
56
65
73
79 AA;
                                                                                                                                                                                                                                                           NCBI_TaxID=5207;
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010326;
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SEQUENCE
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Nature 407:757-762(2000).

-!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
biosynthesis (By similarity).

-!- PATHWAY: De novo fatty acid biosynthesis.

-!- PATHWAY: The propentetheline is transferred from CoA to a specific serie of the apo-ACP-like protein (Potential).

-!- SIMILARITY: Contains 1 acyl carrier domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHOPANTETHEINE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glass J.I., Lefkowitz B.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>.</u>
د.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
NCBI TaxID=134821;
                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30.5; DB 1; Length 77;
Pred. No. 1.6e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                        Length 84;
                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3CDB655FBFA968C6 CRC64;
                                 l protein.
84 AA; 9427 MW; 46F6656120231346 CRC64;
                                                                                                        Score 31; DB 1; I Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Acyl carrier protein homolog (ACP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 77 A.A.
                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR006162; Ppantne_attach.
Pfam, PP00550; pp-binding; 1.
PR051TE; PS50075; ACP DOMAIN; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AE002149; AAF30918.1; -.
InterPro, IPR006163; Pp_bind.
InterPro, IPR006162; Ppantne_attach.
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                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                              1 RRRVYDA--LNVLMAMNII 17
                                                                                                                                                                                                                                               || |:: || :: ||:: 56 RRSFYESLKLNCIVCINVL 74
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77 AA; 8750 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 33.5%;
Similarity 39.1%;
9; Conservative
                                                                                                              34.1%;
31.6%;
EMBL; U75930; AAC59075.1;
Hypothetical protein.
SEQUENCE 84 AA; 9427 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                              Query Match
Best Local Similarity
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Serovar 3;
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MEDLINE=20530297; PubMed=11076505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCP3 MESMA
                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9U8D1;
                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              SCP3_MESMA
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
   8
                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Venom gland;
MEDLINE=99402983; PubMed=10471839;
Zhu S.-Y., Li W.-X., Zeng X.-C., Jiang D.-H., Mao X., Liu H.;
Zhu S.-Y., Li West, Zeng X.-C., Jiang D.-H., Mao X., Liu H.;
"Molecular cloning and sequencing of two 'short chain' and two 'long chain' K(+) channel-blocking peptides from the Chinese scorpion Buthus
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSPNJP7; P58491;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 41, Last snnotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
Meurotoxin BmP02 precursor (Potassium ion channel blocker P02P).
Mesobuthus martenaii (Manchurian scorpion) (Buthus martenaii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Butholdea; Buthidae; Mesobuthus.
                                                                Mitochondrion.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (AGL).
                                                                                                                                                                                                                                                                                                                                                                                                            Hydrogen ion transport, CF(0); Mitochondrion; Transmembrane.
TRANSMEM 12 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB 1; Length 48; Pred. No. 1.2e+02; Mismatches 3; Indels
                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                   0E7876341CAF0747 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 AA.
                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                  STRAIN=CBS 7154 / SP1;
MEDLINE=90332440; PubMed=2143015;
                                                       Candida parapsilosis (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52115; CAA36361.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         martensii Karsch.";
FEBS Lett. 457:509-514(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                 48 AA; 5492 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NWR OF 29-56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :|:| ||| |
LRLLIARNIIIK 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S10465; PWCK8P
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=34649;
                                                                                                   NCBI_TaxID=5480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Venom;
                                                                                                                                                                                                                                                  H(+) (Out)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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MEDLINE=99402983; PubMed=10471839;
MEDLINE=99402983; PubMed=10471839;
Zhu S.-Y., Li W.-X., Zeng X.-C., Jiang D.-H., Mao X., Liu H.;
"Molecular cloning and sequencing of two 'short chain' and two 'long chain' K(+) channel-blocking peptides from the Chinese scorpion Buthus
Xu Y.Q., Wu J.H., Pei J.M., Shi Y.Y., Ji Y.H., Tong Q.C.; "Solution structure of BmP02, a new potassium channel blocker from the venom of the Chinese scorpion Buthus martensi Karsch.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99313193; PubMed=10386622;
Wu J.J., Dai L., Lan Z.D., Chi C.-W.;
"Genomic organization of three neurotoxins active on small conductance
Ca2+-activated potassium channels from the scorpion Buthus martensi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurotoxin BmP03 precursor (Potassium ion channel blocker P03).
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthopoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEBS Lett. 457:509-514(1999).
-!- FUNCTION: Blocks small conductance Calcium-activated potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                    Blockemistry 39:13669-13675(2000).
-!- FUNCTION: Blocks potassium channels.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: BELONGS TO THE SCORPION LEIUROTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: BELONGS TO THE SCORPION LEIUROTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 1; Leng....
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70953032042F8672 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toxin; Neurotoxin; Ionic channel inhibitor;
Potassium channel inhibitor; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF132975; AAF31296.1; -. PDB; 1DU9; 28-MAR-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 452:360-364(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 RLFTLVLIVLAMNVM 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RVYDALNVLMAMNII 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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40 RRRISDRCTVLVDRGLL 56

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein resembling coliphage repressors.";
J. Bacteriol. 173:955-960(1991).
-!- FUNCTION: POSSIBLY PREVENTS RNA POLYMERASE ACCESS TO THE PROMOTERS
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91123222; PubMed=1991733;
Ken R., Hackett N.R.;
"Halobacterium halobium strains lysogenic for phage phi H contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage phi-H.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
NCBI_TaxID=10771;
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                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR LYTIC CELL CYCLE TRANSCRIPTION.
SIMILARITY: TO THE HELIX-TURN-HELIX FAMILY OF DNA-BINDING PROTEINS, AND IN PARTICULAR TO COLIPHAGE REPRESSORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 1; Length 89; Pred. No. 2.3e+02; 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                     Score 30; DB 1; Length 56; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repressor; DNA-binding; Transcription regulation.
DNA BIND 29 38 H-T-H MOTIF.
SEQUENCE 89 AA; 10167 MW; 3D21ED8E53F01741 CRC64;
                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
70953032007E8672 CRC64;
                                                                                                                                                              Porassium channel inhibitor; Signal.
SIGNAL 1 28 BY SIMILARITY.
CHAIN 29 56 NEUROTOXIN BMP03.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   89 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                   Neurotoxin; Ionic channel inhibitor;
                                                                                                                                                                                                                                                                                                8; Mismatches
                                                                                                              EMBL; AF097408; AAF01253.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.0%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X52504; CAA36746.1; -.
                                                                                                                                                                                                                                                                      33.0%;
26.7%;
                                                                                                                                                                                                      47
52
54
6001 MW;
                                                                                                                           EMBL, AF156170, AAF29463.1,
HSSP, Q9NJP7, 1DU9.
Toxin, Neurotoxin, Ionic cha
                                                                                                                                                                                                                                                                                                                                           | :: :::|||::
RLFTLVLIVLAMNVM 17
                                                                                                                                                                                                                                                                                                                            3 RVYDALNVLMAMNII 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 26.7 tes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A38167;
                                                                                                                                                                                                                                                                                                                                                                                                                     BPPHH
                                                                                                                                                                                                                    DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       VREP BPPHH
ID VREP BPI
AC P22562;
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comparative analysis of the frd operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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30-MAY-2000 (Rel. 39, Last sequence update)
38-FBB-2003 (Rel. 41, Last annotation update)
Phorbol-12-myristate-13-acetate-induced protein 1 (PMA-induced protein 1) (Immediate-early-response protein APR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding the fumarate reductase of Proteus vulgaris. Extensive sequence divergence of the membrane anchors and absence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.0%; Score 30; DB 1; Length 96; 66.7%; Pred. No. 2.5e+02; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 AA; 10300 MW; EC094F1F37956EE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           frd-linked ampC cephalosporinase gene.";
Eur. J. Biochem. 167:481-488(1987).
-!- SIMILARITY: BELONGS TO THE HUPF/HYPC FAMILY.
                                                                                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 AA.
                                                                                96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X06151; CAA29511.1; -.
PIR; S00119; S00119.
Interpro; IPR001109; HupE_HypC.
Pfam; PR01455; HupF HypC; 1.
PIRSF; PIRSF005618; HupF HypC; 1.
PRINTS; PR00445; HupFHyPC;
PCDOM; PD0001112; HupF HypC; 1.
TIGRFAMB; TIGR00074; hypC_hupF; 1.
                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
MEDLINE=90376412; PubMed=2398525;
                                                                                                                                                                                                                                                                                                                   FRD operon hypothetical protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=88004470; PubMed=3308458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae; Proteus
NCBI_TaxID=585;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                     STANDARD;
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ETLNALMAM 75
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  Proteus vulgaris.
                                                                                YFRC PROVU
P20927;
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APR_HUMAN
RESULT 12
YFRC PROVU
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Herrmann R.;
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AC P75238;
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                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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;
Hijikata M., Kato N., Sato T., Kagami Y., Shimotohno K.; "Molecular cloning and characterization of a cDNA for a novel phorbol-12-myristate-13-acetate-responsive gene that is highly expressed in an adult T-cell leukemia cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC 33530 / G-37;

MEDLINES-96026346; PubMed=7569993;

Frager C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Muyven D.T., Vutterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).
                                                                                              J. Virol. 64:4632-4639(1990).
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADULT T-CELL LEUKEMIA CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29.5; DB 1; Length 54; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM): 604959; -.
GO; GO:0007048; P:oncogenesis; TAS.
RROUENCE 54 AA; 6030 MW; 291A142B27167E70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FBB-1996 (Rel. 33, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) 28-FBS ribosomal protein L32. RPMF OR RPL32 OR MG363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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InterPro; PR002677; Ribosomal_L32p.
InterPro; IPR005718; 32_bact_org.
Pfam; PF01783; Ribosomal_L32p; 1.
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                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90070; BAA14111.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.48;
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-!- SIMILARITY: BELONGS TO THE L32P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9TKT1;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cytochrome b559 alpha subunit (PSII reaction center subunit V).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                       Score 29.5; DB 1; Length 56;
Pred. No. 1.7e+02;
5; Mismatches 6; Indels
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TIGRFAMS; TIGR01031; rpmF_bact; 1.
Ribosomal protein; Complete proteome.
1 nitT MET 0 0 0 SIMILARITY.
SEQUENCE 56 AA, 6492 MW; B4FCC76E52C4287D CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
SOS ribosomal protein L32.
RPMF OR MPNS40 OR MP302.
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InterPro; IPR002677; Ribosomal L32p.
InterPro; IPR005718; S32 bact org.
Pfam, PF01783; Ribosomal L32p; 1.
TIGRPAMS; TIGR01031; rpmF bact; 1.
Ribosomal protein; Complete proteome.
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MEDLINE=97105885; Pubmed=8948633;
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14 KRRSHDALTA-QALSVCQK 31
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Similarity 36.8%;
7; Conservative
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                                                                                                                                          Query Match
Best Local Similarity
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FUNCTION: Histone H4, along with histone H3, plays a central role
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NULM_DASNO
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                                                                                                                                                                                                                                                                                                                                                   "The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: insights into the architecture of ancestral chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LUMENAL (POTENTIAL).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
B267F4441B857D23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Electron transport; Transmembrane; Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).

-!- FUNCTION: This b-type cytochrome is tightly associated with the reaction center of photosystem II and possibly is part of the water-oxidation complex.

-!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
-!- SIMILARITY: Belongs to the psbE / psbF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97257506; PubMed=9103980;
Salvini M., Bini E., Santucci A., Batistoni R.;
H4 histone in the macronucleus of Blepharisma japonicum (Protozoa,
Ciliophora, Heterotrichida).";
FEMS Microbiol. Lett. 149:93-98(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H41 BLEJA STANDARD; PRT; 97 AA.
P80737; P90815;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Blepharisma japonicum.
Blepharisma japonicum.
Eukaryota; Alveolata; Ciliophora; Heterotrichea; Heterotrichida; Blepharismidae; Blepharisma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.9%; Score 29; DB 1; Length 83; 31.2%; Pred. No. 3.2e+02; tive 5; Mismatches 6; Indels
                                                                             Chloroplast.
Eukaryota, Viridiplantae; Chlorophyta; Prasinophyceae; Chlorodendrales; Chlorodendraceae; Nephroselmis.
NCBI_TaxID=31312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-46, AND SEQUENCE OF 9-97 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF137379; AAD54835.1; -. HAWAP; MF 00642; -; 1. Interpro; 1PR006216; Cyt_b559. Interpro; 1PR006217; Cyt_b559 alpha. Pfam; PF00283; cytcohr_b559; 1. Pfam; PF00284; cytcohr_b559; 1. Pfam; PR00284; cytcohr_b559; 1. Pfam; PR05137; Cytcohr_b559; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                      STRAIN=NIES-484;
MEDLINE=99398694; PubMed=10468594;
                                                                                                                                                                                                                                                                                                                                Turmel M., Otis C., Lemieux C.; "The complete chloroplast DNA se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 39 1
40 83 1
23 23 23 83 83 A3, 9404 MW; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 ITDRFNALQQMDILTE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 31.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Photosystem II; Heme;
                                                   Nephroselmis olivacea.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A5-3;
                                                                                                                                                                                                                                                                                                                                                                                                                           genomes.";
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TRANSMEM
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                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation -
                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for comment is not removed. Usage by and for commencial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
in nucleosome formation.
SUBUNIT: The nucleosome is an octamer containing two molecules
each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding. NON TER 97 97 97 85 SEQUENCE 97 AA; 10722 MW; 64BBB2D65594607C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Edentata, Dasypodidae, Dasypus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 29; DB 1; Length 97;
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
18-UUL-1998 (Rel. 36, Last annotation update)
MINDAL ubdainone oxidoreductase chain 4L (EC 1.6.5.3).
                                                                                                                SIMILARITY: Belongs to the histone H4 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dasypus novemcinctus (Nine-banded armadillo).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS, PROD623; HISTONEH4.
PRODOM; PD001827; Histone H4; 1.
SMART; SM00417; H4; 1.
PROSITE; PS00047; HISTONE H4; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, X97995; CAA66634:1; -.
InterPro; IPR004822; Histone_core.
InterPro; IPR001951; Histone_H4.
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BR; T11449; T11449.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00420; oxidored q2; 1.
ProDom; PD000359; Oxidred4L; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.9%;
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80 RRKTVTALDVVYAL 93
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Best Local Similarity 42.9
Matches 6; Conservative
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AND FUNCTION.
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Q98QN7;
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SEQUENCE
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RL32 MYCPU
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                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
Cytochrome c oxidase polypeptide VID (EC 1.9.3.1) (Fragments).
Thunnus obesus (Bigeye tuna).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Scombridae; Thunnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            liver.",
Eur. J. Biochem. 248:99-103(1997).

-!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
MITOCHONDIAILA ELECTRON TRANSPORT. THIS PROTEIN MAY BE ONE OF THE
HEME-BINDING SUBUNITS OF THE OXIDASE.
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bummalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The subunit structure of cytochrome-c oxidase from tuna heart and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97454291; PubMed=9310366;
Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
Kadenbach B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
LeCCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Retinol-binding protein III, cellular (CRBP-III) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.8%; Score 28; DB 1; Length 34; 85.7%; Pred. No. 1.8e+02; Live 0; Mismatches 1; Indels
                                                          Score 29; DB 1; Length 98;
Pred. No. 3.8e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE PEPTIDES SHOWN IS UNKNOWN
  ase; NAD; Ubiquinone; Mitochondrion.
98 AA; 10840 MW; D0FF9BC309048774 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 AA; 4035 MW; B34A390BA1F05546 CRC64;
                                                                                                                                                                                                                                                                                                34 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; Mitochondrion.
                                                              31.9%;
55.6%;
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                                                                                  Local Similarity 55.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FISSUE=Heart, and Liver;
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                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                               8 LNVLMAMNI 16
                                                                                                                                                                       ||::|| :|
LNIIMAFSI 14
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8241;
    Oxidoreductase;
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P82708;
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P80976;
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SEQUENCE
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                                                              Query Match
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DT 28-FEB

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
-!- SIMILARITY: BELONGS TO THE L32P FAMILY OF RIBOSOMAL PROTEINS.
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma
                                                Calderone V., Ottonello S., Bolchi A., Zanotti G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.8%; Score 28; DB 1; Length 42;
58.3%; Pred. No. 2.3e+02;
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mypuilst; MYPU 3240; -.
HAMAP; MF 00340; -.; 1.
InterPro; IPR002677; 1.
InterPro; IPR002677; 31 bact org.
Pfam; PF01783; Ribosomal_L32p; 1.
TIGRFAMS; TIGR01031; TupH bact; 1.
TIGRFAMS; TIGR01031; TupH bact; 1.
SEQUENCE 61 AA; 6904 MW; B7FD0E475ACA3DB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 AA; 4892 MW; ACB4F1399FDD7F09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-0cT-2001 (Rel. 40, Created)
16-0cT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vitamin A; Retinol-binding; Transport.
                                                                                                                                                                                                                                                                                                                       HSSP; P82980; 1GGL.
InterPro; IPR000463; Fatty acid BP.
InterPro; IPR000566; LipocIn_cyFFABP.
Pfam; PF00061; Lipocalin; 1.
PROSITE; PS00214; FABP; FALSE_NEG.
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MEDLINE=21267165; PubMed=11353084;
TISSUE=Kidney;
MEDLINE=21173623; PubMed=11274389;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 ALNVLMAMNIIS 18
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Mycoplasma pulmonis.
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Best Loc
Matches
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SPECIESE.Coll; STRAIN-C157:H7 / RIMD 0509952;
MEDLINE-21156231; Pubbled-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino E., Nakayama K., Mirata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli Ol57:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES-E.coli; STRAIN=K12 / MG1655;
MEDLINE=92558234; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SPECISS=E.CO.1; STRAIN=O6:H1 / CFT073 / ATCC 700928;
SPECISS=E.CO.1; STRAIN=O6:H1 / CFT073 / ATCC 700928;
MEDLINE=E2.8018624; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Burkles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                            Gaps
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SPECIES=E. Coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
SPECIES=E. Coli; STRAIN=01206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Posta D.G., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Postai G., Hachett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                     Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
                                            ö
                Length 61;
                                                                                                                                                                          YIFL ECOLI STANDARD; PRT; 67 AA.
P39166; 08X3YS;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical lipoprotein yifL precursor.
YIFL OR B3808.1, OR C4729 OR E5325 OR ECS4737.1 OR SF3886.
              Score 28; DB 1; Length 61;
Pred. No. 3.4e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECLES=E.coli; STRAIN=K12;
Glaser P., Sismeiro O., Danchin A.;
submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                        67 AA.
                                                                                                                                                                                                                                                                        Escherichia coli,
Escherichia coli 06,
Escherichia coli 0157:H7, and
                   30.8%;
50.0%;
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                                               5; Conservative
                                                                         1 RRRVYDALNV 10
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16 KRQTHDALKV 25
                   Query Match
Best Local Similarity
                                               Matches
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                                                                                                                                                                                                                          "Genome sequence of Shigella flexneri 2a: insights into pathogenicity intrough comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                       SPECIES_S.flexneri; STRAIN=301 / Serotype 2a; MEDLINE=22272406; PubMed=12384590; Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang J., Yang G., Wu H., Qu D., Dong J., San D., Xue Y., Zhao A., Zhao J., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dacterial genome.";
Nucleic Acids Res. 22:4756-4767(1994).
-1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
Plasmid IncFI ColV2-K94.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                           SPECIES=E.coli;
MEDI-INE=95075659, PubMed=7984428;
Borodovsky M., Rudd K.E., Koonin E.V.;
Intrinsic and extrinsic approaches for detecting genes in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL LIPOPROTEIN YIFL.
N-ACYL DIGLYCERIDE (POTENITAL)
BORSONNY -> MVHPR (IN REF. 2).
4A52CF48A555A7F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 1; Length 67;
Pred. No. 3.8e+02;
4; Mismatches 4; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; E86067; E86067.
Ecodene; EG12233; YIGL
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Hypothetical protein; Nembrane; Lipoprotein; Signal;
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01-FRE-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Replication initiation protein (Fragment).
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EMBL, XE6782; -; NOT ANNOTATED CDS.
EMBL, XE6782; -, NOT ANNOTATED CDS.
EMBL, ARE016769; AANNOTATED CDS.
EMBL, ARE016769; AANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP002567; -; NOT ANNOTATED_CDS.
EMBL; AE015395; AAN45322.1; -.
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nilarity 38.5%;
Conservative 4
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7177 MW;
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ses 5; Conserv
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[6]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION
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ID REPL ECOLI
AC P10396;
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79 AA; 8762 MW;
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Best Local Similarity
Matches 6; Conserv
                              Query Match
Best Local Similarity
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NCBI_TaxID=10255;
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SEQUENCE 79
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01-FEB-1996
Protein 15.
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                                                                                                                                                                                                                                            Protein 15.
                                                                                                                                                                          VACCV
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    SEQUENCE
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P12924;
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P33001;
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VIO5_VACCV
                                                        Matches
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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SEQUENCE FROM N.A.

MEDIATRE-8623772; PubMed=2423502;

MEDIATRE-8623772; PubMed=2423502;

"Incompatibility repressor in a RepA-like replicon of the IncFI
plasmid Coly-V2-K94, ",

"Incompatibility repressor in a RepA-like replicon of the IncFI
plasmid Coly-V2-K94, ",

"Incompatibility repressor in a RepA-like replicon of the IncFI
plasmid Coly-V2-K94, ",

"Incompatibility repressor in a RepA-like replicon of the IncFI
plasmid Coly-V2-K94, "

"Incompatibility repressor in a RepLICATION FROTEIN IS COMPATIBLE WITH THE
REPA REPLICON FOR THE INCFII R PLASMIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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BEDLINE-91021027; PubMed=2219722;
Goebbel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
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Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                            77 AA; 8941 MW; 44784ECC89D965E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete DNA sequence of vaccinia virus."; Virology 179:247-266(1990).
                                                                                                                                                                                                                                                  EMBL; M13472; AAA21195.1; -.
Plasmid; DNA replication; Plasmid copy control.
NON TER 77 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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InterPro; IPR006803; Pox_I5.
Pfam; PF04713; Pox_I5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology 179:517-563 (1990).
                                                                                                                                                                                                                                                                                                                                                6; Conservative
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(Rel. 17,
(Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991
01-FEB-1991
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmitt J.F.C., Stunnenberg H.G.; "Sequence and transcriptional analysis of the vaccinia virus HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccinia virus (strain WR).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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                                     Score 28; DB 1; Leugur-
Pred. No. 4.5e+02;
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Pred. No. 4.5e+02;
2; Mismatches 3; Indels
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76F4826B7009DFAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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                                                                                                    2; Mismatches
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or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                        PRT;
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STRAIN-India-1967 / Isolate Ind3;
MEDLINE-94152154; Pubmed-8109158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J03399; AAB59807.1; -. PIR; E29889; WZVZI5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 30.8%;
Similarity 54.5%;
6; Conservative
                                                   30.8%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006803; Pox_I5.
Pfam; PF04713; Pox_I5; 1.
                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                     6 DALNVLMAMNI 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 DALINVILMAMNI 16
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                                                                                                                                                                                                      3 DAITVLTAIGI 13
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Pasteurellaceae; Haemophilus.
                       NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 28
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                                                                                                                                                             STRAIN=India-1967 / Isolate Ind3;
MEDLINE=93190624; PubMed=8383392;
Shchelkunov S.N., Blinov V.M., Totmenin A.V., Marennikova S.S.,
Kolykhalov A.A., Frolov I.V., Chizhikov V.E., Gytorov V.V.,
Andzhaparidze O.G., Sandakhchiev L.S.;
"Nucleotide sequence analysis of variola virus HindIII M, L, I genome
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=India-1967 / Isolate Ind3;
MEDIJNE=93202281; PubMed=8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
"Genes of variola and vaccinia viruses necessary to overcome the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Potential virulence determinants in terminal regions of variola smallpox virus genome.";
Nature 366:748-751(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-701-1999 (Rel. 38, Created)
15-701-1999 (Rel. 38, Last sequence update)
16-701-2001 (Rel. 40, Last sannotation update)
16-701-2001 (Rel. 40, Last annotation update)
Virulence-associated protein D.
VAPD OR H10450.
VAPD OR H10450.
Bachenjalus influenzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
                                   Sandakhchiev L.S.; "Analysis of the nucleotide sequence of a 43 kbp segment of the hypasis of the nucleotide sequence of variola virus India-1967 strain."; virus Res. 30:239-258(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
           Shchelkunov S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 1; Length 79;
Pred. No. 4.5e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF04713; Pox IS; 1. SEQUENCE 79 AA; 8778 MW; AD4E703B701B5C86 CRC64;
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MEDLINE=94088747; PubMed=8264798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X67119, CAA47559.1; -.
EMBL, X69198; CAA49000.1; -.
EMBL, L22579, AAA60807.1; -.
PIR, C36843; C36843.
PIR, T28497; T28497.
InterPro, IPR006803; Pox_I5.
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54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protective mechanisms.";
FEBS Lett. 319:80-83(1993).
                                                                                                                                                                                                                                                                                                                                                 Virus Res. 27:25-35(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Best Local Similarity
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                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              COMPLETE GENOME
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P71351;
15-JUL-1999 (
15-JUL-1999 (
                                                                                                                                                                                                                                                                                                                               fragments.";
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VAPD HAEIN
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                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Сарв
SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhogh W., Fields C.A., Gocayne J.D., Schirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Geneb C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang C., Qian B., Tu Y., Gu W., Wang Y., Han Z., Chen Z.; "Novel genes expressed in hematopoietic stem/progenitor cells from Myelodysplastic syndromes patient."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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P82221; Q9BST6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mitochondrial 28S ribosomal protein S21 (MRP-S21) (MDS016)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 1; Length 91;
Pred. No. 5.3e+02;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; HI0450; -.
Pfam; PF04605; VapD_N; 1.
Virulence; Complete protecome.
SEQUENCE 91 AA; 10543 MW; 70B23CDE28E083E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.8%;
Best Local Similarity 35.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U32728; AAC22108.1; -. PIR; C64069; C64069.
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50 DMANLFQAMNALKQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 76-80.
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87 AA

STANDARD;

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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SRE-2003 (Rel. 42, Last annotation update)
Mitochondrial 28S ribosomal protein S21 (MRP-S21).
                                                                                                                                                           Mus musculus (Mouse)
         RT21 MOUSE
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                                                                                                                                             MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
MALSTONE T.D., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Artschul M.J., Defin W.F., Casavant T.L., Scheetz T.E., Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worlby D.M., Sodergren B.J., Lu X., Gibbs R.A., Willalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A., Willalon D.K., Murny D.M., Schergren B.J., Lu X., Gibbs R.A., Willalon A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myera M.A.; Schein J.E., Jones S.J.M., Mara M.A., Schein J.E., Jones S.J.M., Mara M.A., Schein J.E., Jones S.J.M., Mara M.A.; Funder S.M., Frankon A., Schein J.E., Jones S.J.M., Mara M.A.; Funder A., Schein J.E., Jones S.J.M., Mara M.A.; Funder A., Schein J.E., Jones S.J.M., Mara M.A.; Funder A., Schein J.E., Schein 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21276436; PubMed=11279123; Moseley A., Spremulli L.L.; Koc B.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.; The small subunit of the mammalian mitochondrial ribosome: andle subunit of the full complement of ribosomal proteins present."; J. Biol. Chem. 276:19363-19374(2001).
-!- SIBUNIT: Component of the mitochondrial ribosome small subunit (28S) which comprises a 12S rRNA and about 30 distinct proteins.
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: BELONGS TO THE S21P FAMILY OF RIBOSOMAL PROTEINS.
  Terasaki M., Takemoto-Hori C., Hanada T., Ueda T., Wada A.,
Suzuki T., Terasaki M., Takemoto-Hori C., Hanada T., Ueda T., Wada Watanabe K.;
Proteomic analysis of the mammalian mitochondrial ribosome.
Identification of protein components in the 28 S small subunit.";
J. Biol. Chem. 276:33181-33195(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.2%; Score 27.5; DB 1; Length 87; 36.8%; Pred. No. 6.1e+02; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     omal subunit; I ribosome; NAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF182417; AAG14953.1; ALT_INIT.
EMBL; BC04556; BAB41008.1; --
EMBL; BC004556; AAH06456.1; --
EMBL; BC006554; AAH06554.1; --
Genew; HGNC:14046; MRPS21.
GO; GO:0005753; C:mitcochondrial small ribosomal sub
GO; GO:0005753; C:mitcochondrial constituent of ribosom
GO; GO:00057153; F:structural constituent of ribosom
InterPro; PR001911; Ribosomal S21.
PROSITE; PS01181; Ribosomal S21.
Ribosomal protein; Mitcochondrion.
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Matches 7; Conservative
                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Mammary gland;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=288828; MEDLINE F.S., Wagner L., Sheamen C.M., Schuler G.D.,

MEDLINE R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

MEDLINE R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

MEDLINE R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

MEDLINE S.A., McEwan P.J., Peters G.J., Abramson R.D., Mullahy S.J.,

MEDRAK S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

MILAGO D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

MILAGO D.K., Muzny D.M., Schergren E.J., Lu X., Gibbs R.A.,

MILAGO D.K., Muzny D.M., Schergren E.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Schergren E.D., Dickson M.C.,

Milakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

MILAGO D.K., Milalon D.K., Milalon D.E.,

MILARITY: BELONGS TO THE S21P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                           MEDLINE-21413863; PubMed=11402041;
Suzuki T., Terasaki M., Takemoto-Hori C., Hanada T., Ueda T., Wada A.,
Watanabe K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                            "Proteomic analysis of the mammalian mitochondrial ribosome. Identification of protein components in the 28 S small subunit."; J. Biol. Chem. 276:33181-33195(2001).
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SEQUENCE 87 AA; 10561 MW; D0F4DAF886AA29DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1913542; MTP821.
InterPro; IPR001911; Ribosomal S21.
PROSITE; PS01181; RIBOSOMAL_S21; FALSE_NEG.
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                                                                                           NCBI_TaxID=10090
                                                                                                                                                                              SEQUENCE
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2 RRVYD-----ALNVLMAMN 15

RESULT 29 RT21_MOUSE

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maize two dimensional gel protein database: towards an integrated
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15 AA; 1853 MW;
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62.5%;
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Guest Local Similarity 62.3°,
Best Local Similarity 63.3°,
Gonservative
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6 RDQVYDAM 13
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Best Local Similarity
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                                                                                                                                                                                                                                    MaizeDB; 123958;
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15-DEC-1998 (
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SECE_TREPA
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YC18_PORPU
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 293:2093-2098 (2001).
-!- FUNCTION: THIS PROTEIN IS ONE OF THE 16S RIBOSOMAL RNA BINDING PROTEINS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE S15P PAMILY OF RIBOSOMAL PROTEINS.
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 688)
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                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
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InterPro; IPR001589; Ribosomal_S15.
InterPro; IPR001589; Ribosomal_S15.
InterPro; IPR001599; Ribosomal_S15; 1.
Prodom; PD157043; RS15_bact; 1.
TIGRRAMs; TIGR00952; S15_bact; 1.
PROSITE; PS00362; RIBOSOMAL_S15; 1.
Ribosomal_Drotein; rRNA-binding; Complete proteome.
SEQUENCE 91 AA; 10594 MW; 5C6D4C302FA49114 CRC64;
                                                                                                                                                   Last sequence update)
Last annotation update)
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RRRLLNYIKKNNVSKYLDLISK 84
                                                                     PRT;
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                                                                                                                                                                                                            30S ribosomal protein S15.
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(Rel. 41,
(Rel. 41,
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tes 8; Conserv
                                                                                                                                                                                                                                                                         Rickettsia conorii
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      RESULT 30

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NCBI_TaxID=2787;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.4, ITS MW IS: 48.4 kDa.
-!- SIMILARITY: TO EXBODES HISTONE-BINDING PROTEIN NI/N2 AND RABBIT
AND HUMAN NUCLEAR AUTOANTIGENIC SPERM PROTEIN.
Maize-2DPAGE; P80633; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Avonport; Reith M.E., Munholland J.; Reith M.E., Munholland J.; (Complete = Complete)
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Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 1; Length 15;
Pred. No. 1.1e+02;
2; Mismatches 1; Indels
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-!- SIMILARITY: SOME, TO SYNECHOCOCCUS PCC 7942 NBLA.
                                                                                                                                                                                                                                                                                                          CA0E12A5DAED8DC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304D4D9EDD0D2371 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Hypochtetical 6.9 kDa protein ycf18 (ORFS8).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 37, Created)
(Rel. 37, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PP04485; nblA, 1.
Chloroplast, Hypothetical protein.
SEQUENCE 58 AA; 6923 MW; 304D4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; TP0420; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TP0420.
                                                                                                                                                                                                                                                                                                                                                                                                                                            TREPA
                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                       Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren B., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                 -!- FUNCTION: ESSENTIAL FOR PROTEIN EXPORT.
-!- SUBCELLULAR LOCATION: Tail-anchored membrane protein (Potential).
-!- SIMILARITY: Belongs to the secE/SEC61-gamma family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prokaryotic
                                                         Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01067; SECE_SEC61G; 1.
Protein transport; Translocation; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=95261545; PubWed=7742976;
Lai C.-Y., Baumann P., Moran N.A.;
"Genes of the tryptophan biosynthetic pathway of the prokaryoti endosymbiont (Buchnera) of the aphid Schlechtendalia chinensis."; Insect Mol. Biol. 4:47-59(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera aphidicola (subsp. Schlechtendalia chinensis).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP-dependent hsl protease ATP-binding subunit hslU (Fragment)
                                                                                                                                                                                                                                           "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.7%; Score 27; DB 1; Length 59; 23.5%; Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 59 POTENTIAL.
59 AA; 6789 MW; 9AC35BA8F48B2A7F CRC64;
 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
16-OCT-2001 (Rel. 40, Last annotatio
Preprotein translocase secE subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGR00964; 3a0501806; 1.
                                                                                                                             MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001901; SecE.
InterPro; IPR005807; SecE_bac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001205; AAC65223.1; -. PIR; E71349; E71349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|: |: |: :: :: 23 RTQVHTAVKVVLVSTVV 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RRRVYDALNVLMAMNII 17
                                                                                                                                                                                                                                                                    Science 281:375-388(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00584; SecE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                          Treponema pallidum
                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=118110;
                                                                                                              STRAIN=Nichols;
                                                                     NCBI_TaxID=160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; TP0235;
                                                                                                                                                                                                                           Venter J.C.;
                                                                                                                                                                                                                                                       spirochete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSLU BUCSC
069227;
                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 34
HSLU_BUCSC
ID HSLU B
AC 06927
DT 30-MAX
DT 28-FEB
DE ATP-de
GN BLChne
OC Bacter
OC Bacter
OC Bacter
OC NCBI TR
RP SEQUEN
RR SEGUEN
RX MEDLIN
RA Lai C.
RT "Genet
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                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gavin M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.,
                        COMPLEX (BY SIMILARITY).
-!- SUBUNIT: Interacts with hslv (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=160;
CHAPERONE SUBUNIT OF A PROTEASOME-LIKE DEGRADATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534077998EAC062A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome.
SEQUENCE 75 AA, 8256 MW; D01376B1670F383B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.7%; Score 27; DB 1; I 54.5%; Pred. No. 6.1e+02; tive 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 1;
Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein TP0420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001219; AAC65408.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U09184; AAC31219.1; -. HSSP; P32168; 1E94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 AA; 8502 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chaperone; ATP-binding.
NON TER 1 1 1 SEQUENCE 72 AA. orn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RRVYDALNVLM 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
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Matches

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                                                                                                                                                                                                                                                                                    STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Wolker C.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma
Hypothetical 9.1 kDa protein in nifx-nifw intergenic region (ORF1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 407:508-513(2000).
-i- SIMILARITY: BELONGS TO THE L31E FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                              Harriott O.T., Hosted T.J., Benson D.R.; "Sequences of nifx, nifw, nifz, nifB and two ORF in the Frankia nitrogen fixation gene cluster.";
                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Frankineae; Frankiaceae; Frankia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoplasma acidophilum.
Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27; DB 1; Length 82;
Pred. No. 7.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Nitrogen fixation.
SEQUENCE 82 AA; 9081 MW; AFBBD86827B4322C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RPL31E OR TA0054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL445063; CAC11202.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                  MEDLINE=95369734; PubMed=7642138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L29299; AAC82972.1; -. PIR; T09234; T09234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF05082; DUF683; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                           Gene 161:63-67(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 RRTYDA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RRVYDA 7
                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2303;
                                                                                        NCBI_TaxID=1859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acidophilum."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RL31 THE
Q9HMI7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 38
RL31 THEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptides..;
J. Biol. Chem. 274:8405-8410(1999)
Acid (LTA). Activated D-alanyl-Dcp donates its D-alanyl
Substituent to membrane-associated LTA (By similarity).
J. CATALYTIC ACTIVITY: ATP + D-alanyl-poly(ribitol phosphate) =
AMP + diphosphate + O-b-alanyl-poly(ribitol phosphate).
J. PATHWAY: D-alanyl-lipoteichoic acid biosynthesis.
J. PYM: 4. -phosphopantetheine is transferred from CoA to a specific serine of apo-DCP (By similarity).
J. SIMILARITY: Contains 1 acyl carrier domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
           Gaps
                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=DSM 20267 / Isolate C2A;
MEDLINE=99185055; PubMed=10085071;
Peschel A., Otto M., Jack R.W., Kalbacher H., Jung G., Gotz F.;
"Inactivation of the dlt operon in Staphylococcus aureus confers sensitivity to defensins, protegrins, and other antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
D-alanine--poly(phosphoribitol)ligase subunit 2 (EC 6.1.1.13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF 00565; -; 1.
InterPro; IPR003230; D-ala_carrier.
InterPro; IPR003230; D-bind.
ProDom; PD015103; D-ala_carrier; 1.
PROSITE; PS50075; ACP_DÖMAIN; FALSE NEG.
Ligase; Cell wall; Phosphopantecheine.
BINDING 36 36 PHOSPHOPANTETHEINE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C64B76620E7074C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus xylosus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.7%; Score 27; DB 1; I
31.6%; Pred. No. 6.7e+02;
iive 4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 AA
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             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
             4; Conservative
                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
hes 6; Conserve
                                                       1 RRRVYD 6
                                                                                                 2 RRRIVE 7
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01-NOV-1995 (
16-OCT-2001 (
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P46041;
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RESULT 36
DITC_STANK
ID DITC_STANK
ID DT 28-FEB
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RESULT 37

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Matches

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Kawano
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ILG1_CAEEL
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RA MEDLINE=21638749; PubMed=11780052;
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Basiley J., Barlow K.F., Bates K.N., Beard D.M.,
RA Beasley O.P., Burder A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.J.,
RA Hunt A.R., Hunt A.R., Hunt A.R., Hall R.B.,
RA Huckle E., Hunt A.R., Hunt S.E., Gorison C.M., Johnson D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McWhirray A.A.,
Milne S.A., Mistry D., Moore M.J.F., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Soderlund C., Steward C.A., Sulston J.E.,
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Walliams S.A.,
RA Rogers J.,
RA Rogers J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                       5
                                                                                                   29.7%; Score 27; DB 1; Length 89; 36.8%; Pred. No. 7.7e+02; wiematches 5; Indels
                                                                   Ribosomal protein; Complete_proteome. _
SEQUENCE 89 AA; 10173 MW; 367E5A1117EACIAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
49-FEB-2003 (Rel. 41, Last annotation update)
47-POCHPICAL BAF-like protein C200rf179.
HAMAP; MF 00410; -; 1.
InterPro; IPR000054; Ribosomal L31e.
Pfam; PF01198; Ribosomal L31e; 1.
PROSITE; PS01144; RIBOSOMAL L31E; FALSE NEG.
                                                                                                                                                                                                                                                                                                              90 AA
                                                                                                                                                                                        1 RRRVYDALNVLMAMNIISK 19
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KRRADTAVSIL--RNFVSK 41
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                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                 Local Similarity
tes 7; Conserv
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Q9H503;
                                                                                                                     Query Match
                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhadditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable insulin-like peptide gamma-type 1 precursor (Ceinsulin-3).
Genew; HGNC:16172; C20orf179.
InterPro; IPR004122; BAF_Drot.
Pfam; PF02961; BAF; 1.
Hypothetićal protein; DNA-binding; Nuclear protein; Polymorphism.
Hypothetićal protein; TNA-> S (in dbSNN:1053993).
/FIId=VAR_013693.
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MEDLINE-98217375; PubMed=9548970;
Duret L., Guex N., Peitech M.C., Bairoch A.;
"New insulin-like proteins with atypical disulfide bond pattern characterized in Caenorhabditis elegans by comparative sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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A-CHAIN-LIKE PEPTIDE (POTENTIAL)
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analysis and homology modeling.";
Genome Res. 8:348-351(198)
Genome Res. Bi348-351(198)
Genome Res. Bi
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Pred. No. 7.8e+02;
7; Mismatches 3; Indels
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                        C7FAB57610ADEF87 CRC64;
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PROSITE; PS00262; INSULIN; 1.
Insulin family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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15-JUL-1998 (Rel. 36, Last seq.
28-FEB-2003 (Rel. 41, Last anno
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                                                                                                                                                                                                                                                                                                   90 AA; 10309 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                      29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 DALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 DGISHELAINLVTK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INS-11 OR C17C3.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
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61
37
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Q18060;
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PEPTIDE
DISULFID
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Matches

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                          MEDLINE-85155495; PubMed-6241581;
Backhaus H., Petri J.B.;
"Sequence analysis of a region from the early right operon in phage
P22 including the replication genes 18 and 12.";
Gene 32:289-303(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBUNIT: Homotetramer.
-1- SIMILARITY: THIS PROTEIN IS RELATED TO THE REGULATORY PROTEIN
CII OF BACTERIOPHAGES LAMBDA AND 434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P(RE) AND PA23 AND ACTIVATE
                                                                                                                                  Viruses, dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
P22-like viruses.
NCBI_TaxID=10754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Krobinski A.M.B., VanderByl C.S.;
"The completed agguence of genome of Salmonella phage P22.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage P22 Cro protein: sequence, purification, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27; DB 1; Length 92;
Pred. No. 8e+02;
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P -> D (IN REF. 4).
D479C6D90085CEE6 CRC64;
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PIR; A91518; ZIBPC2.

Pfam; PF05269; Phage CII; 1.

Transcription regulation; DNA-binding; Activator.

Ac H-T-H MOTIF (PROBABLE).
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥.
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                                                                            Transcriptional activator protein Cl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=86159692; PubMed=3954988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF217253; AAF75026.1; -.
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15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iochemistry 25:251-256(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 AA; 10211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M10074; AAA32274.1; -. EMBL; M12584; AAA32269.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.7%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRRVYDALNV 10
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                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poteete A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAPD ACTAC
ID VAPD ACTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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     SOLUTION SOLUTION SERVICE SERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-TOKYO 1998;
MEDLINE=2045173; DubMed=10993077;
MEDLINE=2045173; DubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Menome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:181-86 (2000)
-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF
PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING
DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME
ENVIRONMENTAL CONDITIONS (BY similarity).
-!- SUBMUNT: Homodimer (By similarity).
-!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                               Length 91;
                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AFVOLIES.
HSSP; P36206; 1B8Z.
INCEPTO; 1PR000119; Bac_DNAbind.
PFOMD; PD000945; Bac_DNA binding; 1.
PRODOM; PD000041; BHL; 1.
SWART; SW0041; BHL; 1.
PROSITE; PS00045; HISTONE LIKE; 1.
DNA-binding; DNA condensation; Complete proteome.
                                      POTENTIAL.
22BF958BF759F254 CRC64;
                                                                                                            Score 27; DB 1; L
Pred. No. 7.9e+02;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 AA.
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             POTENTIAL
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             49 79
65 70
91 AA; 10173 MW;
                                                                                                                  29.78;
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                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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16-OCT-2001 (Rel. 40, La
DNA-binding protein HU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   symbiotic bacterium).
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40 KIFKALNVM 48
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Best Local Similarity
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ID RPCI BPP22
AC P03041;
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P57144;
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DISULFID
SEQUENCE
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Gaps

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2; Indels

Matches

RESULT 42

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us-09-900-147-3.rsp

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modified and this statement is not removed.
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P41301;
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NULM BALMU
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                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Natural electron acceptor for a formate dehydrogenase.
SUBCELLULAR LOCATION: Periplasmic.
PTM: BINDS ONE HEME GROUP PER MOLECULE.
SIMILARITY: BELONGS TO THE CLASS I CYTOCHROME C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=95362676; PubMed=7543479;
Galli D.M., Leblanc D.J.;
"Transcriptional analysis of rolling circle replicating plasmid pVT736-1: evidence for replication control by antisense RNA.";
J. Bacteriol. 177:4474-4480(1995).
-: SIMILARITY: BELONGS TO THE VAPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                     Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27; DB 1; Length 95;
Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid, Virulence. SEQUENCE 95 AA: 11190 MW; 3424348E815BF62A CRC64;
15-JUL-1999 (Rel. 30, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Virulence-associated protein D homolog.
Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Cytochrome C-553 precursor (C553).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
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                                                                                                                                                        Pasteurellaceae; Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L24000; AAC37126.1; -. Pfam; PF04605; VapD_N; 1.
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62.5%;
                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5, Conservative
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                                                                                              actinomycetemcomitans).
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                                                                                                                Plasmid pVT736-1
                                                                                                                                                                                 NCBI_TaxID=714;
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Q9ZJZ9;
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C553 HELPJ
AC 092373 H
AC 092373 H
DT 28-FEBB
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Usage by and for commercial
                      (See http://www.isb-sib.ch/announce/
                                                                                 Gaps
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Arnason U., Gullberg A.;
"Comparison between the complete mtDNA sequences of the blue and the
fin whale, two species that can hybridize in nature.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti;
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-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRON (HEME AXIAL LIGAND)
SIMILARITY).
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01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
MTND4L OR ND4L OR NADH4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3E607AE5D422AD82 CRC64;
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PIR, S41828; S41828.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
Pfam; PF00420; oxidored q2; 1.
Propom; PD000359; Oxidred4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27; DB 1; I
Pred. No. 8.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                           entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Balaenoptera musculus (Blue whale). Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Cetartioda
Balaenopteridae; Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 AA; 10354 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KKVIVALGVLAFANVL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73
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        SQ SEQUENCE
        98 AA; 10747 MW; 9F770651FE65ED1B CRC64;

        Query Match
        29.7%; Score 27; DB 1; Length 98;

        Best Local Similarity
        55.6%; Pred; No. 8.6e+02;

        Matches
        5; Conservative
        3; Mismatches
        1; Indels
        0; Gaps

        Qy
        8 LNVLMARNI 16
        1 | | | ::
        b
        6 MNVLMAFSM 14
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Search completed: February 17, 2004, 10:57:02 Job time: 7.0198 secs

063454 cupha eryma Q8xy31 arlatonia s Q8xy31 arlatonia s Q86468 homo sapien Q8ha80 bacteriopha Q48050 trypanosoma Q8x316 escherichia P92499 apis mellif P92501 apis mellif P92501 apis mellif P92601 apis mellif P92601 arlatobact Q94x1 arabidopsis Q94x1 arabidopsis Q94x1 arabidopsis Q94x1 arabidopsis Q94x1 etraodon f Q5418 eerratia ma Q9hrh halobacteri Q94x0 bacillus ha Q98x10 bacteriopha Q38507 bacteriopha Q98x10 bacillus ha Q98x

092682 08UKS1 099RD1 099RD1 034371 057412 057412 091RH0 091RH0 091RD1 090RD1 09

O63454 Q8XYL3 Q96DE8 Q8HA80 Q44050 Q8X3F6 P92499 P92501

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"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                    [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. PATCC 51768 / DSM 7523; PubMed=11792869; Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

44.0%; Score 40; DB 17; Length 58;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

EMBL; AE009873; AAL64158.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 58 AA; 6342 MW; 110191142AD83792 CRC64;
                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
101-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein PAE2389.
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Q99MV9;
Q99MV9;
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ID Q99M
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                                                            February 17, 2004, 10:50:12; Search time 26.901 Seconds (without alignments) 182.261 Million cell updates/sec
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        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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09HQ82
0979G1
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Q91QF4
Q8EAL3
Q9BM32
Q9BM32
Q9C8H4
Q92 Q22
Q99VZ5
Q99VZ5
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sp_human:*
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Maximum DB seq length: 100
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58 AA.

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Gaps

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Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Kiyokawa C., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Incomplete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                           Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tasahin A., Scott J., Beanan M., Brinkac L., Daugherty S., Boby R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Muller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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Phyllobacteriaceae; Mesorhizobium.
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Pred. No. 1.8e+02;
9; Mismatches 3; Indels
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SEQUENCE 39 AA; 4562 MW; F7426BEB79112768 CRC64;
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SEQUENCE 58 AA; 6919 MW; C5BEBDC3FF061623 CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein ms10755.
                                                       (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Pred. No. 1.2e+02;
5; Mismatches 1;
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                  39 AA.
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MEDLINE=21082930; PubMed=11214968;
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ilarity 29.4%;
Conservative
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EMBL; AP002995; BAB48281.1;
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13 RRRIFERLNLI 23
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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"An abundance of X-linked genes expressed in spermatogonia.";
Nat. Genet. 27:422-426(2001).
EMBL, AF285583; AAX11962.1; --
MGD; MGI:1890547; Tex18.
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Pred. No. 1e+02;
5; Mismatches 5; Indels
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Pred. No. 51;
1; Mismatches 6; Indels
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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                    Last sequence update)
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MEDLINE=21175748; Pubmed=11279525;
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                  (TrEMBLrel. 17, (TrEMBLrel. 19,
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6; Conservative
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les 8; Conservative
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                                                             Testis protein TEX18.
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Submitted (JUN-1999)
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Vacuolar ATP synthase 57KD subunit (Fragment).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-MUSO, and N315;
MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
                                                                                                                                                                                                                                                                                                                                           Berthomieu P., Guerrier D., Giraudat J.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SAV0618 (Hypothetical protein MW0582)
SAV0618 OR SA0575 OR MW0582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                              Last sequence update)
Last annotation update)
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NCBL_TaxID=158878, 158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus (strain Mu50 / ATCC 700699)
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Pred: No. 2.6e+02;
7; Mismatches 5
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                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
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33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 RQIYPPINVLPSLSRLMK
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Best Local Similarity 33.3.
6; Conservative
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18 IYNALKLFMEMN 29
                                                                                       PRELIMINARY;
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Q42022;
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STRAIN-C57BL/6J; TISSUB=Cerebellum;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL: AK047089; BAC32557.1; -.
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=UA159 / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Pred. No. 2.1e+02;
3; Mismatches 3; Indels
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Pred. No. 2.5e+02;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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EMBL. AE014994; AAN59277.1; - protecome.

Hypothetical protein; Complete protecome.

SEQUENCE 68 AA; 7604 MW; EEF457B026865773 CRC64;
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                                                                                                                                                                                               Last sequence update)
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Last annotation update)
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                                    RRRVYDALNVLMAMNII 17
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53.8%;
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Best Local Similarity 53.87
Conservative
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Matches 6; Conservative
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                                                                                                                                        PRELIMINARY;
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01-MAR-2003 (TrEMBLrel.
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01-MAR-2003
01-MAR-2003
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SEQUENCE FROM N.A. Alonso J.C., Luder G., Stiege A.C., Chai S., Weise F., Trautner T.A.; "Analysis of the complete nucleotide sequence and functional
                              MEDLINE=98049343; PubMed=9389475;
MEDLINE=98049343; PubMed=9389475;
MEDLINE=98049343; PubMed=9389475;
MEDLINE=98049343; PubMed=9389475;
Kalank H.-P., Clayron R.A., Tomb J., Hickey B.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Merlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Medlandund J., Lee N.H., Sutron G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Richardson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses, dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
NCBI_TaxID=10724;
                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                            -i- SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01037; ASNC_trans_reg; 1.
DNA-binding; Hypothetical protein; Transcription regulation;
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Pred. No. 3.8e+02;
5; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organization of Bacillus subtilis bacceriophage SPP1.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X97918; CAA66519:1;
InterPro; IPR006479; Holin. SPP1.
Fram: PF04688; Phage holin; 1.
TIGRFAMS; TIGR01592; holin. SPP1; 1.
SEQUENCE 82 AA; 9391 MW; 558P709AD9E0D3A0 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
10-JUNAR-2003 (TrEMBLrel. 23, Last annotation update)
Complete nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.4%; Score 34; DB 17; 70.0%; Pred. No. 3.6e+02; tive 1; Mismatches 2,
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TIGR; AF1404; -.
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity
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MEDINE-2050483; PubMed=11016950;
MEDINE-2050483; PubMed=11016950;
Shukla H.D., Lasky S.P., Baliga N.S., Thorsson V., Sbrogna J.,
Swatrzell S., Walt D., Hall J., Dahl T.A., Welt R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Genome sequence of Halobacterium species NRC-1.";
Froc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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                            Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
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                                                                                                                                                                                                                                            Score 34; DB 16; Length 74;
Pred. No. 3.4e+02;
4; Mismatches 2; Indels
    Iwama N., Asano K., Naimi T., Kuroda H., Cui L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Halobacteria; Halobacteriales
                                                                                                               EMBL; AP003359; BAB56780.1; -.
EMBL; AP003131; BAB41807.1; -.
EMBL; AP0040824; BAB9447.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 74 AA; 8228 MW; 35AFAB2F9FF612AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5D045F8E606B6FC5 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Transcriptional regulatory protein, ASNC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium sp. (strain NRC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRRVYDALNVLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 KQTIHNRLNVLVAAGHVEK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Halobacteriaceae; Halobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 AA; 8286 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 31.6%;
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                        50.0%;
                                                                                                                                                                                                                                                     37.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome
                                                                                       Lancet 359:1819-1827(2002)
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                  |::| |::|||
35 DSMNALVDLNII 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           6 DALNVLMAMNII 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                        Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=64091;
                                                                      acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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RESULT 10
209H01
10 Q9HH02
AC Q9HH04
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RESULT 11
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STRAIN-CSS1 / DSM 4299 / JCM 9571;
Kawashima-T., Amano N., Koike H., Makino S.-I., Higuchi S.,
Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
Nunoshiba T., Yamanoto Y., Aramaki H., Makino K., Suzuki M.;
Nunoshiba T., Yamanoto Y., Aramaki H., Makino K., Suzuki M.;
"Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium."; 14257-14262(2000).
EMBL; Aroboo995; BAB60342.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 66 AA; 7786 MW; 7237A16A6IE3109FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gadus morhua (Atlantic cod).
Bukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygit; Neopterygit; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
NCBI_TaxID=8049;
                                                                                                                                                                                                     Thermoplasma volcanium.
Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 17; Length 66;
Pred. No. 4.5e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.3%; Score 33; DB 13; Length 79; 47.1%; Pred. No. 5.4e+02; tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ong T.L., McNamara P.T., Armstrong R.F., Buckley L.J.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, 1049122, AAA91234.1; --
HSSP; P11952, AAA91234.1; --
InterPro; IPR000183; Decarbxylse2.
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                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                   Created)
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Pfam; PF00278; Orn DAP Arg dec; 1.
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                                                                                             01-0CT-2001 (TrEMBLrel. 18, 01-0CT-2001 (TrEMBLrel. 18, 01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein TV1200. TV1200 OR TVG1229743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  091038;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local Similarity 47...
Best Conservative
State B; Conservative
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                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 LNIIVDKNIISR 61
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SEQUENCE FROM N.A.
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             NON TER
SEQUENCE
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                                                                           Q979G1;
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QBEIV8
                 RESULT 15
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=NEMBL6 / Serotype III;
STRAIN=NEMBL | Serotype III;
MEDUINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
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                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of Streptococcus agalactiae, a pathogen causing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.4%; Score 34; DB 16; Length 99; 46.7%; Pred. No. 4.6e+02; tive 4; Mismatches 4; Indels
                                                                                                                                        Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                       invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513 (2002).

EMBL, AL766850; CAD47009.1; -.

Sagalist; gbs1350; -.

Skypothetical protein; Complete proteome.

SEQUENCE 99 AA; 11302 MW; B83CB8FC1AB03C53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 AA; 6859 MW; B5CD27577F80E8A8 CRC64;
U1-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
GBS1350.
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
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Best Local Similarity 46...
7; Conservative
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nes 8; Conservative
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                                                                                                                                                                                              NCBI_TaxID=216495;
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                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                Kunst F.;
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8; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                            Mitochondrion.
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SEQUENCE
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Q8XYL3
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The preterns of mitochondrial versus nuclear DNA sequence divergence among nymphalid butterfiles: the utility of wingless as a source of among nymphalid butterfiles: the utility of wingless as a source of caracters for phylogenetic inference.";

The characters for phylogenetic inference.";

The characters for phylogenetic inference.";

CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-

CHAIN THAT CATALYZES THE ENEXME. ELECTRONS ORIGINATING IN

CATALYTIC SUBUNIT OF THE ENEXME. COPPER A CENTER OF SUBUNIT 2

CATALYTIC SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME AS AND COPPER B (BY SIMILARITY).

CHAIN THAT CATIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME

C + 2 H(2)O.

--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL

C --- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos B.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Socht J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Wamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldobyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Shewanella oneidensis."
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-Cr-2002 (TrEMBLrel. 22, Last annotation update)
Cytochrome oxidase subunit I (EC 1.9.3.1) (Cytochrome c oxidase polypeptide I) (Fragment).
                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Papilionoidea; Nymphalidae; Heliconiinae; Cupha.
NCBI_TaxID=64452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.3%; Score 33; DB 16; Length 83; 45.0%; Pred. No. 5.7e+02; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Complete proteome.
SEQUENCE 83 AA; 9075 MW; AC5D08F38ACB345C CRC64;
                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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EMBL, AE015517, AAN53799.1; -.
TIGR, S00721; -.
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MEDLINE-98119519; PubMed=9459431;
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                                                                                                                                              Conserved hypothetical protein.
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NC 06345
NC 06345
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-1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY. EMBL, AFO14151; AACO5893.1; -. InterPro; IPR000883; COX1.
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MEDLINE=21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguler P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Ralstoniaceae; Ralstonia.
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                                                                                              Pfam, PF00115; COX1, 1.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Oxidoreductase; Respiratory chain; Transmembrane; Transport;
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                                                                                                                                                                                                                                                                                               Length 92;
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92 AA; 10826 MW; B7B6BEDFFDCE3697 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to 26S proteasome-associated pad1 homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
U-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein RSc1745.
RSc1745 OR RS02033.
                                                                                                                                                                                                                                                                                         36.3%; Score 33; DB 8; 347.1%; Pred. No. 6.3e+02; tive 3; Mismatches 6
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EMBL, AL64666, CAD15447.1; -.
InterPort IRR002634; BolA.
Hypothetical protein; Complete proteome.
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Mitochondrion.
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  Query Match
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"Trypanosoma rangeli sialidase: cloning, expression and similarity to T. cruzi trans-sialidase.";
Glycobiology 7:1167-1173 (1997).
EMBL; U83240; AAC38897.1; -.
NON TER 24 24
SEQÜENCE 24 AA; 2695 MW; 009FE2472BBD3F35 CRC64;
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5698;
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Viruses; daDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
T5-1ike viruses.
VCBI_TaxID=10726;
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Pred. No. 7.4e+02;
5; Mismatches 3; Indels
                                                                                                                             Query Match 36.3%; Score 33; DB 4; Length 95; Best Local Similarity 35.3%; Pred. No. 6.5e+02; Matches 6; Conservative 6; Mismatches 5; Indels
                     Straubberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009524; AAH09524.1; -.
InterPro; IPR003639; Mov34 1.
ProDom; PD363422; Mov34 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Mikoulinskaia G.V., Zimin A.A., Feofanov S.A.;
Mikoulinskaia G.V., Zimin A.A., Feofanov S.A.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY140897;
AY140897;
AY170541;
Hypothetical protein.
SEQUENCE 89 AA; 10284 MW; 59C7EF0AC84D9B3C CRC64;
                                                                                                      95 AA; 11009 MW; D70270AD00529A18 CRC64;
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Last annotation update)
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Last annotation update)
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01-UUN-1998 (TrEMBLrel. 06, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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Best Local Similarity 43.0.,
A. Conservative
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ORF2C.
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SEQUENCE FROM N.A.
                                                                                          Proteasome.
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                                                                                                      SEQUENCE
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"Mitochondrial sequence characterisation of Austrailan commercial and feral honeybee strains (Hymenoptera: Apidae: Apis mellifera Linnaeus), in the context of the species worldwide.";
J. Aust. Entomol. Soc. 0:0-0(1997).
-!- FUNCTIONS SUBUNITS I, II AND III FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME C + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=0157.H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Hida T., Takami H., Honda T., Saaakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterchemorrhagic Escherichia coli

"Complete genome sequence of enterchemorrhagic scherichia coli

"O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Cytochrome oxidase subunit III (EC 1.9.3.1) (Cytochrome c oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Pred. No. 5.4e+02;
  Length 24;
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 53 AA; 6018 MW; 653FBE5407E4B98F CRC64;
                                                                                                                                                                                                                                                          01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
101-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein EC83484.
35.2%; Score 32; DB 5; I
46.2%; Pred. No. 2.5e+02;
tive 4; Mismatches 3;
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EMBL; AP002562; BAB36907.1; -.
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                                             Conservative
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6; Conserva
               Best Local Similarity
Matches 6; Conserv
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NCBI_TaxID=375;
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                                                                                                                          SEQUENCE
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QBJKS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Z682
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Koultanos S., Crozier R.H.;

Mitochondrial sequence characterisation of Austrailan commercial and feral honeybee strains (Hymenoptera: Apidae: Apis mellifera Linnaeus), in the context of the species worldwide.";

J. Aust. Entcomol. Soc. 0:-0.1977).

-I. FUNCTION: SUBINITS I, II AND III FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX (BY SIMILARITY).

-I. ATALYIT CATTVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME C + 2 H(2) 0.

C + 2 H(2) 0.

-I. SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
                                                                                                                                                                                                                                                             Gaps
  -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Cytochrome oxidase subunit III (EC 1.9.3.1) (Cytochrome c oxidase
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                                                                                                                                                                                                                Score 32; DB 8; Length 55;
Pred. No. 5.6e+02;
7; Mismatches 4; Indels
                                                                                 ProDom; PD000382; CytC oxdse_III; 1.
PROSITE; PS50253; COX37 1.
Oxidoreductase; Transmembrane; Mitochondrion.
NON TER 55 55
SEQÜENCE 55 AA; 6506 MW; 650A864ED7C2FC0C CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein MTH186.
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InterPro; IPR000298; CytC_oxdse_III.
Pfam; PF00510; COX3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                        EMBL, U72269, AAB41167.1; -.
InterPro; IPR000298; CytC_oxdse_III
Pfam; PF00510; COX3; 1.
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                                                                                                                                                                                                                       35.2%;
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34 IYSSISMFMILNFIN 48
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion.
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01-JAN-1998 (
01-JAN-1998 (
01-JUN-2002 (
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SEQUENCE
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02628
ID 02628
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DT 01-JA
DE HYPOT
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P92501
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                                                                                                                                                                  MEDLINE-98037514; pubMed=9371463; MEDLINE-98037514; pubMed=9371463; MEDLINE-98037514; pubMed=9371463; MEDLINE-98037514; pubMed=9371463; MEDLINE-98037514; pubMed=9371463; DeLoughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Wiarabowski J., Gbson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietroveki S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; Bacteriol. 179:7135-7155(1997).
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STRAIN=USDAILO;
Mayer R.M., Mathis J.N., McMillin D.E.;
Maper R.M., Mathis J.N., McMillin D.E.;
Mathis J.N., Mathis J.N., McMillin D.E.;
Mathis of a DNA fragment present in Bradyrhizobium japonicum 110
Fix+ derivatives but missing in a Fix- derivative.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
NON_TER 61
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               Archaea; Euryarchaecta; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
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Bacteria; Proteobacteria; Alphaproteobacterja; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Pred. No. 6.2e+02;
2; Indels
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Pred. No. 6.18+02;
4; Mismatches 3; Indels
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SEQUENCE 60 Aa; 6960 MW; A3FACA6838251B4D CRC64;
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61 AA; 6729 MW; FF29A9A1891C986A CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Arginine-rich protein a209R.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Exonuclease I (Fragment).
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Methanobacterium thermoautotrophicum.
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Local Similarity 46.2%;
Les 6; Conservative !
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Best Local Similarity
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Length

8B6BB4B3627F791C CRC64;

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66 AA; 8016 MW;
                                                           35.2%;
66.7%;
                                                                                                                   6; Conservative
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47 RVYDDLNTI 55
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                                                           Query Match
Best Local Similarity
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  SEQUENCE
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094EX1;
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Matches
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Q9GMS9
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                                            SEQUENCE FROM N.A.
MEDLINE=22174892; PubMed=12186886;
Cheng C.H., Liu S.M., Chow T.Y., Hsiao Y.Y., Wang D.P., Huang J.J.,
Chen H.H.;
"Analysis of the Complete Genome Sequence of the Hz-1 Virus Suggests
that It Is Related to Members of the Baculoviridae.";
J. Virol. 76:9024-9034 (2002).
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MBDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi J Baba T., Takeuchi F., Karoda M., Yazawa T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
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1-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SAV2564 (Hypothetical protein MW2422)
SAV2504 OR SA2292 OR MW2422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 12; Length 64;
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheng C.H., Hsiao Y.Y., Liu S.M., Chow T.Y., Chen H.H.; Submitred (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF45189. 2AN04335.1; -7.5234CECE423428 CRC64; SEQUENCE 64 AA, 7698 WW; 775234CECE423428 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Cheng C.H., Liu H.M., Hsiao Y.Y., Chow T.Y., Chen H.H.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus (strain MuSo / ATCC 700699), Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain MW2). Bacteria; Firmicutes; Bacillales; Staphylococcus. NCBI_TAXID=158878, 158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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Lancet 359:1819-1827(2002).
EMBL; AP003365; BAB58666.1; -.
EMBL; AP003137; BAB43595.1; -.
EMBL; AP004830; BAB96287.1; -.
Heliothis zea virus 1.
Viruses, unclassified viruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 31.67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Kim C.J. Chen H., Cheuk R., Koesema E., Meyers M.C., Shinn P.,
Tracy S.E., Banh J., Bowser L., Carninci P., Chung M.K.,
Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 6; Length /1;
Pred. No. 7.3e+02;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS99288; AAG3860.1;
-SEQUENCE 72 AA; 8265 MW; COCA73AC066ECIC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB047839; BAB12265.1; ...
Hypothetical protein.
SEQUENCE 71 AA; 8296 MW; 1A50C4AE703A69C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical 8.3 KDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
Score 32; DB 16; Le
Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                     71 AA.
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                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                     PRT;
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Local Similarity 33.3%;
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RRVYDALNVLMAMNI 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :::|| :|| :
| KKLYDNINVKMLSQV 23
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL; APO01519; BBA117-11.-

Hypothetical protein; Complete proteome.

SEQUENCE 83 AA; 9454 MW; 471552D292B2A44F CRC64;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Taleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                   Yao C.W., Huang C.J.; "Partial genomic sequence of GNDS gene of puffer fish (Tetraodon fluviatilis).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SETRAINSC-125 / JCM 9153;
MEDLINE-20512592; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 16; Length 83;
Pred. No. 8.5e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 78;
                                                                                                                                                                                                                           Submitted (UNV.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF007814; AAB94740.1; -.
HSSP; Q12967; 2RGF.
InterPro; IPR000463; Fatty acid BP.
InterPro; IPR000159; RA_domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEDA65DB7C297A16 CRC64;
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Last annotation update)
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Pred. No. 8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last seq 01-OL-MAR-2002 (TrEMBLrel. 20, Last ann Hypothetical protein BH3512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 01, C
(TrEMBLrel. 01, I
(TrEMBLrel. 08, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.2%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                    78 AA; 9109 MW;
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00788; RA; 1.
PROSITE; PS00214; FABP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.0
Tr Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RVYDALNVLMAMN 15
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01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RRVYDALNVL 11
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REIYDTLNGL
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Matches 6; Conserv
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=86665;
                                                                                                    NCBI_TaxID=47145;
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                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9K761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     054418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Phylogeny of Heliconius butterfiles inferred from mitochondrial DNA sequences (Lepidoptera: Nymphalidae).";
Mol. Phylogenet. Bvol. 3:159-174(1994).
-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CATALYTIC SUBUNIT TO THE ENZYME. BLECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Cytochrome oxidase I (EC 1.9.3.1) (Cytochrome c oxidase polypeptide I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: 4 PERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: RESPIRATORY CHAIN; TERMINAL STEP.
SUBCELLULALAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Papilionoidea; Nymphalidae; Heliconiinae; Dryadula.
NCBI_TaxID=34742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copper; Electron transport; Heme; Inner membrane; Membrane; Oxidoreductase; Respiratory chain; Transmembrane; Transport;
              Score 32; DB 10; Length 72;
Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 8; Length 77;
Pred. No. 7.9e+02;
2; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 AA; 9133 MW; 7CE02EE82BBCC12D CRC64;
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                                                                                                                                                                                                                                                              77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=P-11-7; TISSUE=Head, and Thorax; MEDLINE=94356263; PubMed=8075834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last seq
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                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.18;
                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U08546; AAA20722.1; -
InterPro; IPR000883; COXI.
Pfam; PF00115; COXI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 47.1.
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                Query Match 35.2
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                     33 VMVAKNIVSK 42
                                                                                                           10 VLMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                Dryadula phaetusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion.
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057412;
01-JUN-1998 (
01-JUN-1998 (
01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brower A.V.Z
                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment)
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057412
1D 05741
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DT 01-JU
DT 01-JU
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OF GNDS.
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PERGENOIS TO A NOT A TRC 49558; MEDLINE=98049343; PubMed=9389475; MEDLINE=98049343; PubMed=9389475; MEDLINE=98049343; PubMed=9389475; MEDLINE=98049343; PubMed=9389475; Melbon R.-D., Cayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Rleichmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty M.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fuljii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
  Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
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Pfam; PF01022; HTH_S; 1.
DNA-binding; Hypothetical protein; Transcription regulation;
                                                                            Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyall-Smith "Sequence and transcription of halovirus HP2."; subutted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF222060; AALS4928.1; -. Hypothetical procesin. SEQUENCE 96 AA; 10900 MW; 359249FBD43CF3CB CRC64;
                                                                                                                                                                                                                                        Length 96;
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                                                                                                                                                                                                                                    Score 32; DB 12; Length 96
Pred. No. 9.8e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein AF2404.
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Pred. No. 9.8e+02;
2; Mismatches 4;
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70.0%;
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50.0%;
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Matches 7; Conservative
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LKALMQLNIVEK 71
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Best Local Similarity
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                                                               SEQUENCE FROM N.A.
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                      NCBI_TaxID=33771;
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                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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"Regulation of the Serratia marcescens extracellular nuclease:
positive control by a homolog of P2 Ogr encoded by a cryptic
prophage.";
J. Mol. Biol. 256:264-278(1996).
EMBL: U11698; AAA98439.1;
SEQUENCE 89 AA; 10283 MW; DDAAD9AB4F5DFEAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.2%; Score 32; DB 17; Length 94; Best Local Similarity 36.8%; Pred. No. 9.6e+02; Matches 7; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                            35.2%; Score 32; DB 2; Length 89; 55.6%; Pred. No. 9.1e+02; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium sp. (strain NRC-1).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 AA; 10601 MW; 4EA3976DDC6146B9 CRC64;
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Last annotation update)
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Last sequence update)
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                                                                                                                                                MEDLINE=96174474; PubMed=8594195;
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                                        Enterobacteriaceae; Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
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80 RRKIYDECN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RRRVYDALN 9
Serratia marcescens.
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                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=64091;
                                                               NCBI_TaxID=615;
                                                                                                                            STRAIN=SM6;
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RESULT 36
109HRH
AC 09HRH
AC 09HRH
DT 01-MA
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RA NG MEDLII
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Indels

RESULT 37
Q8V6V2
ID Q8V6V
AC Q8V6V
DT 01-MADT 01-MADT 01-MADT 01-MADT 05-MADT 05-MADT 05-MADDT 05-MADOV

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Bothrops jararaca (Jararaca).
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Best Local Similarity
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EMBL, APOOLIS14; BAB505915.1; - Hypothetical protein; Complete proteome. SEQUENCE 35 AA; 3960 MW; 9F851AF909DB2388 CRC64;
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=8256795; PubMed=6809534;
Yoshikawa H., Ito J.;
"Nucleotide sequence of the major early region of bacteriophage phi-
            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-19996 (TrEMBLrel. 19, Last annotation update)
101-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Left end of bacteriophage phi-29 coding for 15 potential proteins
Annong these are the terminal protein and the proteins encoded by t
Genes 1, 2 (sus), 3, and (probably) 4.

Bacteriophage phi-29.
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                   Viruses, daŭna viruses, no RNA stage; Caudovirales; Podoviridae;
phi-29-like viruses.
NCBI_TaxID=10756;
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                                                                                                                                                                                                                                                    34.6%; Score 31.5; DB 9; Length 52; 43.8%; Pred. No. 6.5e+02; tive 5; Mismatches 3; Indels
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Pred. No. 5.4e+02;
6; Mismatches 3; Indels
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NCBL_TaxID=86665;
                                                                                                                                                                                                                 EMBL, V01155; CAA24488.1; -. SEGUENCE 52 AA; 5979 MW; B7EE0EBBB9ED0690 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9PS47;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
JARARAFIBRASE II (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Local Similarity 35.7%;
nes 5; Conservative
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13 RDVFTSLNVI-RMNVV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein BH2196
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                                                                                                                                                                                                         Gene 17:323-335(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Horikoshi K.;
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Q9PS47
ID Q9PS4
AC Q9PS4
DT 01-MA
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                                                                                                                                                                         Maruyama M., Sugiki M., Yoshida E., Mihara H., Nakajima N.; "Purification and characterization of two fibrinolytic enzymes from Bothrops jararaca (jararaca) venom."; Toxicon 30:853-864(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
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STRAIN=56601 / Serogroup Icterchaemorrhagiae / Serovar lai;
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                       34.1%; Score 31; DB 13; Length 49
36.4%; Pred. No. 7.5e+02;
ive 5; Mismatches 2; Indels
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE011224; AAN47571.1; -.
Complete proteome.
SEQUENCE 62 AA; 7420 MW; D838FE2F7F71B70A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto
                                                                                                                                                                                                                                                                                                                                                                                         88F064DC1DB2E44E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
predicted transcriptional regulator, copG family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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34.1%; Score 31; DB 16;
Best Local Similarity 42.9%; Pred. No. 9.4e+02;
Matches 9; Conservative 3; Mismatches 7;
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                                                                                                                                    SEQUENCE.
MEDLINE=92397346; PubMed=1523677;
                                                                                                                                                                                                                                                                                           HSSP; P15167; 1ATL.
InterPro; IPR001590; Reprolysin.
PEm; PF01421; Reprolysin; 1.
PROSITE; PSS0215; ADAM MEPRO; 1.
SEQUENCE 49 AA; 6112 MW; 88FG
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Search completed: February 17, 2004, 10:56:19 Job time: 28.901 secs
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
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                                                                                                                                                                 "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213 (2001).
Hypothetical protein; Complete proteome.
SEQUENCE 68 AA; 7648 MW; 8876D5D9FFCC4B14 CRC64;
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Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 34.1%; Score 31; DB 16; Length 68; Best Local Similarity 66.7%; Pred. No. 1e+03; Matches 6; Conservative 2; Mismatches 1; Indels
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Pred. No. 1e+03;
5; Mismatches 8; Indels
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
1-MAPOCHETICAL protein TV0729.
1-W0729 OR TVG0736303.
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last seg
01-OCT-2002 (TrEMBLrel. 22, Last ann
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Local Similarity 31.6%;
Local Similarity 51.6%;
Les 6; Conservative
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D8 Hyport
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EMBL, BC007583, AAH07583.1; -.
InterPro; IPR001014; Ribosomal L23.
Bram, PR00276; Ribosomal L23; 1.
ProDom; PD001141; Ribosomal L23; 1.
PROSTITE; PS0050; RIBOSOWAL_L23; 1.
HYPOTHELICAL Protein.
SEQUENCE 70 AA; 7923 MW; AC1C466548F343C1 CRC64;
                                                                                                                                           Score 31; DB 4; I Pred. No. 1.1e+03;
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Best Local Similarity 53.0.
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83.497 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Match Length
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seq length: 100
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Perfect score:
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Maximum DB
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Human musculoskele Novel human muscul Arabidopsis cell c DP-1 transcription E2F activity inhib E2F activity inhib	l transcri I transcri I transcri I transcri no acid se Jment of h an cadheri	le #231 brain #225 brain bone # bone # le #227 le #226 le #226 peptid	Arabidopsis thalia Human jumune/haema Human polypeptide Human DNA binding Repressor protein Human liver poptid Peptide #7053 enco Human brain expres Human bone marrow Peptide #7138 enco
22 ABB03433 24 ABU12727 24 ABU12727 3 AAW30515 19 AAW30506 19 AAW30506 19 AAW57051	AAW3050 AAW3050 AAW3050 AAW3050 AAX3776 AAX3670 ABP3271	22 ABB29659 22 ABB34837 22 ABB20257 22 AAM55645 22 AAM68025 22 AAM68025 22 AAM28353 22 AAM03581 23 ABG37552 22 AAO01170 22 AAM88281	
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ALIGNMENTS

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DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                      DP-1 transcription factor antagonist peptide H3.
                                                                                                                                                      Location/Qualifiers
                 AAW30505 standard; Peptide; 20 AA
                                                                                                                                                                1..10
/note= "Claim 3"
                                                                                                                                                                                                                             97WO-GB03506,
                                                                                                                                                                                                                                              96GB-0026589.
                                                    26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                (PROL-) PROLIFIX LTD
                                                                                                                                     Homo sapiens
                                                                                                                                                                                          WO9828334-A1
                                                                                                                                                                                                                            22-DEC-1997;
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                                                                                                                                                                                                          02-JUL-1998
                                                                                                                            Synthetic
                                   AAW30505;
                                                                                                                                                              Peptide
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RESULT 1
          AAW30505
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La Thangue NB;

Bandara LR,

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AAW30507 standard; Peptide; 30 AA
                          Claim 4; Page 44; 55pp; English.
                                                                                                                                                                                                                                                                                97WO-GB03506
                                                                                                                                                                                                                                                                                        96GB-0026589
                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                      surgical stent; therapy
  WPI; 1998-377596/32.
                                                                                                                            20 AA;
                                                                                                                                                                                              26-OCT-1998
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                 WO9828334-A1
                                                                                                                                                                                                                                                                                22-DEC-1997;
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                                                                                                                                                                                                                              Synthetic
                                                                                                                            Sequence
                                                                                                                                                                                      AAW30507;
                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                     Peptide
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Peptide H7 comprises amino acid residues 170-199 in the DBF box CC (II) (see AAW30501) of transcription factor DP1. Claimed peptides CC (II) (see AAW30504-07) containing one or both of 2 mortifs (see AAW30502-03) of the DBF box are capable of amergonising the AAW30502-03 of the DBF box are capable of antagonising the creatimerisation of the DBF box are capable of antagonising the claimed are variants of these peptides, especially containing and 175 of DP-1, fusion proteins (III) comprising (I) of (II) and and 175 of DP-1, fusion proteins (III) comprising (I) of (II) and and nost cells. (II) comprising (I) or (II) and containing cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in patients who have undergone cardioplasty. (I)-(III) function by inactivating the DNA-binding cardiovascular of DP-1/E2F dimerisation and as immunoassay agents.

Also described is the use of sequences antisense to nucleic acids cenceding (I)-(III) enhance cell killing.
                                                                                                                                                         Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 101; DB 19; Length 30; 100.0%; Pred. No. 3.1e-09; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DP-1 transcription factor peptide H (DEF box).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW30501 standard; Peptide; 37 AA.
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                                                                                                                                                                                                                                                                      Claim 4; Page 44; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 NVLMAMNIISKEKKEIKWIG
                                                                       La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1998 (first entry)
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Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell proliferation; car
surgical stent; therapy
                     (PROL-) PROLIFIX LTD.
                                                                                                                       WPI; 1998-377596/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 AA;
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09828334-A1
                                                                       Bandara LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW30501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                              Peptide H3 comprises amino acid residues 174-193 in the DEF box (I) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07) containing one or both of 2 motifs (see AAW30504-07) containing one or both of 2 motifs (see AAW30502-03) of the DEF box are capable of antagonising the capable of antagonising the certain of a DP protein with an E2F protein. Also chercifications of these peptides, especially containing of substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprishing (I) or (II) and a membrane translocation sequence (see AAW30508), expression vectors coroding (I)-(III) and host cells. (I)-(III) are used to therapeutically to induce apoptosis, specifically in tumour or treat or surgical stents comprising (I)-(III) are used to cardiovascular cells, either in vivo or in vitro, e.g. for purging to antioplasty. (I)-(III) function by inactivating the DNA-binding activity of DP-E2F heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunoassay agente.

They are also escribed is the use of sequences antisense to nucleic acids cencoding (I)-(III) to control DP levels in cells, particularly by centoding (I)-(III) enhance cell killing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                       Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
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5..15
/note= "Claim 3"
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Gaps

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96GB-0026589. 97WO-GB03506.

22-DEC-1997; 20-DEC-1996;

02-JUL-1998.

(PROL-) PROLIFIX LTD

us-09-900-147-4.rag

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/note= "encoded by CNA"
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hes 13; Conservative
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                                                                                                                                                                                                                       56 AA;
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                                                                                                                                                                                                                        Sequence
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Matches
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                                                                                                                       Peptide H (I) comprises residues 163-199, i.e. the DEF box region, of transcription factor DP1. Claimed fragments (II) (see AAM30502-07) of (I) are capable of antagonising the heterodimerisation of a DP protein with an E2F protein. Also claimed are fusion proteins (III) comprising (I) or (II) and a membrane translocation sequence (see AAM30508), expression vectors encoding (I)-(III) and host cells. (I)-(III) are used therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding activity of DP/E2F heterodimers. They are also insentifying antagonists of DP-1/E2F dimerisation and as immunoassay
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                               inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                       agents. Also described is the use of sequences antisense to nucleic acids encoding (1)-(III) to control DP levels in cells, particularly by gene therapy. When formulated with cytotoxic or cytostatic agents, (1)-(III) enhance cell killing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation.
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                                                                                                                                                                                                                                                                                                                                                                          Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fragment from a wheat E2F-dimerisation partner (DP) protein.
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                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 101; DB 19; 100.0%; Pred. No. 3.9e-09;
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                                                                                                    Claim 1; Page 44; 55pp; English.
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            La Thangue NB;
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.'
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-257972/26.
N-PSDB; AAF80148.
                                 WPI; 1998-377596/32.
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                                                                                                                                                                                                                                                                                                                                                  37 AA;
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            Bandara LR,
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                                                                                                                                                                                                                                                                                                                                                    Sequence
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New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size -
                                                                                                                                                                                       (DP) processor. Laggments of a wheat E2F-dimerisation partner (DP) process. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active, transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and particularly to alter cell proliferation characteristic such as to alter plant cell, organ or tissue shape,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.2%; Score 78; DB 22; Length 56; 65.0%; Pred. No. 3.3e-05; ive 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DP-1; soybean; cell cycle regulatory protein;
transcription factor; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY32163 standard; Protein; 83 AA,
                                                                                                                                     Claim 10; Page 50; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NVLMAMNIISKEKKEIKWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 NVLIALRVIAKEKKEIRWMG 41
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97WO-GB03506.
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                                                                      (PROL-) PROLIFIX LTD
                                                                                                                           WPI; 1998-377596/32.
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             22-DEC-1997;
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                                         20-DEC-1996;
                                                                                                 Bandara LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW30504
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                                                                                                                                                                                                                                                                           This sequence represents 42% of the middle region of soybean cell cycle regulatory protein DP-1, as deduced from an isolated collar conscious (see AAZ34575). The invention relates to nucleic acid fragments (see AAZ34575-83) encoding plant CDC-16, DP-1, DP-2 and E2F cell cycle regulatory proteins (see AAZ32159-67). It also crelates to the construction of a chimeric gene encoding allor a portion of the cell cycle regulatory protein, in sense or antisense orientation, where expression of the chimeric gene results in producton of altered levels of the cell cycle regulatory protein in a transformed host cell. The nucleic acids and protein in cused to facilitate studies of cell cycle regulation in plants, cused to facilitate studies of cell cycle regulation in plants, convide genetic tools to enhance cell growth in tissue culture, increase gene transfer efficiency and provide nore stable transfer reficiency and provide targets to transfer the protein may also provide targets to facilitate design and/or identification of cell cycle regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DP-1; transcription factor; B2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69; DB 20; Length 83; Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP-1 transcription factor antagonist peptide H2mt2
                                                                                                                                               Sakai H;
                                                                                                                                                                                                                      Plant-derived cell cycle regulatory proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins that may be useful as herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "R167A mutation"
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                                                                                                                  (DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                   Claim 10; Page 41; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NVLMAMNIISKEKKEIKWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.3%;
70.0%;
                                                          99WO-US07638
                                                                                     98US-0081132
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Best Local Similarity 70.07
Best Local 14; Conservative
                                                                                                                                               Klein TM, Morakinyo LO,
                                                                                                                                                                            WPI; 1999-633830/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 AA;
                                                                                                                                                                                             N-PSDB; AAZ34579
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 WO9953075-A2
                                                                                       09-APR-1998;
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                              21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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RESULT

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Peptide HZmt2 is based on peptide H2 (see AAW10504) from the DEF box (see AAW30501) of transcription factor DP1. In HZmt2, amino acid residues of H2 that correspond to DP1 residues Arg167 and Asp171 are substituted by Ala residues. H2 is an antagonist of the heterodimerisation of DP1 with E2F. HZmt2 retains some, but not all, of this antagonistic activity. H2 and other claimed peptides (see AAW30504-07) from the DEF box region of DP1 can be used to induce apoptosis, specifically in tumour and cardiovascular cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GapB
                                                                                                                                                                                                                                        Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
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Pred. No. 0.22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DP-1 transcription factor antagonist peptide H2
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100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for the prevention of restenosis.
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                                                                                                                                                                                                                                                                                                                                                                              Example D; Page 26; 55pp; English
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96GB-0026589
                                                                                                                         La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             surgical stent; therapy
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Boudolf V, De Veylder L, 14-MAY-2001; 2001WO-IB01307. 15-NOV-2001. Synthetic Sequence AAU72601; Query Match Inze D, RESULT 8 ###X#X\$ ò 셤

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Peptide H2 comprises amino acid residues 166-184 in the DEF box (I) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07) containing one or both of 2 motifs (see AAW30502-03) of the DEF box are capable of antagonising the Claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and a mebrane translocation sequence (see AAW30508), expression vectors encoding (I)-(III) and host cells. (I)-(III) are used to therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding angioplasty of DP-E2P heterodimers. They are also used as research reagents as positive controls in assays for identifying antagonists of DP-1/E2P dimerisation and as immunoassay agents. Also described is the use of sequences antisense to nucleic acids encoding (I)-(III) enhance cell killing.
Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                  Claim 4; Page 44; 55pp; English
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50.5%; Score 51; DB 19; Length 19; 100.0%; Pred. No. 0.22; 0; Indels 100.0%; Preu. ... 0; Mismatches Best Local Similarity 100. Matches 11; Conservative 1 NVLMAMNIISK 11 19 AA;

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Gaps ö

AAU72601 standard; Peptide; 35 AA

DEF domain consensus sequence. 26-FEB-2002 (first entry)

Cell cycle protein, CCP, cell cycle regulation, herbicide, plant growth regulator; plant development, abiotic stress, biotic stress, nutrient deprivation, pathogen attack; crop yield; motif.

WO200185946-A2.

12-MAY-2000; 2000US-204045P

(CROP-) CROPDESIGN NV.

New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators -WPI; 2002-062249/08.

Magyar Z;

Acosta JAT,

The invention relates to a novel cell cycle protein (CCP) and the polynucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antiobdy is useful for detecting the presence of CCP in a sample. A CCP antiobdy is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thalians, rice, wheat, maize, tomato, alfalfa, oilseed rape, sobbean, sunflower and canola. CC cycle or growth oilseed rape, sobbean, sunflower and canola. CC protein or groudction of CCP protein forms which have decreased or agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein or production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CMP polymelectide is useful as nerbicides or plant excellators. The polymucleotide is useful for modifying cell fate, plant development, plant morphology, biochemistry and/or physichology, the length of the GI, S, G2 and/or M phase of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, send development, tuber, fruit, leaf formation, shoot and root initiation and/or development, tuber, fruit, leaf formation, seed act, colerance or resistence to etress CCP, the polymucleotide cord initiation and/or activity of a protein involved in the cell cycle due cold, nutrient deprivation, hat, drought, salt stress, or biotic stress such as pathogen attack, to modulate e.g. enhance crop yields, and attenuate plant architecture, plant quality traits, plant reproduction and seed development, endoreduplication in storage cells, corage tissues and/or storage organs of plants or its parts. CCP manners and or naturally occurring CCP much, or a genetic cold, nutrient deprivation, redeted evelopment, endoreduplication is genetal as an immunogen to generate antibodies. CC lesion in a CCP gene and to modulate CCP activity. The present sequence represents a motif which may be found in a CCP protein of the invention. Disclosure; Page 25; 316pp; English. 35 AA; Sequence

ö 50.5%; Score 51; DB 23; Length 35; 55.0%; Pred. No. 0.43; ive 0; Mismatches 9; Indels 11; Conservative Local Similarity Query Match Best Loca Matches

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DP-1 transcription factor peptide H4 AAW30510 standard; Peptide; 15 AA 26-OCT-1998 (first entry) AAW30510; AAW30510

DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy. Synthetic.

Homo sapiens

WO9828334-A1

02-JUL-1998

97WO-GB03506. 22-DEC-1997;

96GB-0026589 20-DEC-1996;

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2000US-0236370.
2000US-0236802.
2000US-0237037.
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                        Peptide H4 comprises amino acid residues 185-199 in the DEF box region (see AAW30501) of transcription factor DP1. Unlike claimed peptides (see AAW30504-07) that contain one or both of 2 motifs (see aAW30502-03) of the DP1 DEF box, peptide H4 is not capable of antagonising the heterodimerisation of a DP protein with an E2F protein. The claimed peptides, their variants and fusion proteins can be used to induce apptosis, specifically in tumour and cardiovascular cells, e.g. to prevent restenosis.
                                                                                                                                                                  Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human musculoskeletal system related polypeptide SEQ ID NO 1380.
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                                                                                                                                                                                                                                                                                              Example C; Page 41; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB03433 standard; Protein; 29 AA
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24-FEB-2000; 2000US-018664.
02-MAR-2000; 2000US-0186550.
11-MAR-2000; 2000US-019874.
17-MAR-2000; 2000US-0199076.
18-APR-2000; 2000US-0198123.
19-MAY-2000; 2000US-0205515.
07-JUN-2000; 2000US-0205515.
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2000US-0217496.
2000US-0218290.
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                                                         Bandara LR, La Thangue NB;
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Best Local Similarity 100.
Matches 9; Conservative
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(PROL-) PROLIFIX LTD
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                                                                                                               WPI; 1998-377596/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 AA;
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11-JUL-2000;
14-JUL-2000;
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ABB03433
XX
AC ABB03
XX
DT 08-JA
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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, ogstrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hammolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barash SC, Ruben SM,
08-NOV-2000; 2000US-0246475.

08-NOV-2000; 2000US-0246476.

08-NOV-2000; 2000US-0246477.

08-NOV-2000; 2000US-0246527.

08-NOV-2000; 2000US-0246524.

08-NOV-2000; 2000US-0246524.

08-NOV-2000; 2000US-0246525.

08-NOV-2000; 2000US-0246525.

08-NOV-2000; 2000US-024652.

08-NOV-2000; 2000US-024652.

08-NOV-2000; 2000US-0246610.

08-NOV-2000; 2000US-0246610.

08-NOV-2000; 2000US-0246611.

08-NOV-2000; 2000US-0246611.

08-NOV-2000; 2000US-0246611.
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17-NOV-2000; 200003-0249209.
17-NOV-2000; 200003-0249210.
17-NOV-2000; 200003-0249211.
17-NOV-2000; 200003-0249212.
17-NOV-2000; 200003-0249213.
17-NOV-2000; 200003-0249214.
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2000US-0249217.
2000US-0249218.
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17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249265.
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17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0250160.
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05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251988.
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06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
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08-DEC-2000; 2000US-0251990
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17-NOV-2000; 2
17-NOV-2000; 2
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Musculoskeletal system antigen; cancer; metastasis;

re-vascularisation; thrombosis; arteriosclerosis; mineral content;

re-vascularisation; thrombosis; arteriosclerosis; mineral content;

re-vascularisation; thrombosis; arteriosclerosis; mineral content;

macroparative tissue repair; limb regeneration; neuronal growth;

muscrelated complex; chondrocyte growth; bone regeneration;

MIDS. related complex; chondrocyte growth; bone regeneration;

keratinocyte growth; hair loss; melanocyte growth; cell proliferation;

cell growth; organ transplant; cell differentiation; body height;

weight; hair colour; eye colour; skin; percentage of adipose tissue;

pigmentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm;

depression; tendency for violence; pain; reproductive capability;

hormone level; endocrine level; appetite; libido; memory; stress;

nearbohydrate content; vitamin content; protein content;

carbohydrate content; vitamin content; cofactor content;
multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovescular disorders such as myocardial isofabenhas; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                        parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. 0.51;
1; Mismatches
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2000US-216647P.
2000US-216880P.
2000US-217487P.
2000US-217487P.
2000US-218290P.
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2000US-224518P.
2000US-224519P.
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2000US-225758P.
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 MNIISKEKKEIKWIG
                                                                                                                                                                                                                                                                           29 AA;
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14-AUG-2000;
14-AUG-2000;
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reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities, at content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. This is the amino acid sequence of a novel human musculoskeletal system antigen.

Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at

ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140.

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Gaps

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Score 50; DB 24; Length 29; Pred. No. 0.51; 1; Mismatches 4; Indels

49.5%;

Query Match
Best Local Similarity 66.7
Matches 10; Conservative

29 AA;

Sequence

6 MNIISKEKKEIKWIG 20

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The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful cordetecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions such as thrombosis, can treat and prevent conditions, such as, Alzhehmer's disease, Parkinson's disease, and neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzhehmer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to subburn by stimulating keratinocyte growth; prevents hair loss, since FGF family conserved and differentiation of hematopoietic cells and bone stimulates growth and differentiation of hematopoietic cells and bone arrows acils when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; increases the differentiation or proliferation of embryos; increases the differentiation or proliferation of embryos; increases the differentiation or proliferation of embryos; increases the differentiation or colour, every embryonic stem cells besides, had an encount of the embryonic stem cells, such as, body height, weight, hair colour, every colour, skin, percentage of adipose tissue, pigmentation, is and shape (e.g., cosmetic surgery); modulates mammalian metabolism; changes carlcadic rhythms, depression, tendency for violence, tolerance for pain, carlcadic rhythms, depression, tendency for violence, tolerance for pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC;
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02-0CT-2000; 2000US-237033P.
02-0CT-2000; 2000US-237039P.
02-0CT-2000; 2000US-237039P.
13-0CT-2000; 2000US-239935P.
20-0CT-2000; 2000US-24096P.
20-0CT-2000; 2000US-24108P.
20-0CT-2000; 2000US-24108P.
20-0CT-2000; 2000US-24109P.
01-NOV-2000; 2000US-24869P.
08-DEC-2000; 2000US-251868P.
             30-AUG-2000) 2000US-228924P.
01-SEP-2000) 2000US-229343P.
01-SEP-2000) 2000US-229343P.
01-SEP-2000) 2000US-229344P.
01-SEP-2000) 2000US-229345P.
05-SEP-2000) 2000US-229345P.
05-SEP-2000) 2000US-229509P.
06-SEP-2000) 2000US-229513P.
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29-SEP-2000; 2000US-236367P.
29-SEP-2000; 2000US-236368P.
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29-SEP-2000; 2000US-236370P.
02-OCT-2000; 2000US-236802P.
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25-SEP-2000; 2000US-234997P.
27-SEP-2000; 2000US-235834P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ROSE/) ROSEN C A. (RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABX58003
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The invention relates to a novel cell cycle protein (CCP) and the polynucleotides encoding them. CCP is useful for identifying a compound polynucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for modulating the presence of CCP in a sample. A CCP modulator is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP nucleic acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of treat disorders characterion of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP polypeptide are useful as herbicides or plant growth regulators. The polynucleotide is useful for modifying cell fate, plant development,
                                                                                                                                                                                                                                                                               Cell cycle protein; CCP; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield; immunogen; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Veylder L, Acosta JAT, Magyar
                                                                                                                                                                                                                                             Arabidopsis cell cycle protein AtDPa 121-293.
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                                                                                                                     AAU72561 standard; Protein; 93 AA.
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13 MKIFSKEKKKIGWPG 27
                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                 RESULT 12
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stimulation or palancement of cell division, property, seed set, stimulation or enhancement of cell division, DNA replication, seed set, seed size, seed development, tuber, fruit, leaf formation, seed set, seed size, seed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, tuber, fruit, leaf formation, shoot and root initiation and/or development, module function, dwarfism in plants, senescence, tolerance or resistance to stress. CCP, the polynuclectide and the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due to environmental conditions, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic and attenuate plant architecture, plant quality traits, plant reproduction and seed development, endoreduplication in storage cells, storage tissues and/or storage organs of plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to screen for naturally occurring CCP substrates. The polymuclectide is cueful for expressing CCP protein, of detect CCP mRNA, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence represents a deletion mutant of a CCP protein of the invention.
   morphology, biochemistry and/or physiology, the length of the G1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
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Pred. No. 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW30515 standard; Peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 IISKEKKEIKWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ilardkkeirwkg 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 61.5
es 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            surgical stent; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROL-) PROLIFIX LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-1997;
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Best Local
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IID AAM3

AAC AAM3

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XX BP-1

XX BP-1

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                                                      are substituted by Ala residues, behaves in a similar fashion to the wild-type H2 peptide in its ability to inactivate E2F site DNA binding activity in D9 EC cell extracts. H2 is an antagonist of the heterodimerisation of DP1 with E2F. Thus, the Val-169 and Val-175 residues of H2 play little role in this activity. H2 and other claimed peptides (see AAW30504-07) from the DBF box region of DP1 can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g. for the prevention of restenosis.
                                                                                                                                                                                                                                                                   Gaps
         Peptide H2mtl is based on peptide H2 (see AAW30504) from the DEF box (see AAW30501) of transcription factor DP1. The H2mtl peptide, in which H2 residues corresponding to DP1 residues Val169 and Val175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide H5 comprises amino acid residues 168-183 in the DEF box (I) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07) containing one or both of 2 motifs (see AAW30502-03) of the DEF box are capable of antagonising the heterodimerisation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
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                                                                                                                                                                                                                                  Score 47; DB 19; Length 19;
Pred. No. 0.96;
                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DP-1 transcription factor antagonist peptide H5.
                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                AAW30506 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5..11 /note= "Claim 3" 7..16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 44; 55pp; English.
                                                                                                                                                                                                                                    46.5%;
90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell proliferation; card
surgical stent; therapy.
                                                                                                                                                                                                                                                                                                 1 NVLMAMNIISK 11
                                                                                                                                                                                                                                                                                                                             9 NALMAMNIISK 19
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                                                                                                                                                                                                        19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW30506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
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region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.

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Gaps

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Length 28; 0; Indels

DB 19; 2.2;

45.5%; Score 46; DB 100.0%; Pred. No. 2.2 ive 0; Mismatches

28 AA;

Sequence

us-09-900-147-4.rag

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Query Match
Best Local Similarity luc...
Thes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This represents a compound that can inhibit E2F activity. The compound is of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding
embatitutions of residues corresponding to residues 167, 169, 171

and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and a membrane translocation sequence (see AAW30508), expression vectors encoding (I)-(III) and host cells. (I)-(III) are used to therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding cativity of DP/EZP heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-1/E2P dimerisation and as immunoassay agents. C Also described is the use of sequences antisense to nucleic acids encoding (I)-(III) to control DP levels in cells, particularly by gene therapy. When formulated with cytotoxic or cytostatic agents, (I)-(III) enhance cell killing.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E2F activity inhibitors - for treatment and prevention of tumours and arteriosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         E2F activity; inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                                                               45.5%; Score 46; DB 19; Length 16; 100.0%; Pred. No. 1.1; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoshida T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                  E2F activity inhibiting compound Ib-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamasaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                             AAW57051 standard; peptide; 28 AA.
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                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                              1 NVLMAMNIIS 10
                                                                                                                                                                                                                                                                                                   NVLMAMNIIS 16
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                                                                                                                                                                                                         16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                     AAW57051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2F activity inhibitors - for treatment and prevention of tumours
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0
                                                                                                                                                                                                                                                                                                                                            E2F activity; inhibitor; treatment; tumour; arteriosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "N-terminal lauroyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                               E2F activity inhibiting compound Ib-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                            AAW57055 standard; peptide; 28 AA.
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10
                                             19 NVLMAMNIIS 28
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1 NVLMAMNIIS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                               RESULT 16
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Synthetic

AAW30517;

RESULT 17

AAW30517

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The present invention relates to a new method of modulating expression of telomerase reverse transcriptase (TERT) from a TERT expression system that includes a TERT promoter and a Site C repressor binding site. The method of the invention involves modulating TERT transcription repression by the Site C repressor binding site. The method of the invention is useful for modulating expression of TERT for production is antibody. The method is also useful in a variety of different applications, including immortalisation of cells, production of reagents consening applications. Increasing TERT expression therapeutic applications, and the chimson-dilator shortening and/or increasing TERT expression delays natural telomeric shortening and/or increasing telomeric length and selections and to inhibit immune sensecence. The method can be employed to lengthen telomeres of cardiovascular disease, osteoporosis, in skin rejuvenation and to inhibit immune sensecence. The method can be employed to lengthen telomeres of steoblast and osteoclast stem cells, encouraging bone replacement and proper remodeling and reinforcement, and can thus be used in bone marrow transplants for the treatment of encouraging bone replacement and cutting and as such the method improves the survival and effectiveness of
                                                              Human, telomerase reverse transcriptase, TERT; Site C; Progeria; burn; repressor binding site; Hutchinson-Gilford syndrome; AIDS; cancer; acquired immunodeficiency syndrome; cardiovascular disease; osteoporosis; skin rejuvenation; immune senescence; bone marrow transplant; skin graft; neoplastic disease; TERT minimal promoter; DNA binding domain; E2F-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulating expression of telomerase reverse transcriptase (TERT) in a cell, for regulating proliferative capacity of a cell, involves modulating TERT transcription repression by Site C repressor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for treating cellular proliferative disease conditions, inc
neoplastic disease conditions e.g. cancer. The present amino acid
sequence represents the human DNA binding domain E2F-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bone marrow and skin cell transplants. Decreasing TERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser S, Mohammadpour H;
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                                                                                                                                                                                                                                                                                      18..59
/label= DNA_binding_domain
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42.9%; Pred. No. 13;
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                                                                                                                                                                                                                                                          Location/Qualifiers
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NVLEGIQLIAKKSKNHIQWLG 83
                    Human DNA binding domain E2F-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-2000; 2000US-227865P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-230174P.
2000US-238345P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andrews WH, Foster CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SIER-) SIERRA SCI INC.
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                                                                                                                                                                                                                                                                                                                                                               WO200216657-A1
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2000;
05-OCT-2000;
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                                                                                                                                                                                                                                                                                      Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide HZmt3 is based on peptide H2 (see AAW30504) from the DEF box (see AAW30501) of transcription factor DP1. In HZmt3, amino acid residues of H2 that correspond to DP1 residues Leul73 and Leul76 are substituted by Arg residues. H2 is an antagonist of the heterodimerisation of DP1 with B2P. HZmt3 has none of the antagonistic activity of H2. H2 and other claimed peptides (see AAW30504-07) from the DEP box region of DP1 can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                   DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
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                                                                                                                                                                                                                                      DP-1 transcription factor peptide H2mt3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "L173R mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "L176R mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example D; Page 26; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU78095 standard; Protein; 85 AA.
                                                                                          AAW30517 standard; Peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the prevention of restenosis.
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9 NVRMAMNIISK 19
                                                                                                                                                                                                                                                                                                                                     surgical stent; therapy
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les 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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18-JUN-2002

AAU78095;

AAU78095 ID AAU7 XX AC AAU7 XX AAU7 DT 18-J

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Sequence

Query Match Best Loc Matches Length 85; Indels

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This peptide comprises amino acid residues 175-183 in the DEF box region (see AAW30501) of transcription factor DP1. Claimed peptides (11) (see AAW30502-07) containing this and/or another motif (see AAW30503) of the DEF box, are antagonists of the heterodimerisation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (1) or (II) and a membrane translocation sequence (see AAW30508), expression vectors encoding (1)-(III) and specifically in tumour or cardiovascular cells, either in vivo or vitro, e.g. for purging bone marrow. Surgical setups omprising control of 10-(III) are used therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or vitro, e.g. for purging bone marrow. Surgical setups on emprising control of 10-(III) are used therapeutically to induce apoptosis, the DNA-binding activity of DF/E2F heterodimers. They are also case and a sessor of the DNA-binding activity of DF/E2F heterodimers. They are also dentifying artagonists of DP-1/E2F dimerisation and as immunoassay agents. Also described is the use of sequences antisense to mucleic acids encoding (I)-(III) to control DP levels in cells, control and as immunoassay and control and a sumunoassay control and a
                                                                                                                                                                                                                                                                                                                                     Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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                                                                                                                                                      97WO-GB03506.
                                                                                                                                                                                                                                                                      La Thangue NB
                                                                                                                                                                                                                                 (PROL-) PROLIFIX LTD
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                                      Homo sapiens.
                                                                           W09828334-A1
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                                                                                                                 02-JUL-1998
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                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to modulating expression of telomerase reverse transcriptase (TERT) expression system that includes a TERT promoter and a Site C repressor binding site. The method involves modulating TERT transcription repression by the Site C repressor binding site. The methods and compositions of the present invention are useful for the immortalization of cells, production of reagents in life science research, therapeutic agent screening applications diagnosis and treatment of disorders associated with aberrant telomerase activity such as cancer, Progeria, immune senescence, HIV, and in skin rejuvenation. The present sequence represents the DNA binding domain of a repressor protein E2P-1.
                                                                                                                                                                                               Telomerase reverse transcriptase; TERT; Site C repressor; transcription; cytostatic; immunostimulant; anti-HIV; vulnerary; telomerase; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating expression of telomerase reverse transcriptase TERT by blocking repression of TERT transcription, useful for the diagnosis and treatment of disorders associated with aberrant telomerase activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mohammadpour H, Andrews WH;
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                                                                                                                                                            Repressor protein E2F-1 DNA binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 7; 47pp; English.
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NVLEGIOLIAKKSKNHIQWLG 83
                                              ABB82986 standard; Protein; 85 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW30502 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-2002; 2002WO-US17959.
                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-2001; 2001US-296992P
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                                                                                                                        (first entry)
                                                                                                                                                                                                                                          repressor protein; E2F-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such as cancer and HIV
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nes 9, Conserv
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                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                        14-APR-2003
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                                                                                     ABB82986;
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Matches
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        RESULT 19
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                                                                                    Gaps
                                                                                    ;
0
                                     Length 9;
                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a Chlamydia trachomatis protein.
                                       DB 19; Lo
                                  / Match 10.0%; Score 42; DB Local Similarity 100.0%; Pred. No. 9.3 les 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                        AAY37764 standard; Protein; 91 AA.
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1 NVLMAMNII 9
9 AA;
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Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; mamen modulation; hamatopoiesis regulation; tessue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; itssue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.6%; Score 40; DB 20; Length 57; Best Local Similarity 31.6%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cadherin-like ORF1685 protein, SEQ ID NO:3370.
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                                                                                                                                                                                                                               WPI; 1999-418749/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 AA;
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                                                                               19-DEC-1997
                                                                  19-DEC-1997
                                                                                             19-DEC-1997
                                                                                                                                                                           Florence K,
                                                                                                                                                              Carter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                 AAY36754-Y17949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophremia; arthritis; sathma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS.
                                                                                                                                                                                                                                                                                                                                                   diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and veneral lymphogramulomatosis. The polypeptides of the invention may be of use in treating these diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.6%; Score 42; DB 20; Length 91; 56.2%; Pred. No. 36; 7; Indels tive 0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fragment of human secreted protein encoded by gene 62.
                                                                                                                                                                                                                                                       Disclosure; Page 1355-1356; 1755pp; English
                                                                                                                                                                                                                               Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY36705 standard; Protein; 57 AA
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97US-0068006.
97US-0068007.
97US-0068008.
                                                                                         98US-0107077.
97FR-0015041.
97FR-0016034.
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18-DEC-1997;
18-DEC-1997;
18-DEC-1997;
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                                                               27-NOV-1998;
                                                                                          04-NOV-1998;
28-NOV-1997;
                                                                                                                     17-DEC-1997;
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                                       10-JUN-1999.
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                                                                                                                                                                         Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY36705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Gaps

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7; Indels

. 6; Mismatches

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the 110 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 110 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and feetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, achizophremia, arthritis, asthma, psoriasis, sepsis, skin disorders, achizophremia, arthritis, asthma, psoriasis, alsorders, kidney disorders, digestive/endocrine disorders, infections and ALDS. The polypeptides are also useful for identifying their binding the polypeptides are also useful for identifying their binding contains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX97916 to AAX98029 represent 110 isolated human secreted protein
genes. AAX36224 to AAX36727 represent the secreted proteins encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes encoding secreted polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KC, Duan RD, Feng P, Ferrie AM, Florenc
ce K, Greene JM, Janat F, Kyaw H, Moore
Rosen CA, Ruben SM, Shi Y, Soppet DR, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 526; 537pp; English.
                                                                                                                           970S-0068064.
970S-0070923.
970S-0068169.
970S-0068365.
970S-0068365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
97US-0068053.
97US-0068054.
97US-0068057.
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CURA-) CURAGEN CORP.
                                            WPI; 2002-106200/14.
                                                                                                                                                                   Best Local Similarity
Matches 6, Conserv
                                                                                                                                                            63 AA;
                                               N-PSDB; ABN76738.
                                                           ransplantation
               WO200190366-A2
         Homo sapiens.
                   29-NOV-2001.
                                       Leach MD,
                                                                                                                                                             Sequence
                                                                                                                                                                 Query Match
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Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                 Human liver peptide, SEQ ID No 28319.
                                                                             ABG49671 standard; Peptide; 75 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488898/53.
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                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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27-SEP-2000;
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                                                                                                                                                                                               25-FEB-2003
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                                                                                                                                         ABG49671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
                                                        ABG49671
                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       designated ORF (open reading frame) 1-4334 movel numning proteins designated ORF (open reading frame) 1-4334, and sequences ABNY5034-ABNY5087 represent conversation them. The invention also encompasses polypeptides at least 804 identical to the ORF1-ORF434 (collectively) creferred to as ORFX) proteins, polynucleotides at least 8054 identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX the ORFX proteins, methods of Screening for modulators of ORFX proteins, antibodies polypeptides, methods of screening individuals for a predisposition to an operativity, and methods of screening individuals for a predisposition to an operativity, and methods of screening individuals for a predisposition to an open of biological activities, society as creening individuals for a predisposition to an open of biological activities, society activity, themetopolesis regulation, cell differentiation, immune modulation, haematopoiesis regulation, cell differentiation, immune modulation, haematopoiesis regulation, clissue growth, angiogenesis, activinto, tumour inhibit activity, activity, receptor/ligand, antiinflammatory activity, tumour inhibition activity, and antiinflective activity, and may also be involved in the determination of bodily characterisatios, fertility and behaviour. ORFX proteins, other proliferative disorders such as spilepsy and Albahemer's disease, contact the contact of ancers, other proliferative disorders such as spilepsy and Albahemer's diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, disorders of tissue growth and regeneration, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals shich may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases.
neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences ABP31028-ABP35561 represent 4534 novel human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.6%; Score 40; DB 23; Length 63; 50.0%; Pred. No. 50; 1. Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 1101; 2508pp; English.
                                                                                                                                                                                                                                                                                           24-MAY-2001; 2001WO-US17076.
                                                                                                                                                                                                                                                                                                                                                    24-MAY-2000; 2000US-206690P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimkets RA;
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Hanzel DK, Chen W, Rank DR;

2000US-0236359 2000GB-0024263 2000US-0632366 2000US-0234687

2000US-0180312 2000US-0207456 2000US-0608408

(first entry)

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                                                                                                                                             The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high
                                                                                                                                                                                                                                                              stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis,
                                                                                                                                                                                                                                                                                                                                                                                            hyperlipoprofinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 22; Length 75;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                           Claim 27; SEQ ID No 28319; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB29659 standard; Peptide; 75 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 ISKEKKEIKWIG 20
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Best Local Similarity
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Matches
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Gaps

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6; Conservative 9 ISKEKKEIKWIG 20 VOKESKENOWLG 59

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein #2256 encoded by probe for measuring heart cell gene expression.
                                                                Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                      Peptide #2343 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 27472; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, gene expression, heart, microarray, vascular system,
cardiovascular disease, hypertension, cardiac arrhythmia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. 61;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.6%;
                                                                                                                                                                                                                                                                                                                                        03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                    2000US-0207456
2000US-0608408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483447/52
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Best Local Similarity
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                                                                                                                                                   WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157274-A2
                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                          30-JUN-2000;
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                                                                                                                                                                                                                                                                              04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG,
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Matches
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    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 47 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label contacting the expression of regions of genomic DNA predicted to verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias chan expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                        Peptide #2310 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
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                                                                                    Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID NO 12627; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 22; Length 75; Pred. No. 61;
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                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-060B408.
03-MG-2000; 2000US-063366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000; 2000GB-0024263.
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(first entry)
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31 ITKEKSSLRWAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 AA;
                                                                                                           disease; cancer
                                                                                                                                                                                           WO200157271-A2
  01-FEB-2002
                                                                                                                                                   Homo sapiens
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RESULT 26

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AC ABB3
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human bone marrow expressed probe encoded protein SEQ ID NO: 28331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO: 28331; 658pp + Sequence Listing; English
                                                                                                                                                                                           Example 4; SEQ ID NO: 27750; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR
                                                                       В;
                                                                       Rank
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                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00668
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                             the probes of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 ISKEKKEIKWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 ITKEKSSLRWAG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488900/53
                                                                         Hanzel DK,
                                                                                                          WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                 75 AA;
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                                                                       Penn SG,
                                                                                                                                                                  brains
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                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA1305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe encoded protein SEQ ID NO: 27750.
                                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in \ensuremath{\mathsf{human}} hearts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
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                                                                                                                                                                                                                           Rank DR;
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-MQ-2000; 2000US-063336.
21-SEP-2000; 2000US-0236859.
                                       04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-053366.
21-SEP-2000; 2000US-0234687.
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                                                                                                                                   27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
         30-JAN-2001; 2001WO-US00666
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Best Local Similarity 50.v.
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                                                                                                                                                                                                                             Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                              WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 AA;
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Length 75; 3; Indels

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Matches
        Matches
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #2277 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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                                                                                                                                                                        22; Length 75;
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                                                                                                                                                                                                                    3; Indels
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Pred. No. 61;
                                                                                                                                                                        Score 40; DB
Pred. No. 61;
                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                        AAM15843 standard; Protein; 75 AA.
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2000US-0234687.
2000US-0236359.
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50.0%;
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2000US-0207456.
2000US-0608408.
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                  6; Conservative
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                                                                                                                                                                                                                                                                                      31 ITKEKSSLRWAG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488901/53
                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                 75 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer.
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                         Peptide #2390 encoded by probe for measuring placental gene expression.
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Gaps
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                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analyzing gene expression in human placenta
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50.0%; Pred. No. 61;
iive 3; Mismatches
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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2000US-0608408
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                                        ISKEKKEIKWIG 20
                                                                             ITKEKSSLRWAG 42
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ITKEKSSLRWAG 42
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                                                                                                                                                                                                                                                                                                                                                                      genetic disorder
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27-SEP-2000;
04-OCT-2000;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                          Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human peptide encoded by genome-derived single exon probe SEQ ID 27217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; single exon probe; asthma; lung cancer; COPD; LLD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histlocytosis; lymphangioleiomyomtosis; Karagener syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Peptide #2263 encoded by probe for measuring breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 61;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID No 12321; 322pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG37552 standard; Peptide; 75 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-2000; 2000US-0207456.
30-UNA-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.08;
                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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31 ITKEKSSLRWAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG, Hanzel DK,
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Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in a human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 AA;
                                                                                                                                                                                                                                              WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
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                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                09-AUG-2001.
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. His oincluded are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with sample derived from human lung, comprising (a) contacting the array with a array; identifying exons in a eukaryotic gene expression of detectably labeled nucleic acids derived from human lung, comprising (a) contacting the array with a array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, and the above mentioned introarray seafighting exons in the probes from genomic sequence by the method above and (b) measuring the expression of each of the exons in several comprising (a) identifying exons from genomic sequence by the method above and ofor cell types using hybridisation to a single exon it is several expression of the exons in the tissues and/or cell types indicates that expression of the exons in the tissues and/or cell types indicates common partern of expression and/or cell types with the exons subside exons in the specification, or encoded by the expression of the exons in the probes are used for gene components and probes are use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haemosiderosis, pulmonary historytosis, lymphangioleiomytosis, pulmonary haemosiderosis, pulmonary bulmonary bulmonary bulmonary bulmonary bulmonary bulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID No 27217; 634pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  format directly from WIPO at
frp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                   26-MAY-2000; 2000US-207456P.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-23559P.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-114183/15.
                                                                                                                                                       WO200186003-A2.
                                                                                                                                                                                                                                                                                                    04-FEB-2000;
                                                                                                               Homo sapiens
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Sequence

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17-JAN-2001; 2001WO-US01354.
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2000US-0232080
                                                                         (first entry)
                                                                                                                                                                      WO200157182-A2.
                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-SEP-2000;
                                                                         07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2-AUG-2000
                                                    AAM88281;
            RESULT 35
                      AAM88281
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                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the encoded proceins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymolectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. steem cell growth factor activity, nemanopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; accine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human polynucleotides (AAI79941-AAI93841) and
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 15062; 1399pp + Sequence Listing; English.
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Pred. No. 69;
1; Mismatches 1; Indels
  DB 23; Length 75;
                      3; Indels
Score 40; DB 2
Pred. No. 61;
3; Mismatches
                                                                                                                                                                              Human polypeptide SEQ ID NO 15062.
                                                                                                                AAO01170 standard; Protein; 83 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Drmanac RT;
 39.6%;
                                                                                                                                                                                                                                                                                                                                         28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US04927.
                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.3
Query Match 39.6
Best Local Similarity 50.0
Matches 6; Conservative
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                                        9 ISKEKKEIKWIG 20
                                                             31 ITKEKSSLRWAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-514838/56.
N-PSDB; AAI81101.
                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 AA;
                                                                                                                                                                                                                                                                            WO200164835-A2
                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                         06-NOV-2001
                                                                                                                                                                                                                                                                                                07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders
                                                                                                                                      AA001170;
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Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen SEQ ID NO:15874.
AAM88281 standard; Protein; 42 AA.
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08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246528.
08-NOV-2000; 2000US-0246532.
                                                                                                                                                                                                            17-NOV-2000; 2000US-0249299
17-NOV-2000; 2000US-0249300
                                     25-SEP-2000; 2000US-0234998.
26-SEP-2000; 2000US-0235484.
                                                                                                                                                08-NOV-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) antino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) to proteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For treatment of diseases associated with decreased expression by rectifying mutations or deletions in a patient's genome cypression by rectifying mutations or deletions in a patient's genome contact affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inserting protein. (I) proteins and polynucleotides may be used to prevent, concers and carcer metastases of haematopoietic-related diseases, especially cancer metastases of haematopoietic-derived cells. AAK64703 concers and carcer metastases of haematopoietic antigen genomic concers and carcer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK84950 and AAM82169 crepresent invention. AAK54942 to AAK84950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaрв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID NO 15874; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.1%; Score 39.5; DB 22; Length 42; 26.7%; Pred. No. 38; tive 8; Mismatches 3; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 7253.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG09353 standard; Protein; 84
                                                                                    2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                          08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
0S-JAN-2001; 2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                              Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483426/52.
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Best Local Similarity
Matches 8; Conserv
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Arabidopsis thaliana

EP1033405-A2

2000EP-0301439.	9US-0121825	99US-0123180. 99US-0123548.	9US-0126264	9US-0126785 9US-0127462	9US-0128234	9US-0129845	9US-0130077 9US-0130449	9US-0130510	9US-013U891 9US-0131449	9US-0132048	9US-0132484	9US-0132485	9US-0132487	9US-0132863	9US-0134218	9US-0134219	9US-0134370	9US-0134768	9US-0135124	9US-0135353	9US-0135629 9US-0136021	9US-0136392	9US-0136782 9US-0137222	9US-0137528	9US-0137502 9US-0137724	9US-0138094	9US-0138540 9US-0138847	9US-0139119	9US-0139452 9US-0139453	9US-0139492	9US-0139454 9US-0139455	9US-0139456	9US-0139457 9US-0139458	9US-0139459	9US-0139460 9US-0139461	9US-0139462	9US-0139463	9US-0139763	9US-0139817	9US-0139899 9US-0140353	9US-0140354	9US-0140695 9US-0140823	9US-0140991	9US-0141287 9US-0141842	9US-0142154	
06-SEP-2000. 25-PEB-2000;	5-FEB-1999 5-MAP-1999	09-MAR-1999;	5-MAR-1999	9-MAR-1999 1-APR-1999	6-APR-1999 8-APP-1999	6-APR-1999	9-APR-1999 1-APR-1999	3-APR-1999	8-APR-1999 8-APR-1999	0-APR-1999	4-MAY-1999	5-MAY-1999 6-MAY-1999	6-MAY-1999	7-MAY-1999	4-MAY-1999	4-MAY-1999	4-MAY-1999	8-MAY-1999	0-MAY-1999	1-MAY-1999	4-MAY-1999 5-MAY-1999	7-MAY-1999	8-MAY-1999 1-JUN-1999	3-JUN-1999	4-JUN-1999 7-JUN-1999	8-JUN-1999	0-01-NUD-0	4-JUN-1999	6-JUN-1999 6-JUN-1999	7-JUN-1999	8-JUN-1999	8-JUN-1999	8-11999 9-11-WIT:-8	8-JUN-1999	8-1-NUC-8	8-JUN-1999	8-JUN-1999	8-JUN-1999	1-JUN-1999	2-JUN-1999 3-JUN-1999	3-JUN-1999	4-JUN-1999 8-JUN-1999	9-NUL-1999	0-JUN-1999 1-JUL-1999	1-JUL-1999	
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2000US-0231413.
2000US-0231414.
2000US-0232080.
2000US-0232081.
2000US-0232397.
2000US-0232397.
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2000US-0216880.
2000US-0217487.
2000US-0217496.
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14-SEP-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                          Score 39; DB 21; Length 84;
Pred. No. 1e+02;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen SEQ ID NO:17667,
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM90074 standard; Protein; 91 AA
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56 LIARRVVGREAKEIERYWI
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99US-0160814.
99US-0160814.
99US-0160810.
99US-0160980.
99US-0161404.
99US-0161404.
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990S-0161920.
990S-0161992.
990S-0161993.
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
99US-0155139.
99US-0155486.
99US-0156569.
99US-0156596.
99US-01567753.
99US-0157753.
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99US-0159331.
99US-0159637.
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99US-0159294.
99US-0159295.
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99US-0160741
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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.1
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
22-SEP-1999;
24-SEP-1999;
24-SEP-1999;
29-SEP-1999;
04-0CT-1999;
06-0CT-1999;
06-0CT-1999;
06-0CT-1999;
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14-0CT-1999;
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8-0CT-1999;
1-0CT-1999;
1-0CT-1999;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 co AAK87694 represent human immune/haematopoietic antigen genomic cequences from the present invention. AAK54921 to AAK5450 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ren F;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, genome mapping, gene therapy, food supplement, virus, fungus, cell-proliferative disorder, neurodegenerative disease, bacterial, Parkinson's disease, Alzheimer's disease, autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao QA, F
Ghosh M;
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                                                                                                                                                                                                                                                                                                                                         38.6%; Score 39; DB 22; Length 91; 66.7%; Pred. No. 1.1e+02; tive 3; Mismatches 0; Indels
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1 Y, Yamazaki V, Chen R, Wang Z,
Wang D, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP69141 standard; Protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 1188.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAR-2002; 2002WO-US05095.
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Wehrman T, Wang J,
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                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                              91 AA;
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                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP69141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 17667; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000; 20000S-0249300.
01-DEC-2000; 20000S-0250160.
01-DEC-2000; 20000S-0250391.
05-DEC-2000; 20000S-0251980.
05-DEC-2000; 20000S-0251980.
06-DEC-2000; 20000S-0251980.
06-DEC-2000; 20000S-0251856.
08-DEC-2000; 20000S-0251856.
02-OCT-2000; 2000US-0237040.
13-OCT-2000; 2000US-0239935.
13-OCT-2000; 2000US-0239937.
20-OCT-2000; 2000US-0249937.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241860.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246511.
08-NOV-2000; 2000US-0246511.
08-NOV-2000; 2000US-0246611.
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17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
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2000US-0249211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-483426/52
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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful coding protein or complementary sequences. The polynucleotides are useful cfor identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating and identifying and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Carinson's or Alzheimer's disease), autoimmune diseases (multiple of sclerosis, diabetes, lupus) genetic disorders, wound, burns, incision, closers, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, comparabitic), arrhrities, etc.

Co parasitic), arrhrities (archis patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fib. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, telomerase reverse transcriptase, TERT; Site C; Progeria; burn, repressor binding site; Hutchinson-Gilford syndrome; AIDS; cancer; acquired immunodeficiency syndrome; cardiovascular disease; osteoporosis; skin rejuvenation; immune sensecence; bone marrow transplant; skin graft; neoplastic disease; TERT minimal promoter; DNA binding domain; B2F-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating expression of telomerase reverse transcriptase (TERT) in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell, for regulating proliferative capacity of a cell, involves modulating TERT transcription repression by Site C repressor binding site -
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9; SEQ ID NO 1188; 1012pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 23; Length 97;
Pred. No. 1.2e+02;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7..49
/label= DNA binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU78096 standard; Protein; 76 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         38.6%;
53.8%;
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Best Local Similarity 53...
7; Conservative
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14 ILLAMLMVDKEKK 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SIER-) SIERRA SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-280952/32.
                                                                                                                                                                                                                                                                                                                                                                                                    97 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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        Claim
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The present invention relates to a new method of modulating expression of telomerase reverse transcriptase (TERT) from a TERT expression system of telomerase reverse transcriptase (TERT) from a TERT expression system that includes a TERT promoter and a Site C repressor binding site. The method of the invention is entered to be the site C repression of TERT for producing a mammalian to be the Site C repression of TERT for producing a mammalian settli for modulating expression of TERT for production of reagents of the method is also useful in a variety of different applications, including immortalisation of cells, production of reagents for use in life science research, therapeutic applications and the saperic agent screening applications. Increasing TERT expression cells, useful for treating disease conditions such as Progeria or delays natural telomeric shortening and/or increases telomeric length and is useful for treating disease conditions such as Progeria or Cardiovascular disease, osteoporosis, in skin rejuvenation and to inhibit cimmume sensescence. The method can be employed to lengthen telomeres of ortoper remodeling and reinforcement, and can thus be used in bone marrow transplants for the treatment of cancer and skin grafts for burn victims and as such the method improves the survival and effectiveness of the confittions even conditions even conditions, including cellular proliferative disease conditions, including centil for treating cellular proliferative disease conditions, including centil for treating cellular proliferative disease conditions, including center the human DNA binding domain E2F-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Telomerase reverse transcriptase; TERT; Site C repressor; transcription; cycostatic; immunostimulant; anti-HIV; vulnerary; telomerase; human; repressor protein; E2F-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulating expression of telomerase reverse transcriptase TERT by blocking repression of TERT transcription, useful for the diagnosis treatment of disorders associated with aberrant telomerase activity such as cancer and HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.1%; Score 38.5; DB 23; Length 76; 42.9%; Pred. No. 1.1e+02; tive 4; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andrews WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repressor protein E2F-4 DNA binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mohammadpour H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB82987 standard; Protein; 76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NVLMAMNIISKE-KKEIKWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
              Disclosure; Page 8; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 NVLEGIGLIEKKSKNSIQWKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-2002; 2002WO-US17959.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 42.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SIER-) SIERRA SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Foster CA, Fraser S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-167401/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2002101010-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB82987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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(first entry)
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7 NMISKQSRKKKW 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483447/52
                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                    31 AA
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                                                                                                                                                                                                                                                                                                                                                                        ABB39547;
                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
                                                                                                                                                                                                                                                                                                      RESULT 42
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                          The invention relates to modulating expression of telomerase reverse transcriptase (TERT) expression system that includes a TERT promoter and a Site C repressor binding site. The method involves modulating TERT transcription repression by the Site C repressor binding site. The methods and compositions of the present invention are useful for the immortalization of cells, production of reagents in life science research, therapeutic agent screening applications diagnosis and treatment of disorders associated with aberrant telomerase activity such as cancer, Progeria, immune senescence, HIV, and in skin rejuvenation. The present sequence represents the DNA binding domain of a repressor protein E2P-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis,
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
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                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                     Length 76;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                 38.1%; Score 38.5; DB 24;
42.9%; Pred. No. 1.1e+02;
iive 4; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human liver peptide, SEQ ID No 33225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank
Disclosure; Page 7; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                       1 NVLMAMNIISKE-KKEIKWIG 20
                                                                                                                                                                                                                                                                                                                                                                    NVLEGIGLIEKKSKNSIOWKG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG54577 standard; Peptide; 31
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2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00664
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                      9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                   76 AA;
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21-SEP-2000;
27-SEP-2000;
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30-JUN-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG41348-ABG59930 represent human liver single exon encoded peptides of the invention.

The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #7053 encoded by human foetal liver single exon probe
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                                                                                                                                                                                                                                                            Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Length 31;
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                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                        2,
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                                                                                                                                                                                                                                                            DB 22;
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Pred. No. 47;
4; Mismatches
                                                                                                                                                                                                                                                            Score 38; DB 2
Pred. No. 47;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-06336.
21-SEP-2000; 2000US-0236399.
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ilarity 50.0%;
Conservative
                                                                                                                                                                                                                                                            37.6%;
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphona, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #7138 encoded by probe for measuring placental gene expression.
                                   Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemis; lymphoma; myeloma.
Human bone marrow expressed probe encoded protein SEQ ID NO: 33175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO: 33175; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 22; Length 31; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM33101 standard; Protein; 31 AA.
                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.6%;
                                                                                                                                                                                                                       ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
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26-MAY-2000; 2000US-0207456.
                                                                                                                                                                                                                                                                      03-AUG-2000; 2000US-0632366,
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359,
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                      30-JAN-2001; 2001WO-US00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 NIISKEKKEIKW 18
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                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                        WO200157276-A2
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                                                                                                                                                                                                                                                          30-JUN-2000;
                                                                                         Homo sapiens
                                                                                                                                                                                                                                        26-MAY-2000;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                            Human brain expressed single exon probe encoded protein SEQ ID NO: 32350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer.
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Pred. No. 47;
4; Mismatches 2; Indels
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                                                                                                                               AAM60245 standard; Protein; 31 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
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50.0%;
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00667.
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NMISKQSRKKKW 18
                                 |:|||: :: ||
7 NMISKQSRKKKW 18
               NIISKEKKEIKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483446/52
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31 AA;
                                                                                                                                                                                                                                                                                                                                                                   WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM72869;
                                                                                                                                                                  AAM60245;
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AAM72869
ID AAM7
XX
AC AAM7
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Gaps

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2; Indels

Search completed: February 17, 2004, 10:53:42 Job time : 39.0198 secs

7 NIISKEKKEIKW 18 |:|||::|| 7 NMISKQSRKKKW 18

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February 17, 2004, 10:53:48; Search time 29.3069 Seconds (without alignments) 142.889 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    801455 seqs, 209382283 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                    US-09-900-147-4
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Maximum DB seq length: 100
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Seguence 4, Appli	Sequence 6, Appli	Ä	Sequence 10, Appl	Sequence 3, Appli	Sequence 16, Appl	Sequence 10, Appl	Sequence 1380, Ap	Sequence 1380, Ap	Sequence 15, Appl	Sequence 5, Appli	9	17,		Sequence 5, Appli
Descri	Segn	Sed	Segi	Segr	Seg	Seg	Sed	Sed	Sed	Sed	Seg	Sed	Sed	Sed	Seq
ID	US-09-900-147-4	US-09-900-147-6	US-09-900-147-1	US-10-214-188-10	US-09-900-147-3	US-09-900-147-16	US-09-900-147-10	US-09-764-877-1380	US-10-242-515-1380	US-09-900-147-15	US-09-900-147-5	. US-10-214-188-6	US-09-900-147-17	. US-10-214-188-5	. US-09-932-581-5
DB	10	10	10	15	10	10	10	10	12	10	10	15	10	15	11
% Query Aatch Length DB	20	30	37	74	19	19	15	29	29	19	16	74	19	74	82
% Query Match	100.0	100.0	100.0	100.0	50.5	50.5	49.5	49.5	49.5	46.5	45.5	45.0	44.6	44.1	44.1
Score	101	101	101	101	51	51	20	20	50	47	46	45.5	45	44.5	44.5
Result No.	1	8	m	4	S	9	7	80	σ	10	11	12	13	14	15

Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 33, App Sequence 3370, Ap Sequence 3555, A Sequence 9, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1920, Appli Sequence 1920, Appli Sequence 1920, Appli Sequence 1920, Appli Sequence 1920, Appli Sequence 1921, Appli Sequence 1921, Appli Sequence 1921, Appli Sequence 1921, Appli Sequence 723, Appli
12 US-10-338-294-5 14 US-10-165-614-2 15 US-10-110-165-614-2 15 US-09-900-147-2 15 US-09-900-147-2 15 US-09-984-408A-3370 19 US-09-864-761-35555 15 US-10-214-188-9 11 US-09-932-581-6 12 US-10-214-188-9 12 US-10-214-188-9 13 US-10-214-188-9 14 US-10-214-188-9 15 US-10-214-188-9 16 US-09-864-761-43984 17 US-10-165-614-3 18 US-10-165-614-3 19 US-09-864-761-43984 10 US-09-916-790-25 10 US-09-916-790-25 10 US-09-916-790-26 11 US-09-864-761-313-192 12 US-09-864-761-313-192 13 US-10-157-677-73 15 US-10-127-577-73 15 US-10-227-577-73 16 US-10-227-577-73 17 US-10-227-577-73 18 US-10-23-3864-761-47714
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; Sequence 6, Application US/09900147; Patent No. US20020103121A1

RESULT 2 US-09-900-147-6

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Query Match
Best Local Similarity
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US-09-900-147-3
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APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
LENGTH: 30
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Best Local Similarity 100.0%; Score 101; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels
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BERNARDS, RENE
HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 101; DB 10;
100.0%; Pred. No. 2.5e-08;
tive 0; Mismatches 0;
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US-10-214-188-10
Sequence 10, Application US/10214188
Sequence 10, Application US/10214188
Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, General INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NVLMAMNIISKEKKEIKWIG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0°
Matches 20; Conservative
GENERAL INFORMATION:
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Sequence 3, Application US/09900147
; Sequence 3, Application US/09900147
; Patent No. US20020103121A1
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas B
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; FILE REFERENCE: 620-67
; CURRENT FILING DATE: 2001-07-09
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 18
; SCOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 3
; LENDIN: 19
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                                                                                                CITTE ARLINGATOR
STATE: VIRGINIA
CONTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-ANG-2002
CLASSIFICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 520-22
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 620-22
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0.49;
ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
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100.0%; Pred. No.
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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                                                                             CITY: ARLINGTON
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US-09-308-935-6
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 TYPE: PRT
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Sequence 1, Appli
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                                                                                                                          February 17, 2004, 10:50:13; Search time 14.4554 Seconds (without alignments) 58.540 Million cell updates/sec
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Sequence 3
Sequence 3
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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-08-894-139-9
-09-328-352-7148
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| S-09-428-131-11
| S-09-308-935-15
| S-09-308-935-16
| S-09-308-935-16
| S-09-308-935-16
| S-09-308-935-15
| S-09-308-935-15
| S-09-078-596-13
| S-09-078-596-13
| S-09-078-596-13
| S-09-308-935-17
| S-09-308-935-17
| S-09-308-935-17
| S-09-308-935-17
| S-09-308-935-17
| S-09-308-935-17
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-08-894-139-5
-08-894-139-7
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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4, Appli
4, Appli
14, Appl
11, Appl
15, Appl
25, Appl
25, Appl
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Patent No. 626834

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/308,935

CURRENT PILING DATE: 1999-05-27

EARLIER APPLICATION NUMBER: PCT/GB97/03506

EARLIER APPLICATION NUMBER: PCT/GB97/03506

EARLIER APPLICATION NUMBER: PCT/GB97/03506

EARLIER APPLICATION NUMBER: GB 9626589.7

EARLIER PILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 20
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Patent No. 6268334

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lisantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFRENCE: 620-67

CURRENT FILING DATE: 1999-05-27

GEARLIER APPLICATION NUMBER: PCT/GB97/03506

EARLIER APPLICATION NUMBER: GB 9626589.7

EARLIER APPLICATION NUMBER: GB 9626589.7

EARLIER FILING DATE: 1996-112-20

NUMBER OF SEQ ID NOS: 18
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Sequence 9, P
Sequence 9, P
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                                       Sequence
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                                US-00-450-417-4
US-08-449-741-4
US-08-449-741-4
US-09-465-646-4
US-09-308-935-11
US-09-230-548-15
US-09-230-548-26
US-09-230-548-26
US-09-230-548-21
US-09-230-548-21
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US-08-343-443B-8
US-08-743-975-9
US-09-263-811-9
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APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                         single
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Best Local Similarity
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Sequence 1, Application US/09308935

Patent No. 6268334

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

FILE REFERENCE: 1999-05-27

CURRENT FILING DATE: 1999-05-27

EARLIER APPLICATION NUMBER: PCT/GB97/03506

EARLIER APPLICATION NUMBER: B 9626589.7

EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 1

LENGTH: 37

THENGTH: 37
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-1
                                                                                                                        FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-308-935-6
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Best Local Similarity 100.0%; Pred. No. 4.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                         Length 30
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
ZIP: 22201-4714
COMPUTER READABLE FRAN.
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
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Patent No. 5863757
GENERAL INFORMATION:
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                      Query Match
100.0%; Score.101; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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             SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 30
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US-08-428-131-11
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STREET: 1100 No. 6150116th Glebe Road, 8th Floor
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100.0%; Pred. No. 9.2e-09;
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Best Local Similarity 100.0%; Pred. No. 9.2e-09;
Matches 20; Conservative 0; Mismatches 0;
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Patent No. 6150116
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-UN-1995
ATTORNEY/AGENT INFORMATION:
ATTORNEY ATTORNEY R. CTAWFORM
ATTORNEY AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LIENTH: 72 aming acids
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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REGISTRATION NUMBER: 25.32.
REFERENCE/DOCKET NUMBER: 117-1
TELECOMMUNICATION INFORMATION:
TELEFAK: (703) 816-4000
TELEFAK: (703) 816-4100
INFORMATION FOR SEQ ID NO: 11:
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NS-09-308-935-10
Sequence 10, Application US/09308935
Facent No. 62688136
Facent No. 626881304:
Facent No. 626881304:
FILE REPERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1999-05-7
FARLIER APPLICATION NUMBER: PCT/GB97/03506
FARLIER PILING DATE: 1997-12-22
FARLIER PILING DATE: 1996-05-7
FARLIER PILING DATE: 1996-05-7
FARLIER PILING DATE: 1996-05-7
FARLIER PILING DATE: 1996-05-7
FARLIER PILING DATE: 1996-12-20
FARLIER PILING DATE: 1996-12-20
FARLIER PILING DATE: 1996-12-20
FARLIER PILING DATE: 1996-12-20
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US-09-308-935-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: PCT/GB97/03506
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1967-12-20
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-3
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100.0%; Pred. No. 0.12;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                             Query Match 50.5%; Score 51; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/09308935
Patent No. 6268334
GENERAL INFORMATION:
                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.5
Best Local Similarity 100.
Matches 11; Conservative
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      Gaps
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APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CT/GB97/03506
EARLIER PILING DATE: 1996-12-22
EARLIER PILING DATE: 1996-12-20
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   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SATON 
                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08894139
Parent No. 6448376
GENERAL INFORMATION
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/09308935 ; Patent No. 6268334
                                                                1 NVLMAMNIISKEKKEIKWIG 20
                                                                                                     15 NVLMAMNIISKEKKEIKWIG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NVLMAMNIISKEKKEIKWIG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 amino acids
20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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STATE: VIRGINIA
                                                                                                                                                                                                                           RESULT 6
US-08-894-139-10
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US-09-308-935-3
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Matches
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LENGTH: 17 amino acids
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                                                                        1 NVLMAMNIIS 10
                                                                                                7 NVLMAMNIIS 16
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STRANDEDNESS: Si
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Sequence 15, Application US/09308935

Patent No. 626834

GENERAL INFORMATION:

APPLICATE La Thangue, Nicholas B

APPLICANT: La Thangue, Espide antagonists of DP transcription factors

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE REFERENCE: 620-67

CURRENT PAPLICATION NUMBER: US/09/308,935

CURRENT PILING DATE: 1999-05-27

EARLIER APPLICATION NUMBER: BCT/GB97/03506

EARLIER PILING DATE: 1996-12-20

MUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 19
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| Sequence 5, Application US/09308935
| Sequence 5, Application US/09308935
| Patent No. 626834
| Patent No. 626834|
| GENERAL INFORMATION:
| APPLICANT: La Thangue, Nicholas B
| APPLICANT: Bandara, Lasantha R
| TITLE OF INVENTION: Peptide antagonists of DP transcription factors
| TITLE OF INVENTION: Peptide antagonists of DP transcription factors
| FILE REFERENCE: 620-67
| CURRENT FAPLICATION NUMBER: US/09/308,935
| CURRENT FILING DATE: 1999-15-27
| EARLIER APPLICATION NUMBER: GB 9626589.7
| EARLIER FILING DATE: 1996-112-20
| NUMBER OF SEQ ID NOS: 18
| SCOFTWARE: PatentIN Ver. 2.1
| SEQ ID NO 5
| LENGTH: 16
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                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide US-09-308-935-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence PEATURE: OPETURE: OPETURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-5
                   FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-308-935-10
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Pred. No. 0.5;
0; Mismatches 1; Indels
                                                                                                    Length 15
                                                                                                                                            0; Indels
                                                                                                    Score 50; DB 3;
Pred. No. 0.13;
                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 9; Conservative 0; Mismatches
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ORGANISM: Artificial Sequence
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nes 10; Conservat
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US-09-308-935-15
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/428,131
FILLING DATE: 23-UW-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: AATCHUE K. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/POCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
Query Match

45.5%; Score 46; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 10; Conservative 0; Mismatches 0; Indels
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STREET: 1100 No. 6150116th Glebe Road, 8th Floor
CITY: Arlington
STATE: Viginia
ZCUNTRY: U.S.A.
                                                                                                                                                                                                                                                       Sequence 13. Application US/08428131
Sequence 13. Application US/08428131
Patent No. 5863757
GENERAL INFORMATION:
GENERAL INFORMATION:
THE OF INVENTION: Transcription Factor DP-1
TITE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-078-596-13
Sequence 13, Application US/09078596
Patent No. 6150116
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
0.63;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; P:
Matches 10; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Sequence 17, Application US/09308935

Sequence 17, Application US/09308935

Sequence No. 626834

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/308,935

CURRENT FILING DATE: 1999-05-27

EARLIER APPLICATION NUMBER: PCT/GB97/03506

SARLIER APPLICATION NUMBER: PCT/GB97/03506

SARLIER APPLICATION NUMBER: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 17

LENGTH: 19
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; OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide
US-09-308-935-17
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                                                                                                                   45.0%; Score 45.5; DB 4; Length 74; 42.9%; Pred. No. 3.7;
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Pred. No. 1;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08428131
Fatent No. 5863757
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INFORNCES: 14
CORRESPONDENCES: 14
CORRESPONDENCES: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arlington
STATE: U.S.A.
COUNTRY: U.S.A.
                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                1 NVLMAMNIISKEKK-EIKWIG 20
                                                                                                                                                                                                                        53 NVLEGIQLIRKKRKNHIQWVG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.6%;
                                                                                                                                     Best Local Similarity 42.99
Matches 9; Conservative
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Best Local Similarity 90.9
Matches 10; Conservative
                  STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
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      TYPE: amino acid
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US-09-308-935-17
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                                                                , MOLECULE T.
US-08-894-139-6
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                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/078,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-894-139-6
; Sequence 6, Application US/08894139
; Patent No. 6448376
; GENERAL INFORMATION:
; APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: HIJMANS, RENE
; APPLICANT: HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
; CORRESPONDER ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Prec. ...
1.ve 0; Mismatches
                                                                                                                                                                                                                                                  NAME: Archur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELEPONE: (703) 816-4000
TELEPAX: (703) 816-4100
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-UTN-1995
ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  17 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NVLMAMNIIS 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-078-596-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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15 NVLEGIQLIAKKSKNHIQWLG 35

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ATTORNEY/AGENT INFORMATION: NAME: Arthur R. Crawford

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Best Local Similarity 42.9%; Pred. No. 5.2;
Matches 9; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-894-139-5

Sequence 5, Application US/08894139

Sequence 5, Application US/08894139

Patent No. 6448176

GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: LA THANGUE, REANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08894139
; Patent No. 6448376
; GENERAL INFORMATION:
   APPLICANT: LA THANGUE, NICHOLAS B.
   APPLICANT: HITWANS, RENE
   APPLICANT: HITWANS, RELEANORE M.
   TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
   NUMBER OF SEQUENCES: 25
   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NVLMAMNIISKE-KKEIKWIG 20
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ZIP: 22201-4714
COMPUTER READABLE FORM:
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44.1%; Score 44.5; DB 2; Length 73;
Best Local Similarity 42.9%; Pred. No. 5.2;
Matches 9; Conservative 6; Mismatches 5; Indels
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| Sequence 12, Application US/09078596
| Patent No. 6150116
| GENERAL INFORMATION:
| APPLICANT: La Thangue, Nicholas Barrie
| TITLE OF INVENTION: Transcription Factor DP-1
| NUMBER OF SEQUENCES: 14
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Nixon & Vanderhye
| STREET: Nixon & Vanderhye
| STREET: US A. A. Ington |
| STREET: US A. A. Ington |
| STREET: US A. A. Ington |
| COUNTRY: US A. A. Ington |
| COUNTRY: US A. A. Ington |
| COUNTRY: US A. A. Ington |
| CONDUTER: Eloppy disk |
| COMPUTER: ISP PC compatible |
| COMPATIBLE |

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APPLICATION NUMBER: US/09/078,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILLING LALLS

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILLING DATE: 23-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Arthur R. Crawford

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 117-181

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (703) 816-4100

TELEFAX: 
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPRAX: (703) 816-4000
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
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Best Local Similarity 42.9
Matches 9; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) TOPOLOGY: linear
) MOLECULE TYPE: protein
US-08-428-131-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-078-596-12
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US-09-078-596-12
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1 NVLMAMNIISKE-KKEIKWIG 20

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APPLICANT: BERNARDS, RENE
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Fatent No. 626834
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1995-05-27
EARLIER APPLICATION NUMBER: PCT/GB97/03506
BARLIER APPLICATION NUMBER: PCT/GB97/03506
BARLIER APPLICATION NUMBER: QB 9626589.7
BARLIER PILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 9
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US-09-308-935-2
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100.0%; Pred. No. 2.5e+05;
tive 0; Mismatches 0; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDMER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WILLSON, MARY J.
REFERENCE/DOCKET NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEPAX: (703) 816-4100
TELEPAX: CRED ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids

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42.1%; Score 42.5; D
Best Local Similarity 38.1%; Pred. No. 11;
Matches 8; Conservative 7; Mismatches
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US-08-894-139-9
; Sequence 9, Application US/08894139
; Patent No. 6448376
; GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NVLMAMNIISKE-KKEIKWIG 20
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Best Local Similarity
Matches 9; Conservat
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US-09-328-352-7148

Sequence 7148, Application US/09328352

Sequence 7148, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                   STREET: 1100 NORTH GLEBE KOAD
CITY: ARLINGTON
STATE: VIRGINIA
COMPUTER: U.S.A.
ZIP: 22010-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION: S36
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPRAK: (703) 816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUIRNEE CHARACTERISTICS:
APPLICANT: HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
39.1%; Score 39.5;
Best Local Similarity 42.9%; Pred. No. 32
Matches 9; Conservative 5; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 NVLEGIDLIEKKSKNSIQWKG 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 MAMNIISKEKKEIKWI 19
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40 VAMSLITRPRKALDWL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-328-352-7148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-894-139-9
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Gaps
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Complexes Into Higher Eucaryotic Cells
IITLE OF INVENTION: Complexes Into Higher Eucaryotic Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                           CIP: 20036

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/948,357
FILING DATE: 1992033
CLASSTETCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ESENCA, RODERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.0940004
TELEPHONE: (202) 466-0800
TELEPHONE: (202) 466-0800
TELEFRAX: (202) 433-8716
INFORMATION FOR EQUID NO: 3:
SEQUENCE CHRAACTERISTICS:
LENGTH: 26 amino acids
THENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTHARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sterne, Kessler, Goldstein & Fox
                                                              B: Sterne, Kessler, Goldstein & Fox 1225 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.7%; Score 35; DB
50.0%; Pred. No. 50;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldsfreet: 1225 Connecticut Avenue
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08450417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Curiel, David T. APPLICANT: Birnstiel, Max L. APPLICANT: Cotten, Matthew APPLICANT: Wegner, Ernet APPLICANT: Zatloukal, Kurt APPLICANT: Plank, Christian APPLICANT: Coberhauser, Berndt APPLICANT: Schmidt, Walter G.M. TITLE OF INVENTION: Composition TITLE OF INVENTION: Composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 MAMNIISKEKKEIKWI 19
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COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: both
MOLECULE TYPE: peptide
                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
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Best Local Similarity
Matches 8; Conserva
                                                                                        STREET: 1225 Conr
CITY: Washington
STATE: D.C.
                                                                                                                                                      TRY: U.S.A.
20036
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                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-948-357-3
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                              Sequence 5431, Application US/09107532A

Sequence 5431, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
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Plank, Christian
Oberhauser, Berndt
Schmidt, Walter G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.6%; Score 37; DB 4; Length 87; 46.7%; Pred. No. 90;
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998

PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION:
REGISTRATION NUMBER: 40,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...87
SEQUENCE DESCRIPTION: SEQ ID NO: 5431:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                   STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/07948357
Patent No. 5547932
GENERAL INFORMATION:
APPLICANT: Curiel, David T.
APPLICANT: Birnstiel, Max L.
APPLICANT: Cotten, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 87 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5431:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Curiel, David T.
Birnstiel, Max L.
Cotten, Matthew
Wagner, Ernst
                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LMAMNIISKEKKEIK 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-107-532A-5431
                US-09-107-532A-5431
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US-07-948-357-3
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                     Query Match 34.7%; Score 35; DB 3; Length 26; Best Local Similarity 50.0%; Pred. No. 50; Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Legendre, Jean-Yves
APPLICANT: Supersaxo, Andreas
APPLICANT: Supersaxo, Andreas
APPLICANT: True of INVENTION: Peptide Conjugates for Transfecting
TITLE OF INVENTION: Cells
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , LOCATION: 1..2
; OTHER INFORMATION: /note= "Position 1 is fMet."
US-08-782-997A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96100603.8
FILING DATE: 17-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kreisler, Lewis J
REGISTRATION NUMBER: 38,522
REFERENCE/DOCKET NUMBER: RAN 4600/73
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08782997A Patent No. 6030602
                                                                                                                                                                                                                                                                                                                                       1 MAQDIISTIGDLVKWI 16
                                                                                                                                                                                                                                                                                               4 MAMNIISKEKKEIKWI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 MAMNIISKEKKEIKWI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAQDIISTIGDLVKWI 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 amino acids
                                 single
                                                             TOPOLOGY: both
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07110
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nutley
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                                                                                                                    US-08-449-741-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 27
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APPLICANT: Zatloukal, Kurt
APPLICANT: Zatloukal, Kurt
APPLICANT: Plank, Christian
APPLICANT: Benddt
APPLICANT: Schmidt, Walter G.M.
TITLE OF INVENTION: Composition for Introducing Nucleic Acid
TITLE OF INVENTION: Complexes Into Higher Eucaryotic Cells
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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COUNTRY: U.S...

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,741
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fleshner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0652.0940007
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox
ATREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION BATA:
APPLICATION NUMBER:
FILING DATE: 19920923
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.0940004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 26
US-08-449-741-3
Selected 3, Application US/08449741
Patent No. 6022735
GENERAL INFORMATION:
APPLICANT: Curiel, David T.
APPLICANT: Curiel, Max L.
APPLICANT: Cotten, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Curiel, David T.
Birnstiel, Max L.
Cotten, Matthew
Wagner, Ernst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 MAMNIISKEKKEIKWI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAQDIISTIGDLVKWI 16
                                                                                                                                                                                                                                                                                                                                          TELEFANO (201) 833-8016
TELEFANO (201) 833-8016
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-450-417-3
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Gaps

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COMPOSITION FOR INTRODUCING NUCLEIC ACID COMPLEXES INTO HIGHER EUCARYOTIC CELLS
                                                                                                                                                                                       CONTRESCUEDENCE AUGUSTONS
STREET: 1100 New York Ave., N.W., Suite 600
STREET: 1100 New York Ave., N.W., Suite 600
STATE: 1.0.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/09/465,646
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 26;
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Best Local Similarity 50.0%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/827,103
FILING DATE: January 30, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/767,788
FILING DATE: September 30, 1991
CLASSIFICATION NUMBER: 07/767,788
FILING DATE: September 30, 1991
THERENGY AGENT INFORMATION:
TELEFRANTON NUMBER: 43,703
REFERENCE CHARACTERISTICS:
TELEFROWNICATION INFORMATION:
TELEFROWNICATION SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: Ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/105,0016
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,754
FILING DATE: May 25, 1995
CLASSIPICATION:
PRIOR APPLICATION NUMBER: 07/937,786
FILING DATE: September 2, 1992
CLASSIPICATION NUMBER: 07/864,759
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/864,759
FILING DATE: April 7, 1992
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/864,759
FILING DATE: April 7, 1992
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/827,102
FILING DATE: January 30, 1992
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMITITE OF INVENTION: COME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: both
MOLECULE TYPE: peptide
US-09-465-646-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 30
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Sequence 3, Application US/08449754
; Sequence 3, Application US/08449754
; Patent No. 6077663
; GENERAL INFORMATION:
APPLICANT: Curiel, David T.
APPLICANT: Birnstiel, Max L.
APPLICANT: Gotten, Matthew
APPLICANT: Cotten, Matthew
APPLICANT: Plank, Christiel
APPLICANT: Plank, Christiel
APPLICANT: Schmidt, Malter G.M.
TITLE OF INVENTION: Composition for Introducing Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.7%; Score 35; DB 3;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/948,357
FILING DATE: 1992-09-23
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 0652.0940004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09465646; Patent No. 6274322; GENERAL INVORMATION:
APPLICANT: Curiel, David T. APPLICANT: Girnstiel, Max L. APPLICANT: Gotten, Matthew APPLICANT: Wagner, Ernst APPLICANT: Zatloukal, Kurt APPLICANT: Zatloukal, Kurt APPLICANT: Plank, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zatloukal, Kurt
Plank, Christian
Oberhauser, Berndt
Schmidt, Walter G.M.
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1225 Conn
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-465-646-3
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                                                                                 RESULT 28
US-08-449-754-3
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APPLICANT: Cotten, Matthew APPLICANT: Cotten, Matthew APPLICANT: Cotten, Matthew APPLICANT: Magner, Ernst APPLICANT: Magner, Ernst APPLICANT: Magner, Brint APPLICANT: Plank, Christian APPLICANT: Comparing Must Composition for Introducing Nucleic Acid TITLE OF INVENTION: Composition for Introducing Nucleic Acid TITLE OF INVENTION of STATE: 0.0005

COUNTRY: U.S.A.

ZIP: 20005

MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 34.7%; Score 35; DB 2; Length 36; Best Local Similarity 50.0%; Pred. No. 71; Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                           SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,417
FILING DATE:
CLASSIFICATION DATE:
FILING DATE:
APPLICATION NUMBER: US/07/948,357
FILING DATE: 19920923
ATTORNEY/AGENT INFORMATION:
NAME: ESHORICA ROBER: 32,893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REFERENCE/POCKET UNBER: 0652.0940004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,741
Sterne, Kessler, Goldstein & Fox
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                      1225 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08449741 Patent No. 6022735 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Curiel, David T.
Birnstiel, Max L.
Cotten, Matthew
Wagner, Ernst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 MAMNIISKEKKEIKWI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAQDIISTIGDLVKWI 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 'SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: both
MOLECULE TYPE: peptide
                      STREET: 1225 Com
                                                                  : D.C.
RY: U.S.A.
20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
ADDRESSEE:
                                                                  STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                      APPLICANT: Guriel, David T.
APPLICANT: Birnstiel, Max L.
APPLICANT: Cotten, Matthew
APPLICANT: Wagner, Ernst
APPLICANT: Zatloukal, Kurt
APPLICANT: Plank, Christien
APPLICANT: Schmidt, Walter G.M.
TITLE OF INVENTION: Composition for Introducing Nucleic Acid
TITLE OF INVENTION: Composition for Introducing Nucleic Acid
TITLE OF INVENTION: Composition for Introducing Composition
TITLE OF INVENTION: Composition for Introducing Nucleic Acid
TITLE OF INVENTION: Complexes Into Higher Bucaryotic Cells
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
STRRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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APPLICANT: Plank, Christian
APPLICANT: Oberhauser, Berndt
APPLICANT: Schmidt, Walter G.M.
TITLE OF INVENTION: Composition for Introducing Nucleic Acid
TITLE OF INVENTION: Complexes Into Higher Bucaryotic Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.7%; Score 35; DB 1; Length 36; 50.0%; Pred. No. 71; cive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/948,357
FILING DATE: 19920923
CLASSIFICATION: 514
ATTOKNEY/AGENT INPORMATION:
NAME: Essenaid, Robert W.
REGISTRATION NUMBER: 32,893
REFRENCE/POCKET UNBER: 0652.0940004
TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.
COUNTRY: U.S.A.
ZIP. 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMDALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
                 Sequence 4, Application US/07948357
Patent No. 5547932
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08450417; Patent No. 5981273; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Curiel, David T.
Birnstiel, Max L.
Cotten, Matthew
Wagner, Ernst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 MAMNIISKEKKEIKWI 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 36 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-07-948-357-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-450-417-4
US-07-948-357-4
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Gaps

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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GUITEL, David T.
APPLICANT: GUITEL, David T.
APPLICANT: GUITEL, Max L.
APPLICANT: GUITEL, Max L.
APPLICANT: Mathew Mather G.
APPLICANT: Schmidt, Mather G.
APPLICANT: Schmidt, Mather G.
APPLICANT: Schmidt, Mather G.
TITLE OF INVENTION: COMPLEXES INTO HIGHER EUCRYOTIC CELLS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Scenne, Kessler, Goldstein & Fox P.L.L.C.
STATE: D. G.
GONDERSER: Scenne, Kessler, Goldstein & Fox P.L.L.C.
GONDERSER: D. G.
GONDERSER: D. G.
GONDERSER: D. G.
GONDERSER: D. G.
GONDERSER: D. GONDERSER: GONDERSE
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                                                                                                                                                    Query Match
Best Local Similarity 50.0%; Pred. No. 71;
Matches 8; Conservative 2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09465646
Patent No. 6274322
                                                                                                                                                                                                                                                                                              4 MAMNIISKEKKEIKWI 19
                                                                                                                                                                                                                                                                                                                                            1 HAQDIISTIGDLVKWI 16
                     ; TOPOLOGY: both MOLECULE TYPE: peptide US-08-449-754-4
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-465-646-4
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APPLICANT: Curiel, Max L.
APPLICANT: Brinstiel, Max L.
APPLICANT: Cotten, Matthew
APPLICANT: Cotten, Matthew
APPLICANT: Arguer, Ernst
APPLICANT: Arguer, Berndt
APPLICANT: Chinat, Christian
APPLICANT: Openate, Berndt
APPLICANT: Composition for Introducing Nucleic Acid
ITLE OF INVENTION: Composition for Introducing Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LINTO Higher Buca.

LUDRESS:
STREET: 1225 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036
                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fleahner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0652.0940007
TELEPHONE: (202) 371-2600
TELEPAS: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-449-741-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0652.0940004
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CLASIBFECATION:
PRIOR APPLICATION NUMBER: US/07/948,357
APPLICATION NUMBER: US/07/948,357
FILING DATE: 1992-09-23
ATORNEY/AGENT INFORMATION:
NAME: Bamond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.09400
TELEPHONE: (202) 466-0800
TELEPHONE: (202) 466-0800
TELEPHONE: (202) 466-0800
TELEPHONE: (202) 433-8716
; INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
** FARTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-449-754-4; Sequence 4, Application US/08449754; Patent No. 6077663; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 MAMNIISKEKKEIKWI 19
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              25-MAY-1995
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TYPE: amino acid
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RESULT 37
US-09-230-548-15
'Sequence 15, Application US/09230548
'Parent No. 6326466
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                              Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 21
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                      1 NVLMAMNIISKE 12
                                                                                                                                                                  3 NVLVALNILAAD 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FLING DATE: 28-MSR-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MSR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REFERENCE/DOCKET NUMBER: 19,655
REFERENCE/DOCKET NUMBER: NIH101.001DV1
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
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STREET: 620 Newport Center Drive, Sixteenth Floor
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kanage, Andrea J.
REGISTRATION NUMBER: 43,703
REFERENCE/DOCKET NUMBER: 0652.0940009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-6566
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08194338
Patent No. 5474898
GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
INVENTE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, olson and Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 MAMNIISKEKKEIKWI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 63 amino acide
TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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US-08-194-338-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
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US-08-194-338-14
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                                                                                                                                                                                                                                                                                                                                            US-09-465-646-4
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APPLICANT: Bottaro, Donald P.
APPLICANT: Bottaro, Donald P.
APPLICANT: Bottaro, Donald P.
APPLICANT: Bottaro, Naymond F.
APPLICANT: Peryshyn, Raymond by The Secretary,
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Double-Stranded RNA Dependent Protein Kinase Derived
TITLE OF INVENTION: Peptides to Promote Proliferation of Cells and Tissues
TITLE OF INVENTION: in a Controlled Manner
FILE REPERBUE: 015280-286200US
CURRENT APPLICATION NUMBER: US 60/023,307
EARLIER APPLICATION NUMBER: US 60/023,307
BARLIER APPLICATION NUMBER: US 60/023,307
BARLIER FILING DATE: 1996-07-20
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                                                                                                                                                                                                                                                                            US-09-308-315-11
US-09-308-315-11
US-09-308-316-11
US-09-308-318-11
Sequence 11, Application US/09308935
Patent No. 6268334
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
TITLE OF INVENTION:
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1999-06-27
EARLIER APPLICATION NUMBER: PCT/GB97/03506
EARLIER APPLICATION NUMBER: PCT/GB97/03506
EARLIER PILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 14
                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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   Length 63;
Score 35; DB 1; Length 63;
Pred. No. 1.3e+02;
5; Mismatches 1; Indels
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US-09-230-548-25
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Sequence 31, Application US/09230548

Sequence 31, Application US/09230548

GENERAL INFORMATION:

APPLICANT: Betryshyn, Raymond

APPLICANT: The Government of the United States of America

APPLICANT: The Government of the United States of America

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Double-Stranded RNA Dependent Protein Kinase Derived

TITLE OF INVENTION: Double-Stranded RNA Dependent Protein Kinase Derived

TITLE OF INVENTION: In a Controlled Manner

FILE REFERENCE: 015200-286200US

CURRENT FILING DATE: 1999-07-23

EARLIER FILING DATE: 1996-07-30

EARLIER APPLICATION NUMBER: WO PCT/US97/14350

EARLIER APPLICATION NUMBER: WO PCT/US97/14350
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Borlaton:
APPLICANT: Borlaton:
APPLICANT: Borlaton.
APPLICANT: Berveshyn, Raymond
APPLICANT: Perryshyn, Raymond
APPLICANT: Breatened by The Scoretary,
APPLICANT: Brepresented by The Scoretary,
APPLICANT: Bepartment of Health and Human Services
TITLE OF INVENTION: Double-Stranded RNA Dependent Protein Kinase Derived
TITLE OF INVENTION: Double-Stranded RNA Dependent Protein Kinase Derived
TITLE OF INVENTION: In a Controlled Manner
FILE REFERENCE: 015280-2862003
CURRENT APPLICATION NUMBER: US 00/230,548
CURRENT APPLICATION NUMBER: US 60/023,307
EARLIER FILING DATE: 1999-07-23
BARLIER FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIN Ver. 2.1
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; OTHER INFORMATION: antagonist, human PKR site 1 (hR1 peptide)
US-09-230-548-15
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                                                                      Length 21;
                                                                                                                        1; Indels
                                                                      Score 34; DB 4;
Pred. No. 57;
                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/09230548; Patent No. 6326466; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                           33.7%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                33.7
Best Local Similarity 54.5
Matches 6; Conservative
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16 LAVEILNKEKK 26
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11 LAVEILNKEKK 21
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Matches 6; Conserv
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US-09-230-548-31
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LENGTH: 26
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y CENDERAL INFORMATION:

APPLICANT: Bottaro, Donald P.
APPLICANT: Bottaro, Asymond
APPLICANT: Bottaro, Control of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: The Sepresented by The Secretary,
APPLICANT: Sepresented by The Secretary,
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Double-Stranded RNA Dependent Protein Kinase Derived
TITLE OF INVENTION: Double-Stranded RNA Dependent Protein Kinase Derived
TITLE OF INVENTION: Double-Stranded Manner
FILE OF INVENTION: APPLICATION NUMBER: US 60/023,307
EARLIER APPLICATION NUMBER: US 60/023,307
EARLIER FILING DATE: 1995-07-30
EARLIER FILING DATE: 1995-07-30
EARLIER FILING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 25
LENGTH: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:double-stranded OTHER INFORMATION: RNA dependent protein kinase (PKR) peptide OTHER INFORMATION: antagonist, cell-permeable PKR peptide antagonist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Pred. No. 1e+02;
4; Mismatches 1; Indels
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US-08-894-139-8
; Sequence 8, Application US/08894139
; Patent No. 6448376
; GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: BERNARDS, RENE
APPLICANT: HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
; TITLE OF INVENTION: TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/09230548
Patent No. 6326466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.7%;
54.5%;
                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                         Query Match 33.7%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 54.5
Matches 6; Conservative
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 MAMNIISKEKK 14
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36 LAVEILNKEKK 46
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27 LAVEILNKEKK 37
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33.2%; Score 33.5; DB 2; Length 86; 38.9%; Pred. No. 3.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08743975
Patent No. 6057434
GENERAL INFORMATION:
TITLE OF INVENTION:
MUMBER OF SEQUENCES:
CORRESCONDENCE 9,
CORRESCONDENCE ADDRESS:
ADDRESSEE: CARCLIA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER PARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325800-507 (PF212)
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,975
FILING DATE: 01 NOVEMBER 1996
CLASSIFICATION DATA:
APPLICATION TOWEMER 1996
FILING DATE: 02 NOVEMBER 1995
FILING DATE: 02 NOVEMBER 1995
ATTORNEY-AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-507
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1704
SEQUENCE CHARACTERISTICS:
                 APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
CLASSIFICATION NUMBER: US/08/343,443B
FRICH APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION NUMBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY-AGENT INPORMATION:
NAME: Welser, Gerard J.
REGISTRATION NUMBER: 19,763
REFREENCE/DOCKET NUMBER: 989.6121P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEPHONE: 215-875-8384
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AMNIISKEKKEIK---WI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AIGIIKKDKRTMKPKIWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-343-443B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-743-975-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Delattre, Olivier
APPLICANT: Delattre, Olivier
APPLICANT: Desatze, Chantal
APPLICANT: Desatze, Chantal
APPLICANT: Desatze, Chantal
APPLICANT: Peter, Martine
APPLICANT: Thomas Gilles
APPLICANT: Zucman, Jessica
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
TITLE OF INVENTION: TRANSLOCATIONS
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.2%; Score 33.5; DB 4; Length 69; Best Local Similarity 38.1%; Pred. No. 2.5e+02; Matches 8; Conservative 4; Mismatches 8; Indels
                                                                                            CITY: ARLINGIUM
STATE: VIRGINIA
COUNTRY: U. S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
SEOUIRNCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19102
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street
CITY: Philadelphia
                                               ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NVLMAMNIISKE-KKEIKWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08343443B
Patent No. 5968734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 NVLEGIGLIEKKSKNSTOWRG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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EARLIER
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EARLIER
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                                                                                                                                        Query Match 32.7%; Score 33; DB 3; Length 61; Best Local Similarity 31.6%; Pred. No. 2.6e+02; Matches 6; Conservative 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09263811

Patent No. 648222

GENERALI INFORMATION:

APPLICANT: Jian Ni et al.

TITLE OF INVENTION: Mammary Transforming Protein
NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, IN.C

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MARYLAND

COUNTRY: USA

ZIP: 20850

COMPUTER: READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM FS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%; Score 33; DB 4; 1 ilarity 31.6%; Pred. No. 2.6e+02; Conservative 8; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PS/2
COPERATING SYSTEM: MS-DOS
SOCTHARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,811
FILING DATE: MAR-08-1999
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/743,975
FILING DATE: 01-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/006,187
FILING DATE: 02 NOVEMBER 1995
ATTORNEY AGENT INFORMATION:
NAME: MICHELE M. WALES
REGISTRATION NUMBER: 43,975
REGISTRATION NUMBER: 43,975
REGISTRATION NUMBER: 43,975
REGISTRATION NUMBER: 43,975
REGISTRATION NUMBER: 9712D1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 45
US-09-205-258-381
Sequence 381, Application US/09205258
Patent No. 6525/14
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 VVFSINLLSRPERE--WEG 30
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                                                                                                                                                                                                                                                                                                                                      14 VVFSINLLSRPERE--WEG 30
                                                                                                                                                                                                                                                                                         2 VLMAMNIISKEKKEIKWIG 20
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i: 61 AMINO ACIDS
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-263-811-9
TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 44
US-09-263-811-9
                                                                        US-08-743-975-9
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207 Human Secreted Proteins
                                                                                                                                                  CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,831
EARLIER PILING DATE: 1997-06-06
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Pro
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ER FILING DATE: 1997-06-06

ER PILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,884

ER PILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,991

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,971

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,964

ER FILING DATE: 1997-06-06

ER PILING DATE: 1997-06-06
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ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/049,019
ER PILING DATE: 1997-06-06
ER PELING DATE: 1997-06-06
ER PELING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,972
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,916
ER APPLICATION NUMBER: 60/048,916
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/049,373
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,975
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,975
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,975
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,997
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,997
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,997
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,998
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ER APPLICATION NUMBER: 60/048,897
ER FILING DATE: 1997-06-06
ER REPLICATION NUMBER: 60/048,898
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,962
ER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/049,020

R FILING DATE: 1997-06-06

R FILING DATE: 1997-06-06

R FILING DATE: 1997-06-06

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,875
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EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER PELICATION NUMBER: 60/048,877

EARLIER APPLICATION NUMBER: 60/048,878

EARLIER PELING DATE: 1997-06-06

EARLIER PELING DATE: 1997-06-06

EARLIER FILING DATE: 1997-12-18

EARLIER FILING DATE: 1998-07-15

EARLIER PELICATION NUMBER: 60/094,657

SOCHWAR: PART

COCATION: (14)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

LOCATION: (62)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-205-258-381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.7%; Score 33; DB 4; Length 66; Best Local Similarity 35.3%; Pred. No. 2.8e+02; Matches 6; Conservative 6; Mismatches 5; Indels
EARLIER APPLICATION NUMBER: 60/048,963
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Search completed: February 17, 2004, 10:59:40 Job time : 14.4554 secs

|::::||:||:| 38 NLSLLLTLIKKKKKKK 54 1 NVLMAMNIISKEKKEIK 17

0; Gaps

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Gaps

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0; Indels

Mismatches

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11; Conservative

Matches

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Best Local Similarity 66.7
Matches 10, Conservative
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CRGANISM: Homo sapiens
US-10-242-515-1380
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
RESULT 8
US-09-764-877-1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-242-515-1380
                                                                                                                                                                                                                                                                                                                                                                                                         US-09-764-877-1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                               US-09-900-147-16

Sequence 16, Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67-69

CURRENT PILING DATE: 2001-07-09

PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR PELING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR PILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOTTWARE PATENTIN VOIL 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/09900147

Sequence 10, Application US/09900147

Patent No. USS0020103121A1

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors
CURRENT PILING DATE: 2001-07-09

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT PILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR APPLICATION NUMBER: BARLIER PAPLICATION NUMBER: GB 9626589.7

PRIOR PILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 10

LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide US-09-900-147-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-900-147-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 50.5%; Score 51; DB 10; Length 19; Best Local Similarity 100.0%; Pred. No. 0.49; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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  1 NVLMAMNIISK 11
                             9 NVLMAMNIISK 19
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LENGTH: 19
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Outcast Name of the Application US/09764877

Sequence 130, Application US/09764877

Sequence 130, Application Name of the Name of the Wight Name of the Name of th
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JS-10-214-188-6
RESULT 12
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APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
ITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPRENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT PILING DATE: 2001-07-09
PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide
                                                                                                                                                                                                                                           APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
PRIOR PILING DATE: EARLIER FILING DATE: 1996-12-20
WUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%; Score 46; DB 10; Length 16; 100.0%; Pred. No. 2.3; tive 0; Mismatches 0; Indels
                                                                                                                                               US-09-900-147-15; Sequence 15, Application US/09900147; Sequence 15, Application US/09900147; Patent No. US20020103121A1; GENERAL INFORMATION:
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; Sequence 5, Application US/09900147
Sequence 5, Application US/09900147
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
  6 MNIISKEKKEIKWIG 20
                              13 MKIFSKEKKKIGWPG 27
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Best Local Similarity 90.9
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Matches 10; Conservative
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LENGTH: 19
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Sequence 17, Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: La Thangue, Nicholas B

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT FILING DATE: 2001-07-09

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SCOFTWARE: Patentin Ver. 2.1

SEQ ID NO 17
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
Sequence 6, Application US/10214188
Publication No. US2003002260A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
BERNARDS, RENE
HITANAN, BLEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.0%; Score 45.5; DB 15;
42.9%; Pred. No. 13;
tive 6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
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Best Local Similarity 42.99
Matches 9; Conservative
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US-09-900-147-17
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Sequence 5, Application US/09932581
                    US20030050264A1
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US-09-932-581-5
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US-10-338-294-5
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                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide US-09-900-147-17
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ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DESTERN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION: CURNOWn>
                                                                                                                                 Score 45; DB 10; Length 19;
Pred. No. 4;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10214188
Publication No. US20030022560A1
GENERAL INFORMATION:
APPLICANT: LA THANGUB, NICHOLAS B.
BERNARDS, RENE
HIJANNS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
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42.9%; Pred. No. 19;
tive 6; Mismatches
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APPLICATION NUMBER: US/08/894,139
FILING DATE: 13.AUG-1997
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: WILSON, MARY J.
REGISTRATION NUBBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-214-188-5
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STRANDEDNESS: <Unknown>
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SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                  ORGANISM: Artificial Sequence
                                                                                                                                 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative (
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Best Local Similarity 42.9°
Matches 9; Conservative
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                                                                                                                                                                                                                 1 NVLMAMNIISK 11
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  LENGTH: 19
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RESULT 15 US-09-932-581-5

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APPLICANT: Foster, Christopher A. APPLICANT: Fraeer, Stephanie APPLICANT: Fraeer, Stephanie APPLICANT: Fraeer, Stephanie APPLICANT: Fraeer, Stephanie APPLICANT: Mohammadpour, Hamid TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION FILE REPERENCE: SIER-005; CURRENT APPLICATION NUMBER: US/09/932,581
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR PLLING DATE: 2000-09-01
PRIOR PLLING DATE: 2000-09-01
PRIOR PLLING DATE: 2000-09-01
PRIOR PLLING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FRAESRQ for Windows Version 4.0
SEG ID NO 5
LENGTH: 85
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Pred. No. 22;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
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63 NVLEGIQLIAKKSKNHIQWLG 83
                                                                                                                                                                                                                                                                                                                                h 44.1%;
Similarity 42.9%;
9; Conservative 6
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Best Local Similarity 42.9%;
Matches 9; Conservative (
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Best Local Similarity
Matches 9; Conserv
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                                                                                              PAPELICANT: Andrews, William H.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMBRASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REPERENCE: SIER-OHD
CURRENT APPLICATION NUMBER: US/10/165,614
CURRENT PILING DATE: 2002-06-25
PRIOR PILING DATE: 2001-06-07
RIOR FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
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Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
BERNARDS, RENE
HITMANS, BLEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE: 25
CORRESPONDENCE: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 44.1%; Score 44.5; D
Best Local Similarity 42.9%; Pred. No. 22;
Matches 9; Conservative 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 NVLEGIQLIAKKSKNHIQWLG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NVLMAMNIISKE-KKEIKWIG 20
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STRANDEDNESS: <Unknown>
TOPOLOGY: linear
Sequence 2, Application US/10165614 Publication No. US20020193289A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: homo sapiens
US-10-165-614-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 18
US-10-214-188-7
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US-09-900-147-2

Sequence 2, Application US/09900147

Sequence 2, Application US/09900147

Sequence 2, Application US/09900147

Sequence 3, Application US/0900147

GENERAL INFORMATION:

TABLE INFORMATION:

TILE OF INVENTION: Peptide antagonists of DP transcription factors

TILE OF INVENTION: Peptide antagonists of DP transcription factors

TILE OF INVENTION: Peptide antagonists of DP transcription factors

CURRENT APPLICATION WUMBER: US/09/900,147

CURRENT FILING DATE: EARLIER FALLIER APPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: EARLIER FILING DATE: 1990-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 2

LENGTH: 9
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                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-900-147-2
                                                                                                                                        Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                               Indels
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CURRENT APPLICATION NUMBER: US/10/097,065
CURRENT PILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/070,923
PRIOR FILING DATE: 1990-12-17
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR PLING DATE: 1997-12-19
                                                                                                                                     Score 42.5; DB 15;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 9; Conservative 0; Mismatches 0
                                                                                                                                        Query Match
42.1%; Score 42.5; D
Best Local Similarity 38.1%; Pred. No. 38;
Matches 8; Conservative 7; Mismatches
) MOLECULE TYPE: peptide
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US-10-214-188-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 532, Application US/10097065 Publication No. US20030055236A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                            1 NVLMAMNIISKE-KKEIKWIG 20
                                                                                                                                                                                                                                                                                             | | | ::: | |: | :: |: | 53 NVLEGIHLIKKKSKNHVQWMG 73
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ORGANISM: Artificial Sequence
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Gaps
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              IITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 75;
93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS1578, EVALUE 2.50e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN BT474, SIGNAL = 3.5
IN FETAL LIVER, SIGNAL = 2.2
IN PLACENTA, SIGNAL = 2.2
IN HBL100, SIGNAL = 3.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3555
LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 9
Pred. No. 93;
3; Mismatches
                                                                                                      PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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Best Local Similarity 50.0
Matches 6; Conservative
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31 ITKEKSSLRWAG 42
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: MOTHER INFORMATION: E OTHER INFORMATION: E
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US-10-214-188-9
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Sublication No. US20040003474A1

GRNERAL INFORMATION:

APPLICANT: Leach, Martin D.

APPLICANT: Leach, Martin D.

APPLICANT: Shimkets, Richard A.

TITLE OF INVENTION: No. US20040009474A1e1 Human Polynucleotides and Polypeptides Encorners TILE No. US20040009474A1e1 Human Polynucleotides and Polypeptides Encorners TILE OF INVENTION: NOWBER: US/09/864,408A

CURRENT APPLICATION NUMBER: US/09/864,408A

PRIOR PELING DATE: 2000-05-24

PRIOR PELING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 9068

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 3370

LENGTH: 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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OTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid
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Pred. No. 70;
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Pred. No. 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.6%; Score 40; DB Best Local Similarity 31.6%; Pred. No. 70; Matches 6; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
PRIOR APPLICATION NUMBER: 60/068,169
PRIOR FILING DATE: 1997-12-19
PRIOR PELING DATE: 1997-12-19
PRIOR PELING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR PELING DATE: 1997-12-18
PRIOR PELING DATE: 1997-12-18
PRIOR PLILING DATE: 1997-12-18
PRIOR PLILING DATE: 1997-12-18
PRIOR PLILING DATE: 1997-12-18
PRIOR PLILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PACENTIN VET: 2.0
SEQ ID NO 532
LENGTH: 57
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Patent No. US20020048763A1
GENERAL INFORMATION:
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.6
Best Local Similarity 50.0
Matches 6: Conservative
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48 VQKESKENQWLG 59
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                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-10-097-065-532
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)..(1)
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US-09-864-408A-3370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-864-408A-3370
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APPLICANT:
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Sequence 6, Application US/09932581

Publication No. US20030050264A1

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

APPLICANT: Foster, Christopher A.

APPLICANT: Fraser, Stephanie

APPLICANT: Fraser, Stephanie

APPLICANT: Fraser, Stephanie

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING

TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION

FILE REPREMENCE: SIER-005

CURRENT PELING DATE: 2001-08-17

CURRENT FILING DATE: 2000-08-24

PRIOR PELING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: 60/230,174

PRIOR FILING DATE: 2000-09-01

PRIOR PILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 76
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TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION CURRENT APPLICATION NUMBER: US/10/338,294

CURRENT FILLING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: US/09/932,581

PRIOR PILLING DATE: 2000-08-24

PRIOR FILLING DATE: 2000-08-24

PRIOR FILLING DATE: 2000-09-01

PRIOR FILLING DATE: 2000-09-01

PRIOR PRILING DATE: 2000-09-01

PRIOR PRILING DATE: 2000-09-01

PRIOR PRILING DATE: 2000-09-01

PRIOR FILLING DATE: 2000-09-01

PRIOR FILLING DATE: 2000-09-01

PRIOR FILLING DATE: 2000-09-01

PRIOR PRILING DATE: 2000-09-01

PRIOR FILLING DATE: 2000-09-01

PRIOR FILLING DATE: 2000-09-01

PRIOR FILLING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 25

SOUTHWARE: FASTESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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   h 38.6%; Score 39; DB 12; Length 84; Similarity 42.1%; Pred. No. 1.5e+02; 8; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NVLMAMNIISKE-KKEIKWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 NVLEGIGLIEKKSKNSIQWKG 73
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Publication No. US20030171326A1
                                                                                                                                                               3 LMAMNIISKEKKEIK--WI 19
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56 LIARRVVGREAKEIERYWI 74
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APPLICANT: Andrews, William H.
                                                  Best Local Similarity Matches 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: human
US-09-932-581-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEO ID NO 6
LENGIH: 76
                   Query Match
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GENERAL INFORMATION:
APPLICANTE ON THE REFERENCE: 38-21(52703)A

TITLE OF INVENTION: WWB Transcription Factors and Uses for Crop Improvement FILE REFERENCE: 38-21(52703)A

CURRENT APPLICATION NUMBER: US/10/407,920

CURRENT FILING DATE: 2003-06-06

PRIOR APPLICATION NUMBER: US/60/370,759

PRIOR FILING DATE: 2002-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.1%; Score 39.5; DB 15; Length 75; 42.9%; Pred. No. 1.1e+02; ative 5; Mismatches 6; Indel8
Sequence 9, Application US/10214188

Publication No. US20030022260A1

GENERAL INFORMATION:
HIJMANS, RENE
HIJMANS, ELERANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible OS
SOFTWARE: PACHORIES PACHORIES
COMPUTER: EACHORIES
SOFTWARE: PACHORIES
COMPUTER: DATE PACHORIES
SOFTWARE: PACHORIES
SOFTWARE: PACHORIES
PATLING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US-DATA:
PATLING NAMER: NOR-DATA:
PATLING NAMER: NOR-DATA:
PAPLICATION NUMBER: US-DATA:
PAPLICATION NUMBER:
PAPLICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13.AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-214-188-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NVLMAMNIISKE-KKEIKWIG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-407-920-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 39
SOFWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 9
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Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 24
US-10-407-920-19
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PRECENTED. UNCORMATION:
SAPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Ransal, David R.
APPLICANT: Hanzal, David R.
APPLICANT: Hanzal, David R.
APPLICANT: Chen, Wensherg,
TITLE OF INVENTION: CENE PERESION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: LENGTH ENGLANCE. 2001-05-236
TITLE PRICE PERESINGE. Asonica. X-1 ENGLANGE. 2001-05-204
CURRENT TILLING DATE: 2001-05-204
FRICK PRICE APPLICATION NUMBER: US 60/120,132
PRICE APPLICATION NUMBER: US 60/120,132
PRICE APPLICATION NUMBER: US 60/200-05-26
PRICE APPLICATION NUMBER: US 60/200, 456
PRICE APPLICATION NUMBER: US 60/200, 466
PRICE APPLICATION NUMBER: US 60/200, 466
PRICE APPLICATION NUMBER: POT/US01/0066
PRICE APPLICATION NUMBER: POT/US01/0066
PRICE PLICATION NUMBER: POT/US01/0066
PRICE P
                                                                                                    Gaps
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                                 Length 76;
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76
                                                                                                    Indels
      Score 38.5; DB 14;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 43984 LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43984, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                 1 NVLMAMNIISKE-KKEIKWIG 20
                                                                                                                                                                                                                             53 NVLEGIGLIEKKSKNSIQWKG 73
                                    Query Match
Best Local Similarity 42.9%;
Matches 9; Conservative
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                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
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| Publication No. US20020193289A1
| Publication No. US20020193289A1
| GENERAL INFORMATION:
| APPLICANT: Andrews, William H.
| TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
| TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
| FILE REPERENCE: SIER-018
| CURRENT APPLICATION NUMBER: US/10/165,614
| CURRENT FILING DATE: 2002-06-25
| PRIOR APPLICATION NUMBER: 60/296,992
| PRIOR PILING DATE: 2001-06-07
| NUMBER OF SEQ ID NOS: 4
| SEQ ID NOS: 4
| SEQ ID NOS: 4
| LENGTH: 76
                                                                                                                                                                    Gaps
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                                                                                              Query Match
38.1%; Score 38.5; DB 12; Length 76;
Best Local Similarity 42.9%; Pred. No. 1.6e+02;
Matches 9; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
38.1%; Score 38.5; DB 12; Length 76;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N: EXPRESSED IN HELA, SIGNAL = 6.1
N: EXPRESSED IN BRAIN, SIGNAL = 5.4
N: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
N: EXPRESSED IN HEART, SIGNAL = 3.3
N: EXPRESSED IN HEART, SIGNAL = 4.8
N: EXPRESSED IN DOUT LIVER, SIGNAL = 4.4
N: EXPRESSED IN LUNG, SIGNAL = 5.4
N: EXPRESSED IN PLACENTA, SIGNAL = 5.4
N: EXPRESSED IN PLACENTA, SIGNAL = 5.4
N: EXPRESSED IN PLACENTA, SIGNAL = 5.4
N: SWISSPROT HIT: Q01094, EVALUE 1.00e-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 29071, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                             1 NVLMAMNIISKE-KKEIKWIG 20
                                                                                                                                                                                                                                                                      53 NVLEGIGLIEKKSKNSIQWKG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 NVLEGIQLIAKKSKNHIQWL 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: homo sapiens
US-10-165-614-3
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COTHER INFORMATION:
US-10-029-386-29071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
OTHER INFORMATION:
; ORGANISM: human
US-10-338-294-6
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 27
US-10-029-386-29071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 29071
LENGTH: 76
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GREERAL INFORMATION:

APPLICANT: Rachael

APPLICANT: Sipeller-Libermann, Rosana
APPLICANT: Sipeller-Libermann, Rosana
APPLICANT: Sipelsesntiago, Immaculada
TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
FILE REPRENCES: 381552002700
CURRENT APPLICATION NUMBER: 08/09/916,790
CURRENT PILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/221,543
PRIOR PRILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.6%; Score 38; DB 9; Lei
Best Local Similarity 41.2%; Pred. No. 2.5e+02;
Matches 7; Conservative 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
37.6%; Score 38; DB 9; 1
Best Local Similarity 41.2%; Pred. No. 2.1e+02;
Matches 7; Conservative 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Consensus amino acid sequence US-09-916-790-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Consensus amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Meyers, Rachel APPLICANT: Silos-Santiago, Immaculada TITLE OF INVENTION: 1658, 14223, AND 16002, NOVE TITLE OF INVENTION: 1658, 14223, AND 16002, NOVE TITLE OF INVENTION: KINASES AND USES THEREFOR FILE REFERENCE: 38155-20030.00 CURRENT APPLICATION NUMBER: US/09/922,138 CURRENT PILING DATE: 2001-11-28 PRIOR PLICATION NUMBER: US 60/229,299 PRIOR PLILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-922-138-20
; Sequence 20, Application US/09922138
; Patent No. US20020061574A1
; Patent No. USZ0020061574A1
; APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
TENGTH: 100
TYPE: PRT
                                                                                                 US-09-916-790-25
; Sequence 25, Application US/09916790
; Patent No. US20020061573A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NVLMAMNIISKEKKEIK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 NILLDNNMVAKGDSEIK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NVLMAMNIISKEKKEIK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 NILLDNNMVAKGDSEIK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
60 NVISPEKIYVQWL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 34
US-09-867-550-1920
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| Sequence 30735, Application US/20030194704A1
| Sequence 30735, Application No. US20030194704A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. |
| APPLICANT: Rank, David R. |
| APPLICANT: RANK STORMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CITILE OF INVENTION: LUMAN GENOME ANALYSIS TWO FILE REFERENCE: ABOUTCA-X-2 |
| CURRENT APPLICATION NUMBER: US/10/029,386 |
| CURRENT APPLICATION NUMBER: 2001-12-20 |
| NUMBER OF SEQ ID NOS: 34288 |
| SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 |
| SEQ ID NO 30735 |
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OTHER INFORMATION: EXPRESED IN FETAL LIVER, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.62

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.63

OTHER INFORMATION: SWISSPROT HIT: P07271, EVALUE 2.20e-01
US-10-029-386-30735
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46.2%; Pred. No. 2e+02;
tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.6%; Score 38; DB 15; Length 69; 40.9%; Pred. No. 1.7e+02;
                                                                                 Length 31;
                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                               Sequence 694, Application US/10083357

Publication No. US20030054370A1

GENERAL INFORMATION:

APPLICANT: Qiandong Zeng et al.

TITLE OF INVENTION: Systemic Discovery of New Genes

FILE REFERENCE: 032796-090

CURRENT APPLICATION UNMERR: US/10/083,357

CURRENT FILING DATE: 2002-02-27

NUMBER OF SEQ ID NOS: 1346

FROUTH OF SEQ ID NOS: 1346
  ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.72
US-09-864-761-43984
                                                                                 9
                                                                            Score 38; DB 5
Pred. No. 75;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LMAMNIISKE----KKEIKWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 LVCRNIIKKQSITTKEGYKWFG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-083-357-694
                                                                                 37.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 46.2
Local Similarity 66.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 NIISKEKKEIKWI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 40.99
Matches 9; Conservative
                                                                                 Query Match 37.6
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                     7 NIISKEKKEIKW 18
                                                                                                                                                                                                                    7 NMISKQSRKKKW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 31
US-10-029-386-30735
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US-10-083-357-694
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Sequence 4500, Application US/09864408A

Sequence 4500, Application US/09864408A

Publication No. US20040009474A1

GRNERAL INFORMATION:

APPLICANT: Lacach, Martin D.

APPLICANT: Shimkets, Richard A.

TITLE OF INVENTION: No. US20040009474A1e1 Human Polynucleotides and Polypeptides EncorTITLE OF INVENTION: NUMBER: US/09/864,408A

CURRENT FILING DATE: 2001-05-24

CURRENT FILING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 9068

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4500

LENGTH: 98
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IN ADULT LIVER, SIGNAL = 1.1
IN BRAIN, SIGNAL = 1.3
HIT: AA084272.1, EVALUE 7.00e-04
HIT: P15870, EVALUE 4.50e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 12; Length 98; Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BONE MARROW, SIGNAL = 0.85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.7%; Score 35; DB 9; Length 50, 23.5%; Pred. No. 4.1e+02; "**emarches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXPRESSED IN LUNG, SIGNAL = 1
EXPRESSED IN HELA, SIGNAL = 1.1
EXPRESSED IN HEART, SIGNAL = 1.5
EXPRESSED IN PLACENTA, SIGNAL = 0.7
EXPRESSED IN BT474, SIGNAL = 1.4
EXPRESSED IN HBL100, SIGNAL = 1.2
                                     PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR RELICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 33458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                               APPLICATION NUMBER: PCT/US01/00670
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Best Local Similarity 33.3%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LMAMNIISKEKKEIKWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.5%
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRANISM: Homo sapiens
FRATURS:
OTHER INFORMATION: MAP TY
OTHER INFORMATION: EXPRE
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US-09-864-408A-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-864-761-33458
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US-09-864-408A-4500
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TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33458, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.1%; Score 35.5; DB 9; 38.9%; Pred. No. 4.6e+02; tive 7; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR PELLING DATE: 2010-103-23
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-09-03
PRIOR PELLING DATE: 2000-09-07
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PELLING DATE: 2001-01-30
Sequence 1920, Application US/09867550
Patent No. US20020082206A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 ISKSVISLLEKRKLPWIG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 MAMNIIS-KEKKEIKWIG 20
                                                                              APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-1920
                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 35
US-09-864-761-33458
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APPLICANT:
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Gaps
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Sequence 723, Application US/09764869
Parent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: MAP TO AL096704.6
OTHER INFORMATION: EXPERSEED IN PLACENTA, SIGNAL = 6.1
OTHER INFORMATION: EXPERSEED IN BONE MARROW, SIGNAL = 0.92
OTHER INFORMATION: EST_HUMAN HIT: AA250859.1, EVALUE 7.80e-02
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33.7%; Score 34; DB 9; Length 32;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 4; Mismatches 2; Indels
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-03-05
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-864-761-48415
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US-09-764-869-723
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APPLICANT: Kozlov, A. P.
APPLICANT: Kozlov, A. V.
APPLICANT: Lobashev, A. V.
APPLICANT: Lobashev, A. V.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences FILE REFERENCE: 2760-103
CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT APPLICATION NUMBER: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOCTHARE: PatentIn version 3.1
SEQ ID NO 192
LENGTH: 18
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                       GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lesantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION WHERE: US/09/900,147
CURRENT FILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTING UNCY: 2.1
SEQ ID NO 11
LENGTH: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-900-147-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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33.7%; Score 34; DB 15; Length 18
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 3; Indels
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Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 192, Application US/10157031 Publication No. US20030108890A1 GENERAL INFORMATION: APPLICANT: Baranova, A. V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 MAMNIISKEKKEIK 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Patent No. US20020103121A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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US-10-157-031-192
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; LOCATION: (22) 7
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-091-504-723
             Sequence 723, Application US/10091504
; Publication No. US20030059908A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE REPRENCE: PCOO7CI
; CURRENT APPLICATION NUMBER: US/10/091,504
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.7%;
Best Local Similarity 35.7%;
Matches 5; Conservative 6
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7 AIHLSDKKKREKRW 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (22)
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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                                                                                                                                                                                        ; LOCATION: (22); CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-869-723
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                                                                                                                                                                                                                                                                                                                                                       Gaps
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CURRENT APPLICATION Nucleic Acids, Proteins, and Antibodies FIER REPERENCE: PCOO7C2
CURRENT APPLICATION NUMBER: US/10/227,577
CURRENT PILING DATE: 2002-08-26
FRIOR PELICATION NUMBER: 09/764,869
FRIOR PELICATION NUMBER: 09/764,869
FRIOR PELICATION NUMBER: 00/179,065
FRIOR PILING DATE: 2000-01-31
FRIOR PILING DATE: 2000-01-31
FRIOR APPLICATION NUMBER: 60/119,866
FRIOR PILING DATE: 2000-06-29
FRIOR PELING DATE: 2000-06-29
FRIOR PELING DATE: 2000-06-39
FRIOR PILING DATE: 2000-07-11
FRIOR PELING DATE: 2000-07-11
FRIOR PILING DATE: 2000-07-11
FRIOR APPLICATION NUMBER: 60/220,963
FRIOR PILING DATE: 2000-07-26
FRIOR PELING DATE: 2000-07-26
FRIOR PILING DATE: 2000-07-11
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                                                                                                                                                                                                                                                                                            Score 34; DB 9; Length 35;
Pred. No. 3.4e+02;
6; Mismatches 3; Indels
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Publication No. US20040005575A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            Query Match 33.7%;
Best Local Similarity 35.7%;
Matches 5; Conservative
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7 AIHLSDKKKREKRW 20
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 723
LENGTH: 35
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                                                                                                          ORGANISM: Homo sapiens
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                                                                                                                                                            NAME/KEY: SITE
LOCATION: (22)
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US-10-227-577-723
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Length 35; 3; Indels

Score 34; DB 15; Pred. No. 3.4e+02; 6; Mismatches

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR PLING DATE: 2000-02-04
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/32,366
PRIOR PELING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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PILING DAFE: 201-01-30
APPLICATION NUMBER: PCT/USO1/00661
FILING DAFE: 2001-01-30
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Sequence 47714, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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AIHLSDKKKREKRW 20

RESULT 42

Gaps

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Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 845
LENGTH: 59
                                                                                                                                                                                                                                 Score 34; DB 9; Length 59;
Pred. No. 5.9e+02;
7; Mismatches 3; Indels
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                                                                                                                                                                                                                                    33.7%;
illarity 28.6%;
Conservative 7
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                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-764-869-845
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Best Local Similarity
Matches 4; Conserva
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| Publication No. US20030194704A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. APPLICANT: Penn, Sharron G. APPLICANT: Penn, David R. APPLICANT: Penn, David R. APPLICANT: Rank, David R. APPLICANT: Penn, SHARESSION ANALYSIS TWO FILE REFERENCE: APPLICATION HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CITILE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: ABOUTCA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386
| CURRENT FILING DATE: 2001-12-20 | NUMBER OF SEQ ID NOS: 34268
| SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 | SEQ ID NO 33245 | LENGTH: 56
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Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 33.7%; Score 34; DB 9; Length 49; Best Local Similarity 41.2%; Pred. No. 4.9e+02; Matches 7; Conservative 4; Mismatches 6; Indels
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.41
OTHER INFORMATION: SWISSPROT HIT: Q22703, EVALUE 7.30e-01
                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: MAP TO AL035670.16
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 12
OTHER INFORMATION: SWISSPROT HIT: Q63688, EVALUE 6.00e+00
US-09-864-761-47714
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR ADDRESS OF SEQ 1D NOS: 49117
SEQ 1D NO 47714
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19 NILHQEELIAQKKREIE 35
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Best Local Similarity 35.3
Matches 6; Conservative
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ORGANISM: Homo sapiens
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US-10-029-386-33245
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US-09-764-869-845
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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 17, 2004, 10:50:13; Search time 6.33663 Seconds (without alignments)
148.428 Million cell updates/sec Run on:

US-09-900-147-4 101 1 NVLAMANNIISKEKKEIKWIG 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

13973 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O72899 fowloar vir		029015 archaeoglob	4	P76073 escherichia	029947 archaeoglob		Q9hj79 thermoplasm					0	P39230 bacteriopha	P58124 streptococc	Q8dun9 streptococc						P21007 vaccinia vi	-			σ.	P81486 phyllomedus	O43262 homo sapien	Q58612 methanococc	~	17 lotus jap		P57596 buchnera ap
SUMMARIES	ū	V089 FOWPV	HLD STAAM	YCS3 ARCFU		YNAE ECOLI	Y295 ARCFU	Y511_BUCAP		RS16_STRA3		VAPD_HAEIN	RS14_CARRU	Y117_NPVAC	SPAC_BPT4	RS16_STRPY	RS16_STRMU	RL32 MAIZE	CSPA_RICCN	CSPA_RICPR	VB11_VACCV	RL29 SULTO	VB11_VACCC	GBGU_MOUSE	YS46_METJA	SECE_BACLI		DMS4 PHYBI	LEU2 HUMAN	YC15 METJA	BOFA_BACSU		5,	Y530_BUCAI
d	Length DB	65 1	45 1		88 1			95 1	98 1	90 1	72 1	91 1	95 1	95 1	97 1	90 1	91 1		70 1			88 1		35 1	56 1	59 1	59 1	76 1	84 1	86 1	87 1	90 1	90 1	90 1
	Query Match	37.6	Š.	ŝ.	35.6	Š.	4.	4.	4.	4.		33.7			33.7	33.2	33.2	32.7	32.7	32.7	32.7	32.7	32.7	31.7	ᆏ	31.7	31.7	31.7	31.7	31.7	31.7	•	31.7	31.7
	Score	38	36	36	36	36	35	35	m	34.5	34	34	34	34	m	33.5	ë.	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32
	Result No.	-	7	٣	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	26	27	28	29	30	31	32	33

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MEDLINE=91126037; PubMed=2281085; Raghunathan G., Seetharamulu P., Brooks B.R., Guy H.R.; Models of delta-hemolysin membrane channels and crystal structures."; Proteins 8:213-225(1990).
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STRAID=MUSO / ATCC 700699, and N315;
STRAID=MUSO / ATCC 700699, and N315;
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
Mixuraniam., Optenti A., Aokti K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=NCTC 8325-4;
MEDLINE-90158509; PubMed=2622452;
Janzon L., Loefdahl S., Arvidson S.;
"Identification and nucleotide sequence of the delta-lysin gene, hld, adjacent to the accessory gene regulator (agr) of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eins 8:213-225(1990).
FUNCTION: DELTA-TOXIN LYSES ERYTHROCYTES AND MANY OTHE MAMMALIAN
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STRAIN=ISOLAte GAL.
STRAIN=ISOLAte GAL.
MEDINE=96004766; PubMed=7565609;
Novick R.P., Projan S.J., Kornblum J., Ross H.F., Ji G.,
Kreiswirth B., Vandenesch F., Moghazeh S.;
"The agr P2 operon: an autocatalytic sensory transduction system in staphylococcus aureus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA for hld, agrB, and agrD genes of Staphylococcus aureus strain
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Fitton J.E., Dell A., Shaw W.V.;
"The amino acid sequence of the delta haemolysin of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEAIN=Canine variant; Fitton J.E., Hunt D.F., Marasco J., Shabanowitz J., Winston S.,
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28-FEB-2003 (Rel. 41, Last annotation update)
Delta-hemolygin precursor (Delta-toxin).
HLD OR SAV2035 OR SAS065.
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain N315), and
Staphylococcus aureus.
Staphylococcus aureus.
Staphylococcus aureus.
Staphylococcus aureus.
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Staphylococcus aureus.
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Mol. Gen. Genet. 219:480-485(1989)
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FEBS Lett. 169:25-29(1984).
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STRAIR=VC-16, DSM 4304 / ATCC 49558;
STRAIR=VC-16, DSM 4304 / DSM 4304 DSM V. Cabbun R.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Fleischmann R.D., Dodsoberty B.A., McKenney K., Adams M.D., Loftus B., Rixhness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., MoNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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Nature 390:364-370(1997).
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Hemolysis; Formylation; Toxin; Transmembrane; 3D-structure;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                 EMBL, AP003364; BAB58197.1; ALT_INIT.
EMBL, X52543; CAA56780.1; ALT_INIT.
EMBL, X52543; CAA56780.1; ALT_INIT.
EMBL, AF230358; AAF43204.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5140 MW;
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Best Local Similarity 44.4%;
Matches 8; Conservative
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PDB; 1DTC; 31-OCT-93.
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PIR; A89995; A89995.
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STRAIN=K12 / MG1655;
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                                                                                                                                        Escherichia coli.
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MEDLINE=9745617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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Pred. No. 46;
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BCOGGERE; EG13823; YdfK.
Hypothetical protein; Complete proteome.
SEQUENCE 88 AA; 10136 MW; 534B06E2287CC6A0 CRC64;
                                                                                                                                                                             PIR; D69406; D69406.
TIGR; AF1253; -.
Hypothetical protein; Complete proteome.
SEQUENCE 64 AA; 7418 MW; CD6CF9F885F4FF15 CRC64;
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15-JUL-1998 (Rel. 36, Last seq.
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Hypothetical protein ydfK.
YDPK OR B1544.
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Matches 8; Conservative
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Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
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                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12 / MG1655;
MEDLINE=97426617; PubNed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Kriley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000234; AAC74457.1; -.
PIR, B64888; B64888.
EcoGene; EG1373; ynas
Hypothetical protein; Complete proteome.
SEQUENCE 88 AA; 10109 WW; 534B1813C77CC6A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF0295.
                                                                          15-JUL-1998 (Rel. 36, Last sequence update)
15-SFP-2003 (Rel. 42, Last annotation update)
Hypothetical protein ynaE.
88 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB
Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 277:1453-1474(1997).
-!- SIMILARITY: STRONG, TO B.COLI YDFK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
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                                                15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last seq.
15-SEP-2003 (Rel. 42, Last annomale.)
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STRAIN=NEM316 / Serctype III;
MEDLINE=2224508; PubMed=12354221;
Glaser P., Rusnick C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek I., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                               Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nature 40/:508-514(2000).
-!- SIMILARITY: BELONGS TO THE S24E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                            Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.7%; Score 35; DB 1; Length 98; 40.9%; Pred. No. 1e+02; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   036ED0B0443CF8C1 CRC64;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
RPSP OR GBS1428 OR SAG1358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus agalactiae (serotype III), and Streptococcus agalactiae (serotype V).
                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
30S ribosomal protein S24e.
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                                     98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00545; -; 1.
InterPro; IPR001976; Ribosomal_S24E.
Pfam; PP01282; Ribosomal_S24e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                 STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL445066; CAC12220.1; -.
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Best Local Similarity 40.93
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                              Thermoplasma acidophilum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 407:508-513(2000)
                                       STANDARD;
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                                                                                                                                                                           RPS2E OR TA1092
                                     RS24 THEAC
Q9HJ79;
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                                                                                                                                                                                                                                                                                                         SEQUENCE
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RS16_STRA3
RESULT
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                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEQUENCE FROM N.A.

MEDLINE-22084549; PubMed=12089438;

MEDLINE-22084549; PubMed=12089438;

Tamas I., Klasson L., Canbaeck B., Nacslund A.K., Eriksson A.-S.,

Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;

Wernegreen J.J., Sandstroem J.P., Moran N.A., Anderston S.G.E.;

So million years of genomic stasis in endosymbiotic bacteria.";

Science 296:2376-2379(2002).

I. SIMILARITY: STRONG, TO E.COLI YHEL.
                                            The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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    Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 1; Length 74; Pred. No. 77; 7; Indels 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 1; Length 95;
Pred. No. 99;
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Pfan; PF04077; DsrH; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 95 AA; 10992 MW; 51E8A2023BE57141 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein, Complete proteome.
SEQUENCE 74 AA; 8839 MW; ODCFSEF3B444B2F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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T
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TIGR; AF0295; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein BUSG511.
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52.9%;
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Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                             Nature 390:364-370(1997)
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nes 9; Conserv
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Query Match

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Y511 BU(Q8K946;

Y511_BUCAP
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DT 28-FEBDT 28-FEB-

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EMBL; U32728; AAC22108.1; -.
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                                                                                                                                                                                                                                                                                              Best Local Similarity 36.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 76-80.
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                                                                                                                                                                                                                                                SEQUENCE
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                                       MEDLINE-2222988; PubMed=12200547;
MEDLINE-22222988; PubMed=12200547;
Tettelin H., Masignani V., Cisslewicz M.J., Eisen J.A., Peterson S. Tettelin H., Masignani V., Cisslewicz M.J., Bisen J.A., Dead T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBOY R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora Piacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione I Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=93062802; PubMed=1435726;

Tschauder S., Driessen A.J.M., Freudl R.;

Tschauder S., Driessen A.J.M., Freudl R.;

"Cloning and molecular characterization of the secY genes from Bacillus licheniformis and Staphylococcus carnosus: comparative analysis of nine members of the SecY family.";

Mol. Gen. Genet. 235:147-152(1992).

-i- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

-i- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                             "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34.5; DB 1; Length 90;
Pred. No. 1.1e+02;
8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Complete proteome. SEQUENCE 90 AA; 10282 MW; CDCA763D78007CBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
50S ribosomal protein L15 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Promis Professional S16; 1.
Prodom; PD003791; Ribosomal S16; 1.
TIGREAMS; TIGR00002; S16; 1.
PROSITE; PS00732; RIBOSOMAL S16; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_00385; -; 1.
InterPro; IPR000307; Ribosomal_S16.
Mol. Microbiol. 45:1499-1513(2002)
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 NPLVAENOVTIKEERVLEWL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL766850; CAD47087.1; -. EMBL; AE014254; AAN00229.1; -.
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01-FEB-1994 (Rel. 28, Last seqn
01-FEB-1994 (Rel. 28, Last anno
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Best Local Similarity 35.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sagalist; gbs1428; -.
TIGR; SAG1358; -.
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RL15 BACLI
AC P35138;
DT 01-FEB-1994
DT 01-FEB-1994
DT 01-FEB-1994
DT 01-FEB-1994
DE 50S ribosoma
GN RPLO.
OC Bacteria; Fi
OX NCBL TaxID=1
RP SEQUENCE FRO
RX MEDLINE=9306
RA TSCHAUGE SO
RY MOLIUS 1C
CC --- SIMITARI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehn C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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Pasteurellaceae, Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.7%; Score 34; DB 1; Length 72; 36.8%; Pred. No. 1.1e+02; tive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 AA; 7441 MW; 6DC3BA681492E6C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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-!- SIMILARITY: BELONGS TO THE VAPD FAMILY.
                                                                                                                                                              entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                 PIR; S34404, S34404. —
Interpro; IPR001196, Ribosomal_L15.
Pfam; PP00256; L15; 1.
Pfam; PF01305; Ribosomal_L15; 1.
PROSITE; PS00475; RIBOSOMAL_L15; 1.
Ribosomal protein; rRNA-binding.
NON_TER
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PIR; S34404; S34404.
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21 LLLETGVISKLKSGVKILG 39
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NCBI_TaxID=46015;
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                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21125546; PubWed=11222582; MEDLINE=21125546; PubWed=11222582; MEDLINE=21125546; PubWed=11222582; Clark M.A., Baumann P.; Clark M.A., Baumann P.; Clark M.A., Baumann D.; Thao M.L., Moran N.A., Baumann P.; J. Bacteriol. 183:1853-1861(2001).
J. Bacteriol. 183:1853-1861(2001).
J. Bacteriol. 183:1853-1861(2001).
J. Bacteriol. 183:1853-1861(2001).
L. FUNCTION: Known to be required for the assembly of 30S particles and may also be responsible for determining the conformation of the 16S rRNA at the A site (By similarity).
L. SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
NCBI_TaxID=114186;
                                                                                                           Gaps
                                                                                                            4
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 11.0 kDa protein in HB65-PK2 intergenic region.
Autographa californica unclear polyhedrosis virus (AcMNPV).
Viruses, dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.7%; Score 34; DB 1; Length 95; 36.8%; Pred. No. 1.4e+02; Live 6; Mismatches 6; Indels
                                                                             Query Match
33.7%; Score 34; DB 1; Length 91;
Best Local Similarity 36.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 AA; 11392 MW; 4BF942A9C3A61AD7 CRC64;
                                                     70B23CDE28E083E7 CRC64;
                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
38-FEB-2003 (Rel. 41, Last annotation update)
RPSN OR RPS14
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PROSITE; PS00527; RIBOSOWAL_S14; FALSE_NEG.
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53 NLFQAMNAL----KQLAWI 67
                                                                                                                                      1 NVLMAMNIISKEKKEIKWI 19
    PIR; C64069; C64069.
TIGR; H10450; -.
Pfam; PF04605; VapD_N; 1.
Virulence; Complete proteome.
SEQUENCE 91 AA; 10543 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 36.8'
Conservative
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Q9AIF4;
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P41670;
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ID Y117_N
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DT 01-NOV
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Kai T., Ueno H., Otsuka Y., Morimoto W., Yonesaki T.;

"Gene 61.3 of bacteriophage T4 is the spackle gene.";

Virology 260:254-259(1999).

-i. FUNCTION: NOT KNOWN. MUTANTS ALLOW SURVIVAL OF LYSOZYME MUTANTS.

-i. SUBCELLULAR LOCATION: Periplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
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               Ayres M.D., Howard S.C., Kuzlo J., Lopez-Ferber M., Possee R.D., "The complete DNA sequence of Autographa californica nuclear polyhadrosis virus.", Virology 2021:86-665 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage T4.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
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Mesyanzhinov V., Kuger W., Stidham T., Thomas E.;
"Bacteriophage T4 genome analysis.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 95;
Pred. No. 1.4e+02;
7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 AA; 10992 MW; 68897B745ECE51C6 CRC64;
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.7%; Scor.
36.8%; Pred. No. 1...
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MEDLINE=94303173; Pubmed=8030224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
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PIR; F72864; F72864.
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Best Local Similarity 36.0.
Local 7; Conservative
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SP OR 61.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
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28-FEB-2003
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EMBL; AE014928; AAN58580.1; -.
                                                                                     outbreaks.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The genome of invasive Streptococcus pyogenes; a comparative analysis of S. pyogenes SSI-1, SF370 and MGAS8232.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes.";
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STRAIN-MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., van Gompel J.J., Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=SERING / ATCC 700294 / Serotype M1;
MEDLINE=21192664; PubMed=11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.
Perimeaux C., Sezete S., Suvozov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
Complete genome sequence of an M1 strain of Streptococcus pyogenes."
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=22133808; PubMed=12122206;
Bereas S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Bereas S.B., Shith T.W., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.W., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=SSI-1 / Serotype M3;
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori
  and
                                                                                                                                                                                                                                                      Score 34; DB 1; Length 97; Pred. No. 1.5e+02; 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30S ribosomal protein S16.
RPSP OR SPY0840 OR SPYM3_0567 OR SPS1287 OR SPYM18_0900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes (serotype M3), and
Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
  Usage by
                                                                                                                                                                                         SPACKLE PROTEIN.
E0A5E5E076C97965 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 AA
modified and this statement is not removed.
                 entities requires a license agreement (S. or send an email to license@isb-sib.ch).
                                                                                                                                                                          POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                97 AA; 10994 MW;
                                                                                EMBL; S57514; AAB25710.1; -. EMBL; AF158101; AAD42510.1; PIR; C45681; C45681.
                                                                                                                                                                                                                                                                            41.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                     5; Conservative
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49 MNIVKRDRPEMK 60
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97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 42,
                                                                                                                                               Signal, Periplasmic. SIGNAL 1
                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRANIB-ALS9 / ArCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., 'Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UA159, a cariogenic dental
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.; "Genome sequence and comparative microarray analysis of serotype M18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
-!- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 90;
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TIGREAMS; TIGRO0002; S16; 1.
PROSTE; PS00732; RIBOSOMAL_S16; FALSE_NEG.
RIDOSOMA! Drotein; Complete proteome.
TIGROSOMA! 10252 MW; CDC5E92FEAAB660E CRC64;
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Pred. No. 1.6e+02;
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InterPro; IPR000307; Ribosomal S16.
Pfam; PF00886; Ribosomal S16; 1.
ProDom; PD003791; Ribosomal S16; 1.
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15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last seq
15-SEP-2003 (Rel. 42, Last ann
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0050; COLDSHOCK.
PRODOM; PRO00621; Cold_shock; 1.
SMART; SM00357; CSP; 1.
PROSITE; PS00352; COLD_SHOCK; 1.
Transcription regulation; DMA-binding; Activator; Complete proteome.
DOMAIN 7 67 CSD.
                                                                                                                                                                                                                                                                                                                                                                                                        "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                            STRAIN=Malish 7;
MEDLINE-21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 396:133-140(1998).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI TaxID=782;
                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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Pred. No. 1.5e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 67 CSD.
70 AA; 7771 MW; 822E9714229FE03A CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
CSPA OR RP670.
28-FEB-2003 (Rel. 41, Last annotation update)
Cold shock-like protein cspA.
CSPA OR RC1021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 AA.
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MEDLINE-99039499; PubMed-9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002059; Cold_shock. Pfam; PF00313; CSD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE008653; AAL03559.1; -.
PIR; E97827; E97827.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MATNIVGK----VKW 11
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Best Local Similarity 46.7%
Matches 7; Conservative
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                                                                                                Rickettsia conorii.
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=781;
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ID _CSPA_RICPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 19
            SOUR THE PROPERTY OF THE PROPE
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade, Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. HD5 X HD7;
Bates E.B.M., Vergne P., Dumas C.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE L32E FAMILY OF RIBOSOWAL PROTEINS.
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                                                                                                                                                                                                                                                                            Query Match 33.2%; Score 33.5; DB 1; Length 91; Best Local Similarity 33.3%; Pred. No. 1.7e+02; Matches 7; Conservative 7; Mismatches 6; Indels
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Pred. No. 92;
5; Mismatches 2; Indels
                                                                                                                                                                                                                            1E7329D1BDFF6EC2 CRC64;
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42 AA; 4709 MW; FA9E004E030D1BF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-00T-1996 (Rel. 34, Created)
01-00T-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
60S ribosomal protein L32 (Fragment).
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(Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 AA
                     HAMAP, MF_00385; -; 1.
InterPro; IPR000370; Ribosomal_S16.
Prom, PF00086; Ribosomal_S16; 1.
ProDom; PD00379; Ribosomal_S16; 1.
TIGRFAMS; TIGR00002; S16; 1.
PROSITE; PS07032; RIBOSOMAL_S16; FALSE_NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 91 AA; 10410 MW; IE7329DIBDFF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001515; Ribosomal_L32E.
Pfam; PF01655; Ribosomal_L32e; 1.
ProDom; PD003823; Ribosomal_L32E; 1.
PROSITE; PS00580; RIBOSOWAL_L32E; PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                  1 NVLMAMNIIS-KEKKEIKWIG 20
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IAHNVSTKKRKEI 18
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Matches 6; Conserv
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Q92GV1;
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RL32 MAIZE
P51421;
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SEQUENCE
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SO TEN DE RECORDE DE LA COMPANSION DE LA

RL32_MAIZE

a

CSPA RICCN ID CSPA R AC Q92GVI DT 28-FEB DT 28-FEB

RESULT 18

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Сарв

4.

us-09-900-147-4.rsp

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RESULT 21
RL29_SULTO
ID _RL29_SU
                                                                         SEE BEER AND DESCRIPTION OF THE PROPERTY OF TH
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                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91259063; PubMed=2045793;
Smith G.L., Chan Y.S., Howard S.T.;
"Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near
the right inverted terminal repeat.";
J. Gen. Virol. 72:1349-1376(1991).
                                                                                                                                                                                                                                                                                                                                   PRINTS, PRO0050; COLDSHOCK.
Probom; PRO00621; Cold shock; 1.
SMART; SM00357; CSP; 1.
PROSITE; PS00352; COLD SHOCK; 1.
Transcription regulation; DNA-binding; Activator; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 67 CSD.
70 AA; 7785 MW; F49FBF2FB344903E CRC64;
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SEQUENCE 72 AA; 8184 MW; 372BE3DCE6AFAE07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 1; I
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Scor. 46.7%; Pred. No. 1...
                                                                                                                                                                                                                                       PIR; B71673; B71673.
HSSP; B41016; LC90.
InterPro; IPR002059; Cold_shock.
Pfam; PF00313; CSD; 1.
                                                                                                                                                                                                                   EMBL; AJ235272; CAA15108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D11079; BAA01841.1; -.
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7 NVEDIINEIDREKEEI
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Best Local Similarity 46.7%
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les 8; Conservative
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Matches
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A. Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.,
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                       Sulfolobus tokodaii.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-91021027; PubMed=2219722;
Gobbel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain?."; DNA Res. 8:123-140(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9A5B120EB10382C2 CRC64;
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                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
RPL29P OR STS061.
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
88 AA.
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TIGRPAMS; TIGRO0012; L29; 2.
PROSITE; PS00579; RIBOSOMAL L29; 1.
Ribosomal protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_00374; atypical; 1.
InterPro; IPR001854; Ribosomal_L29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=JCM 10545 / 7;
MEDLINE=21456156; PubMed=11572479;
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=111955;
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NCBI_TaxID=10249;
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VB11_VACCC
ID VB11_VACCC
AC P21007;
SULTO
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Pfam; PF00631; G-gamma; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annaschii.";
                                                                                                                                                                                                                Y546 METJA
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SECE_BACLI
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                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-T2 subunit
(G gamma-C) (G-gamma-B) (Fragment).
GNGT2 OR GNG8 OR GNGT8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                         Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFFECTOR INTERACTION.
SUBUNIT: G proteins are composed of 3 units (alpha, beta and
                                                                                                                                                                                                                                                                       ;
0
                                                 "Appendix to 'The complete DNA sequence of vaccinia virus'.";
Virology 179:517-563(1990).
                                                                                                                                                                                                                2 19 9 X 2 AA TANDEM REPEATS OF D-T.
88 AA; 9897 MW; F81B3D279229AE02 CRC64;
                                                                                                                                                                                                                                               Score 33; DB 1; Length 88;
Pred. No. 1.9e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE G PROTEIN GAMMA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                           35 AA.
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                                                                                                                                                                              EMBL; M35027; AAA48208.1; -.
PIR; A42527; A42527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001770; G-gamma
                                                                                                                                                                                                                                                   32.7%;
50.0%;
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                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                   23 NVEDIINEIDREKEEI 38
  Virology 179:247-266(1990)
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50...
8; Conservative
                                                                                                                                                                                                                                                                                                1 NVLMAMNIISKEKKEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
               [2]
COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                             GBGU_MOUSE
                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     961017;
                                                                                                                                                                                                         Repeat
                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAINS-JAL-1 / DSM 2661 / ATCC 43067;
STRAINS-JAL-1 / DSM 2661 / ATCC 43067;
STRAINS-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., George J.D.,
Skerlawage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                        Gaps
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Pred. No. 1.8e+02;
7; Mismatches 4; Indels
                                                                                                                                                                                                     Score 32; DB 1; Length 35;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Transmembrane; Complete proteome. TRANSMEM 2 22 POTENTIAL. DOMAIN 27 47 GLU-RICH.
ProDom; PD003783; G-gamma; 1.
PROSITE; PS50058; G_PROTEIN_GAMMA; 1.
Transducer; Prenylation; Lipoprotein; Multigene family.
NON_TER 1 1 3 35
NON_TER 35 35
SEQÜENCE 35 AA; 3852 MW; 6F1D53CC6BFAF97D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Buryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66CBFC395548BA5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AA
                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NVLMAMNII--SKEKKEIK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |::: :| || :|:|
14 NILGIKVIMLQKELEEVK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.7%;
Similarity 31.6%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U67504; AAB98548.1; -.
PIR; B64368; B64368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein MJ0546.
                                                                                                                                                                                                     31.7%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 AA; 6460 MW;
                                                                                                                                                                             Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                    7 NIISKEKKEIK 17
                                                                                                                                                                                                                                                                                                                                                        B DLISKTGKEIK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIGR; MJ0546; -.
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PIR; S39858; S39858.
Subtilist; BG10161; secE.
InterPro; IPR001901; SecE.
InterPro; IPR005807; SecE.
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D13303; BAA02559.1; -. EMBL; Z99104; CAB11876.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 AA; 6927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : || |:: |
10 VGKEMKKVSW 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 ISKEKKEIKW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95058172; PubMed=7968510;
Jeong S., Yoshikawa H., Takahashi H.;
"Isolation and characterization of the secE homologue gene of
                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 1; Length 59;
Pred. No. 1.9e+02;
6; Mismatches 7; Indels
                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                     59 AA; 6775 MW; BD40479D9FA5837B CRC64;
                                                                                                                                                                                                                                                                                                                                          TIGRPAMS; TIGR00964; 3a0501806; 1.
PROSITE; PS01067; SECE_SEC61G; 1.
Protein transport; Translocation; Transmembrane.
                  (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECE BACSU STANDARD; PRT; 59 AA. 006799; P3689; P3689; P3689; P3689; P3691-JUN-1994 (Rel. 29, Last sequence update) PFEB-2003 (Rel. 41, Last annotation update) Preprotein translocase secE subunit.
  59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                            01-OCT-1994 (Rel. 30, Last annotatic
Preprotein translocase secE subunit.
PRT;
                                                                                                                                                                                                                                                                                                 EMBL; M29694; -; NOT_ANNOTATED_CDS.
InterPro; IPR001901; SecE.
InterPro; IPR005807; SecE_bac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Microbiol. 10:133-142(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VLMAMNIISKEKKEIKW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 IIKFLKNVGKEMKKVTW 19
                                                                                                                                                                                                                                                                                                                                                                                                          31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                   23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
 STANDARD;
                                                                        Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00584; SecE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis."
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis
                                                                                             NCBI_TaxID=1402;
                     01-OCT-1994
                                01-OCT-1994
                                          01-OCT-1994
 BACLI
                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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SECE BACSU
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Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Benizot F.V., Deviner K.M., Dusterhoft A., Erhilch S.D., Emmerson P.T.,
B. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
R. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
R. Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Glim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A. Hibert H., Holsappel S., Hosono S., Hallo M.F., Itaya M., Jones L.,
A. Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A. Kobayashi Y., Koetter P., Koningstein G., Frogh S., Kumano M.,
A. Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A. Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,
A. Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,
A. Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Persecan E., Pujic P., Purnalle B., Rapoport G., Rey M., Reynolds S.,
R. B. Pujic P., Purnalle B., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
A. Tacconi E., Takagi T., Takahashi H., Takemaru K.,
A. Yasanoto V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Vanta A., Wambutt R., Wedler E., Wedler H., Waitzenegger T.,
Winters P., Winder A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390:249-256(1997).
-!- FUNCTION: ESSENTIAL FOR PROTEIN EXPORT.
-!- SUBCELLULAR LOCATION: Tail-anchored membrane protein (Potential).
-!- SIMILARITY: Belongs to the secE/SEC61-gamma family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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TIGRPAMs; TIGR00964; 3a0501806; 1.
PROSITE; PS01067; SECE SECGIG; 1.
Protein transport; Translocation; Transmembrane; Complete proteome.
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LoCT-2001 (Rel. 40, Last sequence update)
15-SRP-2003 (Rel. 42, Last annotation update)
Dermaseptin BIV precursor (Dermaseptin B4).
Phyllomedusa bicolor (Two-colored leaf frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Annra; Neobetrachia; Bufonoidea; Hylidee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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40.0%; Pred. No. 1.9e+02;
tive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 AA.
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Oncogene 15:2463-2473(1997).
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIGR: MJ1215:
                                                                                                                                                                                                                                                                                                    Anti-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METJA
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                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           058612;
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                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Liu Y., Corcoran M., Rasool O., Ivanova G., Ibbotson R., Grander D.,
Liu Y., Corcoran M., Rasool O., Ivanova G., Ibbotson R., Gardiner A.,
Ilyengar A., Baranova A., Kabuba V., Merup M., Wu X., Gardiner A.,
Mullenbach R., Poltaraus A., Hulstrom A.L., Juliusson G., Chapman R.,
Tiller M., Cotter F., Gahrton G., Yankovsky N., Zabarovsky E.,
Einhorn S., Oscier D.;
"Cloning of two candidate tumor suppressor genes within a 10 kb region on chromosome 13q14, frequently deleted in chronic lymphocytic
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-PEB-2003 (Rel. 41, Last annotation update)
Leukemia associated protein 2 (Deleted in lymphocytic leukemia 2)
DLEUZ OR LEUZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
AMIDATION (G-74 PROVIDE AMIDE GROUP)
ABA0525F0709F447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nouwo вернець (попами).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amphibian defense peptide; Antibiotic; Multigene family; Signal;
Cleavage on pair of basic residues; Amidation.
SIGNAL 1 22 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                         SEQUENCE FROM N.A., SEQUENCE OF 46-73, AND MASS SPECTROMETRY.
TISSUE-Skin secretion;
MEDLINE-98278974; PubMed=9614066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 1; Length 76;
Pred. No. 2.4e+02;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DERMASEPTIN BIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y16565; CAA76289.1; -.
InterPro; IPR004275; Brevenin.
      Phyllomedusinae; Phyllomedusa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 43
46 73
75 76
73 73
76 AA; 8642 MW;
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nes 6; Conservative
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                            NCBI_TaxID=8393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukemia.";
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SEQUENCE
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LEU2_HUMAN
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                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- SIMILARITY: BELONGS TO THE M.JANNASCHII MJ0126 / MJ0128 / MJ0141 /
MJ0435 / MJ0604 / MJ1215 / MJ1217 / MJ1305 / MJ1379 FAMILY.
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
Bult C.J. White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., George J.D.,
Soutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weingtock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 2.7e+02;
2; Mismatches 2; Indels
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Methanocaldococcaceae; Methanocaldococcus
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Pfam; PF01909; NTP transf.2; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 86 AA; 10281 MW; CD9296D0B135FD14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 AA; 10196 MW; DIEE021072A0E03B CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ1215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 AA.
-! - FUNCTION: MAY ACT AS A TUMOR SUPPRESSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 605766; -.
GO; GO:0008181; F:tumor suppressor; TAS.
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PIR; F64451; F64451.
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Genew; HGNC:13748; DLEU2.
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DOMAIN
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RR15_LOTJA
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Ravedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Bruschi C., Brans A., Brann M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

R. Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Brouillet S., Brington J., Connerton I.F., Cummings N.J., Daniel R.A.,

R. Britz C., Fujita M., Fujita Y., Funa S., Gallaria R.D., Emmerson P.T.,

R. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

R. Ariz C., Fujita M., Fujita Y., Harwood C.R., Henaut A.,

R. Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Chim S.Y., Caliser P., Goffeau A., Golightly E.J., Grandi G.,

R. Malbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Chaiseppi G., Guy B.J., Haga K., Haisch J., Harwood C.R., Henaut A.,

R. Malbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Coris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

R. Kobayashi Y., Kootter P., Mizuno M., Moeell D., Nakai S., Kumano M.,

R. Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

R. Pescan B., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

R. Reger M., Rivolta C., Rocha B., Roche B., Roche B., Sorfone F.,

Schowska A., Seror S.J., Schroeter R., Yosenotti A.,

Takeuchi M., Tamakoshi H., Tarkayai T., Tarkemaru K.,

R. Sorokin A., Tacconi E., Takagi T., Tarkahashi H., Takemaru K.,

R. Sorokin A., Tacconi E., Takagi T., Terpetra P., Tognoni A.,

Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

Tosato V., Wambutt R., Wedler H., Weitzenegger T.,

R. Winters P., Wambutt R., Wedler H., Weitzenegger T.,

R. The complete genome sequence of the Gram-positive bacterium Bacillus

R. Thillis ".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sigma-K factor processing regulatory protein BOFA (Bypass-of-forespore
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168;
MEDLINE=96051385; PubMed=7584024;
Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus shromosome containing the replication origin.";
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91088245; PubMed=2124672;
Alonso C., Shirahige K., Ogasawara N.;
"Molecular cloning, genetic characterization and DNA sequence
analysis of the reck reckin of Bacillus subtilis.";
Nucleic Acids Res. 18:6771-6777(1990).
Score 32; DB 1; Length wo; Pred. No. 2.7e+02; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                       87 AA.
                                                                                            2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last seq
28-FEB-2003 (Rel. 41, Last ann
                        31.7%;
60.0%;
                        Query Match 31.7
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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SEQUENCE FROM N.A.
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P24282;
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BOF ARCSU
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DT 01-MARR
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
      Ricca E., Cutting S.M., Losick R.;
"Characterization of bofA, a gene involved in intercompartmental regulation of pro-sigma K processing during sporulation in Bacillus subtilis.";
                                                                                                                                                                                                                             MEDLINE=97286525; PubMed=9141672;

Warcamonti M., Marasco R., de Felice M., Sacco M.;

Wambrane topology analysis analysis analysis bord protein
involved in pro-sigma K processing.";

Microbiology 143:1053-1058(1997).

-!- FUNCTION: INVOLVED IN THE MEDIATION OF THE INTERCOMPARTMENTAL
COUPLING OF PRO-SIGMA K PROCESSING TO EVENTS IN THE FORESPORE.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
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MEDINDE=21082929; PubMed=11214967;
MEDINDE=21082929; Sato S., Nakamura Y., Tabata S.;
"Complete structure of the chloroplast genome of a legume, Lotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 7:323-330(2000).
-!- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.
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Pred. No. 2.8e+02;
1; Mismatches 1; Indels
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EXTRACELLULAR (PROBABLE).
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PubMed=1577688;

    Bacteriol. 174:3177-3184(1992)

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28-FEB-2003 (Rel. 41, Last seq
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71.4%;
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Q9BBN7;
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Best Local
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RESULT 34
YHBY_ECOLI
ID _YHBY_ECOLI
                                                                                                                                                                            Query Match
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Y530_BUCAI
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Wagnoliophyta; eudicotyledons, core eudicots; Caryophylidae, Caryophyllales, Chenopodiaceae, Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Geant d'hiver, and cv. Monatol;
MEDLINE=21187424; PubMed=11292076;
Schmitz-Linneweber C., Maier R.M., Alcaraz J.-P., Cottet A.,
Hermann R.G., Mache R.;
Hatermann R.G., Mache R.;
Hithe plastid chromosome of spinach (Spinacia oleracea): complete
nucleotide sequence and gene organization.";
Plant Mol. Biol. 45:307-315(2001).
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                                                                                                                                                                                                                                      31.7%; Score 32; DB 1; Length 90; 75.0%; Pred. No. 2.9e+02; tive 2; Mismatches 0; Indels
                                                                                                                             InterPro; PR000589; Ribosomal S15.
InterPro; IPR005290; RS15 bact
Pfam, PR00312; Ribosomal S15; 1.
ProDom; PD157043; RS15 bact; 1.
TIGRPAMS; TIGR00952; S15 bact; 1.
PR0STIE; PS00352; RISOSOMAL S15; 1.
RRDSTE; PS00352; RISOSOMAL S15; 1.
SEQUENCE 90 AA; 10904 MW; ECGAA9312D6D7EE5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-20, FUNCTION, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chloroplast 30S ribosomal protein S15.
                                                                                                                                                                                                                                                                                                                                                                       90 AA
                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                        EMBL; AP002983; BAB33252.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spinacia oleracea (Spinach)
                                                                                                                                                                                                                                                   Best_Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                       8 IISKEKKE 15
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                                                                                                                       HSSP; P80378; 1AB3
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Q9M3I4; P82138;
16-OCT-2001 (Re
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BRDILNES-20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Renome sequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                symbiotic bacterium).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Pred. No. 2.9e+02;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Length 90;
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Pfam, PR04077; DBrH; ..
Hypothetical protein; Complete proteome.
SEQUENCE 90 AA; 10501 MW; 4D9FF2FDB25E338F CRC64;
                                                                                                           HSSP; P80378; 1AB3.
InterPro; IPR000589; Ribosomal_S15.
InterPro; IPR000589; RS15 bact.
Pfam; PF00312; Ribosomal_S15; 1.
ProDom; PD157043; RS15_bact; 1.
PTGRPAMs; TGR00952; S15_bact; 1.
PROSITE; P800362; RIBOSOMAL_S15; 1.
Ribosomal protein; Chloroplast; rR.
CONFLICT 12 12 D -> P (IN REF. 2).
SEQUENCE 90 AA; 10754 MW; F93B9E70B1310413 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  31.7%; Score 32; DB 1; I
60.0%; Pred. No. 2.9e+02;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein BU530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buchnera sp. APS.";
Nature 407:81-86(2000).
-!- SIMILARITY: STRONG, TO E.COLI YHEL.
     entities requires a license agreement (
or send an email to license@isb-sib.ch)
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                                                            EMBL; AJ400848; CAB88791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Buchnera
NCBI_TaxID=118099;
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Similarity 27.8%;
5; Conservative
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7 ISVISDEKKE 16
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Best Local Similarity
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P57596;
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                                                                                                                                                                                                                                                                                                  through comparison with genomes of Escherichia coli K12 and O157.";
Nucleic Acids Res. 30:4432-4441(2002).
-!- SIMILARITY: BELONGS TO THE UPF0044 FAMILY. STRONG, TO H.INFLUENZAE
                                                                                                                                                                                                                                                           "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=56337999; PubMed=868087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Flizderald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
                           MEDLINE-22272406; PubMed-12386590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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Pred. No. 3.1e+02;
5; Mismatches 2; Indels
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Archaea; Euryarchaeota; Methanococci; Methanococcales;
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SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1126 METJA

1D Y126 METJA STANDARD; PRT; 98 AA.

AC Q57590;

DT 10-100-1997 (Rel. 35, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein MJ0126.
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PROSITE; PS01301; UPF0044; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 97 AA; 10784 MW; 5284F7AAG
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EMBL; X54718; -; NOT ANNOTATED CDS.
EMBL; AE015333; AAN44686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000399; AAC76212.1; -.
EMBL; U01376; -; NOT ANNOTATED_CDS.
EMBL; AE01676; AANST377.1; -.
EMBL; AE005546; AAG58314.1; -.
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InterPro; IPR001890; UPF0044.
Pfam; PF01985; UPF0044; 1.
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PIR, C91136; C91136.
PIR, F65108; F65108.
PIR, F85981; F85981.
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=2238824; PubMed=12471157; MEDLINE=2238824; PubMed=12471157; MEDLINE=2238824; PubMed=12471157; MEDLINE=2238824; PubMed=12471157; Medlor R.A., Burland V., Plunkett G. III, Redford D., Roesch P., Rasko D., Buckles E.L., Liou S.-K., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence of urcopathogenic Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plumkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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"The nucleotide sequence of greA, a suppressor gene that restores
growth of an Escherichia coli RNA polymerase mutant at high
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SPECIES=E.coli; STRAIN=C157:H7 / EDL933 / ATCC 700927;
SPECIES=E.coli; STRAIN=C11206551;
BRDLINE=21074935; Pubmed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Fosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECLESE.coli; STRAIN=K12;
Wang R., Kushner S.R.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein ybby.
YHBY OR B3180 OR C3937 OR Z4542 OR ECS4059 OR SF3220.
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Nucleic Acids Res. 18:6443-6443(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                     Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
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                                                                                                                                                                                                                                                       Escherichia coli 06,
Escherichia coli 0157:H7, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 64-97 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                          Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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15-JUL-1998
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                                                                                                                                                                                               YF50 MET
Q58945;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 38
GBGU BOVIN
                                                                                                                                                                   YFSO_METJA
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                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                 Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE M.JANNASCHII MJ0126 / MJ0128 / MJ0141
MJ0435 / MJ0604 / MJ1215 / MJ1217 / MJ1305 / MJ1379 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Mol. Biol. Rep. 13:336-342(1995).
-!- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, stramenopiles, Bacillariophyta, Coscinodiscophyceae,
Biddulphiophycidae, Eupodiscales, Eupodiscaceae, Odontella,
NCBI_TaxID=2839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 3.2e+02;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002934; NTP transf.
Pfam; PR01909; NTP transf 2; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 98 AA; 11604 MW; 0748F07131F29685 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FBB-1996 (Rel. 33, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
1-FBB-1996 (Rel. 33, Last annotation update)
Chloroplast 30S ribosomal protein S14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; iPR001209; Ribosomal S14.
Pfam; PF00253; Ribosomal S14; I.
PROSITE; PS00527; RIBOSOWAL S14; I.
Ribosomal protein; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.7%;
54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U67469; AAB98106.1; -.
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Best Local Similarity 60.v.
6; Conservative
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Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast.
                                                                               annaschii.
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RR14_ODG
RR16_ODG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
STRAIN=9633999; PubMed=8688089;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Rikhases E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
Complete genome sequence of the methanogenic archaeon, Methanococcus
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01-OCT-1996 (Rel. 34, Lat sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-T2 subunit (G gamma-C) (G-gamma-B).
GNGT2 OR GNG8 OR GNGT8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinne; Bos
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Pred. No. 2.8e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Archaea, Euryarchaeota, Methanococci, Methanococales,
Methanocaldococcaceae, Methanocaldococcus.
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Hypothetical protein; Complete proteome.
SEQUENCE 61 AA; 7106 MW; 52C0B8011E728F12 CRC64;
                                                                                                                                                                                                          (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                              61 AA.
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                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                           Hypothetical protein MJ1550.
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                                                                                                                                                                                                                                                                                                                                                                Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 ISKEKKEIKWIG 20
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                                                                                                                                                              STANDARD;
S SMIEREKKRIK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 5; Conserv
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Complete proteome.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                    Fung B.K.-K.;
"Molecular cloning and characterization of the G protein gamma subunit of come photoreceptors";
J. Biol. Chem. 270:8495-8500(1952).
-!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.
-!- SUBUNIT: G proteins are composed of 3 units (alpha, beta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FARNESYL (BY SĪMILARITY).
REMOVED IN MATURE FORM (BY SIMILARITY).
210C8319D1520314 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 407:757-762(2000).
-!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid biosynthesis (By similarity).
-!- PATHWAY: De novo fatty acid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
                                          MEDLINE=95238332; PubMed=7721746;
Ong O.C., Yamane H.K., Phan K.B., Fong H.K., Bok D., Lee R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 1; Length 69;
Pred. No. 3.2e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD003783; G-gamma; 1.
SMART; SM00224; GGL; 1.
PROSITE; PS50058; G PROTEIN GAMMA; 1.
Transducer; Prenylation; Lipoprotein; Multigene family.
                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE G PROTEIN GAMMA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Acyl carrier protein homolog (ACP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P02698; 1A0R.
InterPro; IPR001770; G-gamma.
Pfam; PP00631; G-gamma; I.
PRINTS; PR00321; GPROTEING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.7%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U20085; AAB61306.1; -. PIR; A56378; A56378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 AA; 7728 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 IISKEKKEIK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||| ||||
28 LISKTGKEIK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Serovar 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               urealyticum.";
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 [1]
SEQUENCE 1
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ID ACPH UR

DT 28-FEB-1

CO WCBI-TF

RP SEQUENC

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RR MEDLINE

RC CS -1-FUN

CC -1-FUN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibc.ch).
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J. Bid. Chem. 267:1056-10569 (1992).

J. Bid. Chem. 267:1056-10569 (1992).

J. Bid. Chem. 267:1056-10569 (1992).

C. I. FUNCTION: DOES NOT FUNCTION AS A GLUTATHIONE DISULFIDE
OXIDOREDUCTASE IN THE PRESENCE OF GLUTATHIONE AND GLUTATHIONE
C. REDUCTASE. MAY BE A COMPONENT OF A RIBONUCLEOTIDE-REDUCING SYSTEM
DISTINCT FROM THE PREVIOUSLY DESCRIBED SYSTEMS UTILIZING
THIOREDOXIN OR GLUTAREDOXIN.

C. I. SUBCELLULAR LOCATION: Cytoplasmic.
C. I. SUBCELLULAR LOCATION: Cytoplasmic.
C. I. SUBCELLULAR LOCATION: Cytoplasmic.
R. InterPro; IPR004502; Thio_glut.
R. InterPro; IPR004502; Thio_glut.
R. InterPro; IPR004602; Glutaredoxin.
R. InterPro; IPR004603; Glutaredoxin.
R. Ffam; PF00462; Glutaredoxin.
R. TIGRRAMS; TIGR00411; redox disulf. 1.
R. PROSITE; PS00199; GLUTAREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a small
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PTM: 4'-phosphopantetheine is transferred from CoA to a specific
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE002149; AAF30918.1; -.
InterPro; IPR006163; Pp_bind.
InterPro; IPR006162; Ppaintne_attach.
Plan; PF00550; pp-binding.1.
PROSITE; PS50075; ACP DOMAIN; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
Hypothetical protein; Fatty acid blosynthesis; Phosphopantetheine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHOPANTETHEINE (BY SIMILARITY) 3CDB655FBFA968C6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 15 REDOX-ACTIVE (BY SIMILARITY) 83 AA; 9147 MW; F538E8023A83F800 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 1; Length 83;
Pred. No. 3.8e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                             serine of the apo-ACP-like protein (Potential).
-!- SIMILARITY: Contains 1 acyl carrier domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable Thioredoxin (Glutaredoxin-like protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 1; I Pred. No. 3.5e+02; 3; Mismatches 4;
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DISULFID 12 15 REDOX-ACTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 30.7%;
Similarity 41.7%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 36
77 AA; 8750 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.7%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Cytochrome C6 (Soluble cytochrome f) (Cytochrome c553) (Cytochrome c553)
                                                                                                                                                                           Dorden D., Margoliash E.;
Submitted (DEC-1979) to the PIR data bank.
-!- FUNCTION: Functions as an electron carrier between membrane-bound cytochrome b6f and photosystem I in oxygenic photosynthesis (By
            Cytochrome C6 (Soluble cytochrome f) (Cytochrome c553) (Cytochrome c-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBCULLUIAR LOCATION: Cytoplasmic (Potential).
-:- SUBCELLUIAR LOCATION: Cytoplasmic (Potential).
-:- PIW: Binds one heme group per molecule.
-:- SIMILARITY: Belongs to the cytochrome c family. PetJ subfamily.
-- BIMILARITY: Belongs to the cytochrome c family. PetJ subfamily.
-- HSSP; P56534; IC6S.
-- HAMAP; MF 00594; -; 1.
-- InterPro; IPR0013329; Cyt CI.
-- InterPro; IPR0013329; Cyt CIC.
-- InterPro; IPR0013329; Cyt CIC.
-- InterPro; IPR001345; Cyt CIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aitken A.;
"Purification and primary structure of cytochrome c-552 from the cyanobacterium, Synechococcus PCC 6312.";
Eur. J. Biochem. 101:297-308(1979).
-i. FUNCTION: Functions as an electron carrier between membrane-b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEME (COVALENT).
HEME (COVALENT).
IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).
37713EC6405EBEEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechococcus sp. (strain PCC 6312 / ATCC 27167).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBL_TaxID=195253;
                                                                         Synechococcus lividus.
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBL_TaxID=33070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 1;
Pred. No. 4e+02;
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00034; cytochrome_C; 1.
PRINTS; PRODO605; CYTCHROMECIC.
PROSITE; PS00190; CYTCHROME C; 1.
Electron transport; Photosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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InterPro; IPR003088; Cyt CI.
InterPro; IPR002329; Cyt CIC.
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9129 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 46.7 hes 7; Conservative
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P00115;
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                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Delta H;

STRAIN=Delta H;

MEDLINE=98037544; PubMed=9371463;

Smith D.R., Doucete-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,

Smith D.R., Doucete-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,

A Aldredge, T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

A Harrison D., Hoang L., Keagle P., Lumm W., Pothlier B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

Jiwani N., Caruso A., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Woelling J., Reeve J.N.,

T. Gomplete genome sequence of Methanobacterium thermoautotrophicum

T. deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155 (1997).

-I. FUNCTION: ACTS TO MAINTAIN REDOX HOMEOSTASIS; FUNCTIONS AS A

PROFILE IN SEDUCHARE REDUCHASE (BY SIMILARITY).

-I. SUBCELLULAR LOCATION: CYtoplasmic (By similarity).

-I. SIMILARITY: BELONGS TO THE GLUTAREDOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriacae; Methanobacteriacae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redox-active center; Electron transport; Complete proteome.
INIT_MET 0 0 0 BY SIMILARITY.
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Pred. No. 3.9e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last annotation update)
Probable Thioredoxin (Glutaredoxin-like protein).
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(Rel. 01, Last sequence update)
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Last annotation updat
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Premis Provess, glucaredoxin; 1.
TIGREAMS; TIGRO0411; redox disulf_1; 1.
PROSITE; PSO0195; GLUTAREDOXIN; 1.
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InterPro; IPR002109; Glutaredoxin.
InterPro; IPR004502; Thio_glut.
InterPro; IPR006663; Thioredox_dom2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                              Created)
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17 MAIEVVDEAKKE 28
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                                      ||: :: : |||
17 MAIEVVDEAKKE 28
                                                                                                                                                        STANDARD;
              MAMNIISKEKKE 15
                                                                                                                                                                                              15-JUL-1998 (Rel. 36,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
hes 5; Conserv
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P00114;
21-JUL-1986
21-JUL-1986
                                                                                                                                                          THIO METTH
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DISULFID
SEQUENCE
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CYC6_SYNLI
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Matches
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SOTITE SOURCE COURT STANTANT SERVICE SOURCE SOURCE

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Length 87; 6; Indels

LIGAND). LIGAND).

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Query Match
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"Anomalies in amino acid sequences of small cytochromes c and cytochromes of term two species of purple photosynthetic bacteria.";

"Atomalies in amino acid sequences of small cytochromes c and cytochromes of from two species of purple photosynthetic bacteria.";

"Ature 278:661-662(1979)

"In The Cytochrome C2 IS FOUND MAINLY IN PURPLE, NONSULFUR, THE STOCHROME C2 IS FOUND MAINLY IN THE PHOTOSHORYLATION DATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATION PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATION PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATION CONTINUES OF CYTOCHROME C551 FROM PRESEUDOMONAS AND AZOTOBACTER THAN TO THE SEQUENCES OF CYTOCHROME C2 FROM OTHER SPECIES OF RHODOSPIRILLUM. PRINT, A000999; 4C51C.

"InterPro; IPR000398; CYt_Cheme_bind.

"RESPIRATION OF CYTOCHROME C; I."

"THE PRO; IPR000345; CYt_Cheme_bind.

"THE PROSULES PROORED C; I."

"THE PROSULES PROORED C; I."
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Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
Rhodocyclaceae; Rhodocyclus.
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Pred. No. 4.2e+02;
5; Mismatches 4; Indels
                                                                                                                                   Score 31; DB 1; Length 87;
Pred. No. 4e+02;
2; Mismatches 6; Indels
                                                                                 ABEME (COVALENT).
IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).
41FC9734E3DF83F2 CRC64;
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IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).
5A51C1E372162F9F CRC64;
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HEME (COVALENT).
IRON (HEME AXIAL
IRON (HEME AXIAL
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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BINDING 12 12 HEME (COVALE
InterPro; IPR000345; CytC heme bind. Pfam; PF00034; cytochrome_c; 1. PRINTS; PR00605; CYTCHROMECIC. PROSITE; PS00190; CYTOCHROME_C; 1. Blectron transport; Photosynthesis; BINDING
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58 58
87 AA; 9098 MW;
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Best Local Similarity 33.3%;
Matches 6; Conservative
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Best Local Similarity 46...
T; Conservative
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ID RPOL_METAC
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P00098;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 51935 / DSM 2834;

MEDLINE=21929760; PubMed=11932238;

A land J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

A lalen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., Maylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McKewan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Frry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

Pritchett M., Sowens K.R., Swanson R.V., Zinder S.H., Lander E.,

Metcalf W.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
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-!- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPOL / EUKARYOTIC RPB11/
RPC19 RNA POLYMERASE SUBUNIT FAMILY.
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Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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Pred. No. 4.2e+02;
5; Mismatches 4; Indels
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PROSITE; PS01154; RNA POL L 11KD; FALSE NEG.
Transferase; Transcription; DNA-directed RNA polymerase;
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28-FEB-2003 (Rel. 41, Created)
8-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase subunit L (EC 2.7.7.6)
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Job time : 7.33663 secs
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InterPro; IPR001306; RNA pol L.
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Genome Res. 12:532-542(2002).
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1: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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8: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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DP-1 transcription E2F activity inhib Soybean DP-1 prote Fragment from a wh DP-1 transcription Human liver peptid Human brain expres Human bone marrow Human bone marrow Human bone marrow Human bone marrow Human Drain expres E2F protein DP-1 transcription DEF domain consens E2F activity inhib Human DNA binding	Repressor protein Human DNA binding Repressor protein Tyrosine activation wheat E2F derived Human Getal protein Human Getal protein Human immune/haema Human colon cancer Staphylococcus epi Human colon cancer Staphylococcus aur Human from E5F E5F relat Human prostate can Propionibacterium Fuman brain express Polypeptide sequen	apoptosis; tumour;
AAW30517 AAW57052 AAX32163 AAX32163 AAB30505 ABB42955 ABM63859 AAW30509 AAW30509 AAW30509 AAW30509 AAW30509 AAW30509 AAW30509 AAW30500	ABB2986 ABB2987 AAUT8096 ABB2987 AARS6646 AAY44493 AAY44493 AAV25567 AAM06343 AAM2530 AAB53284 AAM79339 AAY565070 AAB80361 AAR80361 AAR80362 AAR80362 AAR80362 AAR80362 AAR80362	1506 standard; Peptide; 16 AA. 1506; T-1998 (first entry) transcription factor antagonist peptide H5. transcription factor; antagonist; E2F protein; proliferation; cardiovascular cell; restenosis; cal stent; therapy. Location/Qualifiers de
11000000000000000000000000000000000000	22 23 23 25 25 25 25 25 25 25 25 25 25 25 25 25	ide; 1 ry) or ant tor; a diovasClaim "Claim "6589.
	85 95 96 97 98 98 98 98 98 98 98 98 98 98	istandard; Peptide; 16 AA. i) 998 (first entry) unscription factor antagonis liferation; cardiovascular stent; therapy. c. iens. Location/Qualifiers 511 /note= "Claim 3" 716 /note= "Claim 3" 716 /note= "Claim 3" 998. 997; 97WO-GB03506.
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RESULT 3
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                                                                                                                           Peptide H5 comprises amino acid residues 168-183 in the DEF box (I) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07) containing one or both of 2 motifs (see AAW30502-03) of the DEF box are capable of antagonising the terrodimerisation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and a membrane translocation sequence (see AAW30508), expression vectors encoding (I)-(III) and host cells. (I)-(III) are used to therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardioplasty. (I)-(III) function by inactivating the DNA-binding cardioplasty. (I)-(III) function by inactivating the DNA-binding reagents as positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunoassay agents. Candagonists (I)-(III) to control DP levels in cells, particularly by gene therapy. When formulated with cytotoxic or cytostatic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                 Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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                                                                                                            Claim 4; Page 44; 55pp; English
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               La Thangue NB;
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Best Local Similarity 100.
Matches 16; Conservative
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                                      WPI; 1998-377596/32.
                                                                                                                                                                                                                                                                                                                                                                                                                    16 AA;
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                Bandara LR,
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Peptide H2 comprises amino acid residues 166-184 in the DEF box CC (I) (see AAW30501) of transcription factor DP1. Claimed peptides CC (II) (see AAW30504-07) containing one or both of 2 motifs (see CAW30504-07) containing one or both of 2 motifs (see CC AM330502-03) of the DEF box are capable of antagonising the CC claimed are variants of these peptides, especially containing the peterodimerisation of a DP protein with an E2F protein. Also CC claimed are variants of these peptides, especially containing CC claimed are translocation sequence (see AAW30508), expression vectors membrane translocation sequence (see AAW30508), expression vectors candiovascular cells. (I)-(III) are used to therapetrically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging condiovascular cells, either in vivo or in vitro, e.g. for purging treat or prevent restencies in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding activity of DP/E2F heterodimers. They are also used as research areagents, as positive controls in assays for identifying cartivity of DP/E2F dimerisation and as immunoassay agents. Also described is the use of sequences antisense to nucleic acids encoding (I)-(III) hearpy. When formulated with cytotoxic or cytostatic agents, (I)-(III) in the largely.
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                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 44; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I) - (III) enhance cell killing.
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                                                              La Thangue NB;
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Best Local Similarity 100.
Matches 16; Conservative
(PROL-) PROLIFIX LTD
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Modified-Bite
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                                                              Bandara LR,
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28 AA;
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                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                 Sequence
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                                                                                                             This represents a compound that can inhibit E2F activity. The compound also of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoyvarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumours
                                                                       activity inhibitors - for treatment and prevention of tumours
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                                                                                                                                                                                                                                                                                                                                                            inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                                      Length 28;
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                                                                                                                                                                                                     Score 76; DB 19;
Pred. No. 6.4e-08;
                                       Yoshida T;
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                                       Yamasaki M,
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                                                                                              Example 3; Page 27; 52pp; Japanese.
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                                                                                                                                                                                                                                                                                            AAW57055 standard; peptide; 28 AA
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100.0%;
                       (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                                                                                                                                                             Local Similarity 100.
nes 16; Conservative
                                      Mizukami T, Shibata K,
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                                                                                and arteriosclerosis
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                                                       WPI; 1998-240020/21
                                                                                                                                                                                     28 AA;
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         30-SEP-1996;
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This represents a compound that can inhibit E2F activity. The compound is of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide H (I) comprises residues 163-199, i.e. the DEF box region, of transcription factor DP1. Claimed fragments (II) (see AAW30502-07)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 76; DB 19;
Pred. No. 6.4e-08;
; Mismatches 0;
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROL-) PROLIFIX LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-377596/32.
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DP-1; transcription factor; antagonist; E2P protein; apoptosis; cell, proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                                                                                                                                                                                                                                       DP-1 transcription factor peptide H2mtl.
                                                                                                                                                            AAW30515 standard; Peptide; 19 AA.
             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                  26-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                          AAW30515;
                                                                                                                         RESULT 7
                                                                                                                                               AAW3053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide H2mt2 is based on peptide H2 (see AAW30504) from the DEF box residues of transcription factor DP1. In H2mt2, amino acid are sidues of H2 that correspond to DP1 residues Arg167 and Asp171 are substituted by Ala residues. H2 is an antagonist of the heterodimerisation of DP1 with E2F. H2mt2 recains some, but not all, of this antagonistic activity. H2 and other claimed peptides (see AAW30504-07) from the DEF box region of DP1 can be used to induce apoptosis, specifically in tumour and cardiovascular cells,
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
nucleic acids encoding (I)-(III) to control DP levels in cells, particularly by gene therapy. When formulated with cytotoxic or cytostatic agents, (I)-(III) enhance cell killing.
                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DP-1; transcription factor; B2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 19; Length 19;
pred. No. 1.5e-06;
0; Mismatches 1; Indels
                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP-1 transcription factor antagonist peptide H2mt2.
                                                                                                                         y Match 100.0%; Score 76; DB 19; Local Similarity 100.0%; Pred. No. 9.3e-08; hes 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "R167A mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "D171A mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g. for the prevention of restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example D; Page 26; 55pp; English
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                                                                                                                                                                                                                                                                                                                                                                    AAW30516 standard; Peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.8%;
Matches 15; Conservative
                                                                                                                                                                                                                     1 RVYDALNVLMAMNIIS 16
                                                                                                                                                                                                                                                           RVYDALNVLMAMNIIS 21
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                                                                                            37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9828334-A1
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                                                                                              Sequence
                                                                                                                                      Query Match
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Matches
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'note= "V169A mutation" Location/Qualifiers

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.5%; Score 68; DB 19; L
87.5%; Pred. No. 1.5e-06;
Live 0; Mismatches 2;
/note= "V175A mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example D; Page 26; 55pp; English.
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                                                                                                                                                                97WO-GB03506.
                                                                                                                                                                                                                       96GB-0026589
                                                                                                                                                                                                                                                                                                                                    La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                             (PROL-) PROLIFIX LTD.
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 AA;
                                                                                                                                                                      22-DEC-1997;
                                                                                                                                                                                                                       20-DEC-1996;
                                                               WO9828334-A1
                                                                                                                                                                                                                                                                                                                                    Bandara LR,
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0; Gaps

1 YDALNVLMAMNIIS 14

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(I) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07) containing one or both of 2 motifs (see AAW30504-07) containing one or both of 2 motifs (see AAW30504-07) containing one or both of 2 motifs (see AAW30504-07) containing one or both of 2 motifs (see AAW30504-03) of the DEF box are capable of antagonising the heterodimerisation of a DP protein with an BZP protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and membrane translocation sequence (see AAW30508), expression vectors cardiovascular cells. (I) (III) are used to therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging treat or prevent restenosis in patients who have undergone angioplasty. (I) (III) function by inactivating the DNA-binding activity of DP/BZP heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-1/EZP dimerisation and as immunossay agents. Also described is the use of sequences antisense to nucleic acids encoding (I) (III) to control DP levels in cells, particularly by gene therapy. When formulated with cytotoxic or cytostatic agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                 DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide H7 comprises amino acid residues 170-199 in the DEF box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 88.2%; Score 67; DB 19; Length 30; Best Local Similarity 100.0%; Pred. No. 4.2e-06; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   DP-1 transcription factor antagonist peptide H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                    AAW30507 standard; Peptide; 30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Claim 3"
5..15
/note= "Claim 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-GB03506
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                                                                                                                                                                             26-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9828334-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                          AAW30507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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AAW330507
XXD AAW30507
XXD AAW307
XXD AAW3
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Peptide H6 comprises amino acid residues 167-180 in the DEF box region (see AAW30501) of transcription factor DP1. Unlike claimed peptides (see AAW30504-07) that contain one or both of 2 motifs (see attagonism) of the DP1 DEF box, peptide H6 is not capable of antagonising the heterodimerisation of a DP protein with an E2F protein. The claimed peptides, their variants and fusion proteins can be used to induce apportosis, specifically in tumour and cardiovascular cells, e.g. to prevent restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                                                               DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19; Length 14;
6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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100.0%; Pred. No. 6e-
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP-1 transcription factor peptide H2mt3.
                                                                                    DP-1 transcription factor peptide H6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example C; Page 41; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW30517 standard; Peptide; 19 AA.
AAW30511 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                         97WO-GB03506.
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                                                                                                                                                                                                                                                                                                     96GB-0026589
                                                                                                                                                                                                                                                                                                                                                           La Thangue NB;
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                                                        26-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Conservative
                                                                                                                                            surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                 (PROL-) PROLIFIX LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14 AA;
                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                  WO9828334-A1.
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                                                                                                                                                                        Synthetic.
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                            AAW30511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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3 YDALNVLMAMNIIS 16

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Gaps

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This represents a compound that can inhibit E2F activity. The compound is of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                             E2F activity inhibitors - for treatment and prevention of tumours and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.3%; Score 58; DB 19; Length 15
100.0%; Pred. No. 0.0001;
.ive. 0; Mismatches 0; Indele
                                                                                                                                                                Yoshida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DP-1; soybean; cell cycle regulatory protein;
transcription factor; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "encoded by NAT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "encoded by GGN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "encoded by GNC"
                                                                                                                                                                Shibata K, Yamasaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "encoded by
                                                                                                                                                                                                                                                                                                    Example 4; Page 28; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY32163 standard; Protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soybean DP-1 protein fragment
                                                                                                                             (KYOW ) KYOWĄ HAKKO KOGYO KK
                                                  97WO-JP03442.
                                                                                       96JP-0259432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RVYDALNVLMAM 12
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                                                                                                                                                                                                      WPI; 1998-240020/21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 AA;
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Misc-difference
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                                                  26-SEP-1997;
                                                                                                                                                                    Mizukami T,
                09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY32163;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide HZmt3 is based on peptide H2 (see AAW30504) from the DEF box (see AAW30501) of transcription factor DP1. In HZmt3, amino acid residues of H2 that correspond to DP1 residues Leu173 and Leu176 are substituted by Arg residues. H2 is an antagonist of the heterodimerisation of DP1 with E2F. H2mt3 has none of the antagonistic activity of H2. H2 and other claimed peptides (see AAW30504-07) from the DEF box region of DP1 can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g. for the prevention of restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E2F activity; inhibitor; treatment; tumour; arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

84.2%; Score 64; DB 19; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.9e-06;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                   'note= "L173R mutation"
                                                                                                                                                          /note= "L176R mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2F activity inhibiting compound Ib-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAWS7052 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example D; Page 26; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RVYDALNVLMAMNIIS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RVYDARNVRMAMNIIS 18
                                                                                                                                                                                                                                                                         97WO-GB03506
                                                                                                                                                                                                                                                                                                                96GB-0026589
                                                                                                                                                                                                                                                                                                                                                                                         La Thangue NB;
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                                                                                                                                                                                                                                                                                                                                                       (PROL-) PROLIFIX LID
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-377596/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AA;
                                                                                                                                          Misc-difference
                                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-1998
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                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                20-DEC-1996;
                                                                                                                                                                                                  WO9828334-A1
                                                                                                                                                                                                                                                                                                                                                                                             Bandara LR,
                                                                                                                                                                                                                                       02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                            Synthetic
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RESULT 11 AAW57052

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Gaps

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Length 15;

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New isolated, enriched, cell free and/or recombinant nucleic acid useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size -
                                                                                                                                                                                                                                                                                                                                                                                       AB67764-68 represent fragments of a wheat E2F-dimerisation partner (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be modulated to alter plant cell, organ or tissue shape, and alter plant cell, organ or tissue shape, and alter plant cell, organ or tissue shape, and alter plant cell, organ or tissue shape.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.4%; Score 55; DB 22; Length 56; 62.5%; Pred. No. 0.0023; ive 4; Mismatches 2; Indels
                                                                                                                                  (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DP-1 transcription factor antagonist peptide H3.
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                                                                                                                                                                            Ramirez-Parra
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                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 50; 77pp; English.
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/note= "Claim 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-2000; 2000WO-EP09325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-GB03506
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                                                                            99ES-0002127
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les 10; Conservative
                                                                                                                                                                            Gutierrez-Armenta C,
                                                                                                                                                                                                                 WPI; 2001-257972/26.
N-PSDB; AAF80148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 AA;
                                                                            24-SEP-1999;
11-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1997;
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29-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents 42% of the middle region of soybean cell cycle regulatory protein DP-1, as deduced from an isolated CDNA clone (see AAZ34575-9). The invention relates to nucleic acid fragments (see AAZ34575-83) encoding plant CDC-16, DP-1, DP-2 and E2F cell cycle regulatory proteins (see AAX32159-67). It also calates to the construction of a chimeric gene encoding all or a portion of the cell cycle regulatory protein, in sense or antisense corientation, where expression of the chimeric gene results in producton of altered levels of the cell cycle regulatory protein in a transformed host cell. The nucleic acids and proteins may be used to facilitate studies of cell cycle regulation in plants, provide genetic tools to enhance cell growth in tissue culture, increase gene transfer efficiency and provide more stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transformations. The proteins may also provide targets to facilitate design and/or identification of cell cycle regulatory proteins that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fragment from a wheat E2F-dimerisation partner (DP) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.7%; Score 56; DB 20; Length 83; 81.2%; Pred. No. 0.0024; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                          Sakai H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant-derived cell cycle regulatory proteins
/note= "encoded by NAT"
                                       "encoded by GNG"
                                                                                                                                                                                                                                                                                                                 (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                        Odell JT,
                                                                          'note= "encoded by
                                                                                                                  /note= "encoded by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 41; 44pp; English
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                                                                                                                                                                                                                                    99WO-US07638.
                                                                                                                                                                                                                                                                           98US-0081132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                        Klein TM, Morakinyo LO,
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les 13; Conservative
                                       note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ34579
                  Misc-difference
                                                        Misc-difference
                                                                                               Misc-difference
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                                                                                                                                                                                                                                      08-APR-1999;
                                                                                                                                                                                                                                                                           09-APR-1998;
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                                                                                                                                                         WO9953075-A2
                                                                                                                                                                                                 21-OCT-1999
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Matches

ઠ 셤 RESULT 13 AAB67766

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Gaps

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Query Match
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Matches
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                                                                                                                                    Peptide H3 comprises amino acid residues 174-193 in the DEF box (I) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07) containing one or both of 2 motifs (see AAW30502-03) of the DFF box are capable of antagonising the heterodimerisation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding respectably containing and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and a membrane translocation sequence (see AAW30508), expression vectors encoding (I)-(III) and host cells. (I)-(III) are used to therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding cartivity of DP-I/E2F dimerisation and as immunoassay agents.

Also described is the use of sequences antisense to nucleic acide encoding (I)-(III) to control DP levels in cells, particularly by gene therapy. When formulated with cytotoxic or cytostatic agents, cells (I)-(III) enhance cell killing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    60.5%; Score 46; DB 19; Length 20; 100.0%; Pred. No. 0.034; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human liver peptide, SEQ ID No 37013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG58365 standard; Peptide; 96 AA.
                                                                                                                     Claim 4; Page 44; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00664.
                            Bandara LR, La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.5
Best Local Similarity 100.
Matches 10; Conservative
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   (PROL-) PROLIFIX LTD.
                                                 WPI; 1998-377596/32
                                                                                                                                                                                                                                                                                                                                                                                                                 20 AA;
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.5%; Score 46; DB 22;
43.8%; Pred. No. 0.28;
iive 7; Mismatches 2;
                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID No 37013; 658pp; English
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                                                                                                   DR;
                                                                                                   Rank
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                                               (MOLE-) MOLECULAR DYNAMICS INC.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                      Chen W,
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04-OCT-2000; 2000GB-0024263.
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| RIYDIVNVLESLHLVS
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nes 7; Conserva
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                                                                                                      Hanzel DK,
                                                                                                                                                        WPI; 2001-488898/53
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the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                         AAM76672;
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                                                     Sequence
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                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe encoded protein SEQ ID NO: 35964.
                                                                                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
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                                                                      Claim 27; SEQ ID NO 35590; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                  60.5%; Score 46; DB 22; Length 96; 43.8%; Pred. No. 0.28; ive 7; Mismatches 2; Indels
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
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27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                             96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epilepsy; cancer
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                                                                                                                                                                                                                                                                                                                                                             Sequence
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IID AAM6

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AAM6

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                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone marrow expressed probe encoded protein SEQ ID NO: 36978.
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43.8%; Pred. No. 0.28;
rive 7; Mismatches 2; Indels
     22; Length 96;
                                                        2; Indels
     Score 46; DB 22
Pred. No. 0.28;
                                                           7; Mismatches
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                                                                                                                                                                                                                                                                                                          AAM76672 standard; Protein; 96 AA
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RIYDIVNVLESLHLVS 20
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RIYDIVNVLESLHLVS 20
     60.5%;
43.8%;
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30-UJN-2000; 2000US-0608408.
23-AUG-2000; 2000US-053366.
21-SRP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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                                                                                                              1 RVYDALNVLMAMNIIS
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Matches 7; Conservative
                                                           7; Conservative
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Query Match
Best Local Similarity
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                                                                                Peptide #10814 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human peptide encoded by genome-derived single exon probe SEQ ID 35546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, single exon probe; asthma; lung cancer; COPD; LLD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous aclarosis; daucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.5%; Score 46; DB 22; Length 96; 43.8%; Pred. No. 0.28; 2; Indels tive 7; Mismatches 2; Indels
                                                                                                             Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        claim 27; SEQ ID No 37046; 654pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Rank
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AAM36777 standard; Protein; 96 AA.
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27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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2000US-0608408.
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5 RIYDIVNVLESLHLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 AA;
                                                                                                                               genetic disorder
                                                                                                                                                                                          WO200157272-A2
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                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                              AAM36777;
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived cuche nucleic acid probes for measuring gene expression in a manple derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes; the novel set of probes which hybridise at high extragency to a nucleic acid expression in the human lung, comprising (a) contacting the novel set of probes which hybridise at high extragent of a collection of detectably labeled nucleic acid derived from human lung, comprising (a) contacting the array with a complete care of the label detectably bound to each probe of the array; identifying exons in a eukaryotic genomic sequences of the eukaryote; and (b) detecting at least one exon from genomic sequence of the eukaryote; and (b) detecting at least one exon from genomic sequence of the eukaryote; and (b) detecting at least one exon from genomic sequence by the method copprising (a) identifying exons to a single exon probe, having a fragment identical to the predicted exon, the probe is included copprising (b) measuring the expression of each of the exons in several compression of the exons in the tissues and/or cell types using hybridisation to a single exon in several copperator of the exons in the tissues and/or cell types using hybridisation to a single exon in expression of the exons in the tissues and/or cell types using frames (lip). The probes are used for gene of 12011 sequences, mentioned in the specification, or encoded by the expression analysis, and for the set suddy or cell types using frames (lip). The probes are used for gene or probes/open reading frames (lip). The probes are used for gene or probes/open reading frames (lip). The probes are used for gene or such as asthma. Jung cancer, chronic obstructive pulmonary dysplasis, primary chilary dysplasis, primary chilary dy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
primary ciliary dyskinesis; pulmonary hypertension;
hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID No 35546; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                     30-JAN-2001; 2001WO-US00665.
                                                                                                                                                                                                                                            2000US-207456P.
2000US-0608408
                                                                                                                                                                                                                                                                                 2000US-0632366
2000US-234687P
                                                                                                                                                                                                                                                                                                                         27-SEP-2000; 2000US-236359P-04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                       Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-114183/15.
                                                                                                       WO200186003-A2
                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                   30-JUN-2000;
                                                                                                                                                                                                                                                                                                        21-SEP-2000;
                                                                                                                                                                                                                                                 26-MAY-2000;
                                                                                                                                                15-NOV-2001.
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96 AA

Sequence

RESULT 21

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This sequence represents 10% of the middle region of soybean cell cycle regulatory protein E2F, as deduced from an isolated cDNA clone (see AAZ34583). The invention relates to nucleic acid fragments (see AAZ34575-93) encoding plant CDC-16, DP-1, DP-2 and E2F cell cycle regulatory proteins (see AAX32159-67). It also relates to the construction of a chimeric gene encoding all or a portion of the cell cycle regulatory protein, in sense or antisense orientation, where expression of the chimeric gene results in producton of altered levels of the cell cycle regulatory protein in a transformed host cell. The nucleic acids and proteins may be used to facilitate studies of cell cycle regulation in plants, provide genetic tools to enhance cell growth in tissue culture, increase gene transfer efficiency and provide more stable
                                                            soybean; cell cycle regulatory protein; transcription factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transformătions. The proteins mây also provide targets to
facilitate design and/or identification of cell cycle regulatory
proteins that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.9%; Score 44; DB 20; Length 80; Best Local Similarity 43.8%; Pred. No. 0.54; Matches 7; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP-1 transcription factor antagonist peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant-derived cell cycle regulatory proteins
                                                                                                                                                                                                                                                                                                                                                    Odell JT, Sakai
                                                                                                                                                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 44-45; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW30502 standard; Peptide; 9 AA.
                        Soybean E2F protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 RIYDIVNVLESIGVLS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RVYDALNVLMAMNIIS 16
                                                                                                                                                                                                                                    99WO-US07638.
                                                                                                                                                                                                                                                                          98US-0081132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                      Klein TM, Morakinyo LO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            surgical stent; therapy
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-633830/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ34583
                                                                                                                                                                                                                                    08-APR-1999;
                                                                                                                                                                                                                                                                          09-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9828334-A1
                                                                                                                                                                                              21-OCT-1999
                                                                                                                      Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW30502;
                                                              E2F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PXSSXXXXXXXXXXXXXXX
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide H1 comprises amino acid residues 166-176 in the DEF box region (see AAW30501) of transcription factor DP1. Unlike claimed peptides (see AAW30504-07) that contain one or both of 2 motifs (see AAW30502-03) of the DP1 DBF box, peptide H1 is not capable of antagonising the heterodimerisation of a DP protein with an B2P protein. The claimed peptides, their variants and fusion proteins can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g. to prevent restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                    DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
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100.0%; Pred. No. 0.038;
tive 0; Mismatches 0; Indels
60.5%; Score 46; DB 23; Length 96; 43.8%; Pred. No. 0.28; tive 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                DP-1 transcription factor peptide H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example C; Page 41; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY32167 standard; Protein; 80 AA.
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                                    7;
                                                                                                                                                                                                              AAW30509 standard; Peptide; 11
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RIYDIVNVLESLHLVS 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96GB-0026589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bandara LR, La Thangue NB;
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                                                                                                                                                                                                                                                                                          (first entry)
                                                                              1 RVYDALNVLMAMNIIS
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100
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Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RVYDALNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                          26-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9828334-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                    AAW30509;
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Matches

RESULT 22

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AAY32167
ID AAY3
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AC AAY3
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Bandara LR, La Thangue NB;
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Best Local Similarity 100.
                                                                                                                                                                                               (PROL-) PROLIFIX LTD.
                                                                                                                                                                                                                                                                                                           4PI; 1998-377596/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2002
                                                                                   22-DEC-1997;
                                                                                                                                         10-DEC-1996;
                             02-JUL-1998.
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The invention relates to a novel cell cycle protein (CCP) and the polymetric conditions are according them. CCP is useful for identifying a compound which but a carrivity of the polymetride and which bluds to the polymetride and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for modulating the cell polymetride and an anti-CCP antibody is useful for modulating the cell of CCP in a sample. A CCP modulator such as Arabidopsis thalians, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CC crossist control of CCP protein control of CCP modulating of CCP modulating cell cycle progression in plants. CCP is useful to agents in regulating cell cycle progression in plants. CCP is useful to compound that bind to or modulate the activity. Compounds that bind to or modulate the activity of CCP protein forms which have decreased or cCC protein corner with a control of CCP polypepide are useful as herbicides or plant growth regulators. CC cCP polypepide are useful as herbicides or plant growth regulators. CC cCP polypepide are useful for modifying cell face, plant development, the polymorlectical substance of the cell cycle of a plant, initiation, shoot and or development, thouse, fruit, leaf formation, seed set, initiation and/or development, though function, dwarfism in plants. CS seed size, seed development, thouse, fruit, leaf formation, seed set, cand the anti-CCP antibody are useful in agriculture to modulate the contribution and seed development, and application, and set of a protein involved in the cell cycle due content and seed development, seed about a strass such as pathogen at tack, to modulate set. Grants or the path of a continion, had attended to strasse such as pathogen at actack, to modulate set. Grants or the path of contrained contents of strasses such as a such as an immunogen to generate antibodies. CCP protein is useful to represents a motif which may be found in a CCP protein in a CCP protein to a continity or cour
                                                                                                                                                                                                                                  New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 53.9%; Score 41; DB 23; Length 35; Local Similarity 66.7%; Pred. No. 0.7; conservative 0; Mismatches 5; Indels
                                                                                                                               Acosta JAT, Magyar Z;
                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 25; 316pp; English
                                                                                                                                     De Veylder L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAWS7054 standard; peptide; 29 AA
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                    12-MAY-2000; 2000US-204045P.
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                                                                                (CROP-) CROPDESIGN NV
                                                                                                                                     Boudolf V,
                                                                                                                                                                                              WPI; 2002-062249/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 AA;
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                                                                                                                                     Inze D,
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Matches
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SXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This peptide comprises amino acid residues 175-183 in the DEF box region (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30502-07) containing this and/or another motif (see AAW30503-06 the DEF box, are antagonists of the heterodimeriation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and a membrane translocation proteins (III) comprising (I) or (II) and a membrane translocation proteins (III) are used therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vivo. e.g. for purging bone marrow. Surgical stens comprising (I)-(III) are used the purging bone marrow. Surgical stens comprising (I)-(III) are used to treat or prevent restencists in patients who have undergone angioplasty. (I)-(III) function by inactivating the DPAEP heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunoassay capents. Also described is the use of sequences antisense to mucleic acids encoding (I)-(III) to control DP levels in cells, incleasing chartcularly by gene therapy. When formulated with cytotoxic
                                                                                                                                                                                                                                                                                                                                                                 Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or cytostatic agents, (I)-(III) enhance cell killing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU72601 standard; Peptide; 35 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 44; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEF domain consensus sequence.
                                                                                               97WO-GB03506.
                                                                                                                                                       96GB-0026589
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E2F activity; inhibitor; treatment; tumour; arteriosclerosis.

Synthetic.

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14-MAY-2001; 2001WO-IB01307

WO200185946-A2.

15-NOV-2001.

E2F activity inhibiting compound Ia-3.

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Yoshida

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This represents a compound that can inhibit E2F activity. The compound also of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoyycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, telomerase reverse transcriptase; TERT; Site C; Progeria; burn; repressor binding site; Hutchinson-Gilford syndrome; AIDS; cancer; acquired immunodeliciency syndrome; cardiovascular disease; osteoporosis; skin rejuvenation; immune senescence; bone marrow transplant; skin graft; neoplastic disease; TERT minimal promoter; DNA binding domain; E2F-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating expression of telomerase reverse transcriptase (TERT) in a
                                                                                                                                         activity inhibitors - for treatment and prevention of tumours
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                                                                                                                                                                                                                                                                                                                                                                                             51.3%; Score 39; DB 1
43.8%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
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/label= DNA_binding_domain
                                                                            Yamasaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                     Example 1; Page 24; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU78095 standard; Protein; 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DNA binding domain E2F-1.
                                             (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RVYDALNVLMAMNIIS 16
                 96JP-0259432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-2000; 2000US-227865P.
01-SEP-2000; 2000US-230174P.
05-OCT-2000; 2000US-238345P.
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14 RIYDITNVLEGIQLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foster CA,
                                                                            Shibata K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SIER-) SIERRA SCI INC.
                                                                                                                                                         and arteriosclerosis
                                                                                                           WPI; 1998-240020/21
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                                                                                                                                                                                                                                                                                                                                                              29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200216657-A1
                30-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                            Mizukami T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andrews WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU78095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        is of the formula R1 - A - R2 where R1 is an optionally substituted altanoyl, alloyl, alloyl, hetero-arylcarbonyl, altoxycarbonyl, arylcxycarbonyl, hetero-arylcxycarbonyl, or M. R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding capion, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                         This represents a compound that can inhibit E2F activity. The compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                         E2F activity inhibitors - for treatment and prevention of tumours and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B2F activity; inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 19; Length 29;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                              Yoshida
                                                            /note= "N-terminal,lauroyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "N-terminal acetyl"
                                                                                        /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2F activity inhibiting compound Ia-1.
                                                                                                                                                                                                                                                                              Yamasaki M,
                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW57049 standard; peptide; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.3%;
                                                                                                                                                                                     97WO-JP03442.
                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KK
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14 RIYDITNVLEGIQLIA
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Matches 7; Conservative
                                                                                                                                                                                                                                                                              Mizukami T, Shibata K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                             WPI; 1998-240020/21
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                                          Modified-site
                                                                         Modified-site
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Homo sapiens
                                                                                                                       WO9814474-A1
                                                                                                                                                                                     26-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Gaps

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Indels

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DB 19; Length 29;

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The present invention relates to a new method of modulating expression of telomerase reverse transcriptase (TERT) from a TERT expression system that includes a TERT promoter and a Site C repressor binding site. The method of the invention involves modulating TERT transcription repression to be the invention is consisted to be a site. The method of the invention is consisted to be a site. The method of the invention is consisted to be a strength of the invention is consisted to be a site. The method is also useful in a variety of different applications, including immortalisation of cells, production of reagents of or use in life science research, therapeutic applications, and therapeutic applications, increases telomeric length and cellsys natural telomeric shortening and/or increases telomeric length and is useful for treating disease conditions such as Progeria or the proper disease, osteoporosis, in skin rejuvenation and to inhibit cardiovascular disease, osteoporosis, in skin rejuvenation and to inhibit of proper remodeling and reinforcement, and can thus be used in bone marrow and sense tem cells, encouraging bone replacement and continue and such the method improves the survival and effectiveness of continue and skin deficiency such and stin cell transplants. Decreasing TERT expression is needful for treating cellular prolliferative disease conditions, including concern the present amino acid cegerane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Telomerase reverse transcriptase; TERT; Site C repressor; transcription; cytostatic; immunostimulant; anti-HIV; vulnerary; telomerase; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating expression of telomerase reverse transcriptase TERT by blocking repression of TERT transcription, useful for the diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
cell, for regulating proliferative capacity of a cell, involves modulating TERT transcription repression by Site C repressor binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.3%; Score 39; DB 23; Length 85; 43.8%; Pred. No. 5.7; Live 4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB82986 standard; Protein; 85 AA
                                                                           Disclosure; Page 8; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RVYDALNVLMAMNIIS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|| ||| ::|:
57 RIYDITNVLEGIQLIA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-2002; 2002WO-US17959
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 AA;
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ABB82986
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                                                                                      transcriptuse (TERT) expression system that includes a TERT promoter and a Site C repressor binding site. The method involves modulating TERT transcription repression by the Site C repressor binding site. The method and compositions of the present invention are useful for the immortalization of tells, production of reagents in life schence research, therapeutic agent screening applications, diagnosis and treatment of disorders associated with aberrant telomerases activity such as cancer, Progeria, immune senescence, HIV, and in skin rejuvenation. The present sequence represents the DNA binding domain of a repressor protein E2F-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modulating expression of telomerase reverse transcriptase (TERT) in a cell, for regulating proliferative capacity of a cell, involves modulating TERT transcription repression by Site C repressor binding
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treatment of disorders associated with aberrant telomerase activity such as cancer and \ensuremath{\mathrm{HIV}} -
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                                                                                   The invention relates to modulating expression of telomerase
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                                                                                                                                                                                                                                                                                                                                    5; Indels
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                                                                                                                                                                                                                                                                                                   Score 39; DB 2; Pred. No. 5.7; 4; Mismatches
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/label= DNA_binding_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU78096 standard; Protein; 76 AA.
                                                    Disclosure; Page 7; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DNA binding domain E2F-4.
                                                                                                                                                                                                                                                                                                        51.3%;
                                                                                                                                                                                                                                                                                                                                                                      1 RVYDALNVLMAMNIIS 16
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01-SEP-2000; 2000US-230174P.
05-OCT-2000; 2000US-238345P.
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                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 43.5
Local Similarity 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SIER-) SIERRA SCI INC.
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                                                                                                                                                                                                                                                                            85 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2002
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                                                                                                                                                                                                                                                                              Sequence
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The present invention relates to a new method of modulating expression of telomerase reverse transcriptase (TERT) from a TERT expression system that includes a TERT promoter and a Site C repressor binding site. The method of the invention is needed to the invention involves modulating TERT transcription repression by the Site C repressor binding site. The method of the invention is caseful for modulating expression of TERT for producting a mammalian antibody. The method is also useful in a variety of different applications, including immortalisation of cells, production of reagents of the repentic agent screening applications. Increasing TERT expression delays natural telomeric shortening and/or increases telomeric length and the useful for treating disease conditions such as Progeria or cardiovascular disease, osteoporosis, in skin rejuvenation and to inhibit immune sensescence. The method can be employed to lengthen telomerse of osteoblast and osteoclast stem cells, encouraging bous replacement and proper remodeling and reinforcement, and can thus be used in bone marrow transplants for the treatment of cancer and skin grafts for burn victims and as such the method improves the survival and effectiveness of the merrow and skin cell transplants. Decreasing TERT expression is useful for treating cellular proliferative disease conditions, including cellular proliferative disease conditions, including cepace represents the human DNA binding domain E2F-4. ö Gaps ö 23; Length 76; 5; Indels Score 38; DB Pred. No. 7.7; 3; Mismatches 50.0%; 1 RVYDALNVLMAMNII 15 |:|| || :| RIYDITNVLEGIGLI 61 Query Match
Best Local Similarity 46...
7; Conservative 76 AA; 47 Sequence g

Repressor protein E2F-4 DNA binding domain. ABB82987 standard; Protein; 76 AA. (first entry) repressor protein; E2F-4. 14-APR-2003 Homo sapiens ABB82987;

transcription; Telomerase reverse transcriptase; TERT; Site C repressor; transcript cytostatic; immunostimulant; anti-HIV; vulnerary; telomerase; human;

WO2002101010-A2

06-JUN-2002; 2002WO-US17959. 19-DEC-2002.

07-JUN-2001; 2001US-296992P.

(SIER-) SIERRA SCI INC

Foster CA, Fraser S,

Mohammadpour H, Andrews WH;

Modulating expression of telomerase reverse transcriptase TERT by blocking repression of TERT transcription, useful for the diagnosis treatment of disorders associated with aberrant telomerase activity such as cancer and HIV WPI; 2003-167401/16. Modulating

and

Disclosure; Page 7; 47pp; English.

The invention relates to modulating expression of telomerase reverse

ö ö transcriptase (TERT) expression system that includes a TERT promoter and a Site C repressor binding site. The method involves modulating TERT transcription repression by the Site C repressor binding site. The methods and compositions of the present invention are useful for the immortalization of cells, production of reagents in life science research, therapeutic agent screening applications, diagnosis and treatment of disorders associated with aberrant telomerase activity such as cancer, progeria, immune senescence, HIV, and in skin rejuvenation. as cancer, Progeria, immune senescence, HIV, and in skin rejuvenation. The present sequence represents the DNA binding domain of a repressor protein E2F-4. associated with immune responses and inflammation, e.g. arthritis, systemic lupus erthyematosus, asthma, inflammatory bowel disease, allergies, allograft rejection, etc. This peptide probably prevents natural activation of target proteins so inhibit signal transduction. (Updated on 25-MAR-2003 to correct PN field.) Gaps Gaps Sundaramoorthi R, Dalgarno DC, Zydowsky LD; ል ö ; 0 New tyrosine activation motif analogues - for treating and preventing immune and inflammatory disorders, e.g. allergies, inhibiting activation of mast cells, lymphocytes, etc. Tyrosine activation motif mimic; arthritis; asthma; allergy; systemic lupus erythematosus; inflammatory bowe; disease; allograft rejection; antiinflammatory. DB 15; Length 24; DB 24; Length 76; This TAM mimic may be used to treat or prevent conditions Indels Indels Tyrosine activation motif mimic Fc-epsilon-RI-beta. ., 2 5 Similarity 63.6%; Score 37; DB 3 Similarity 63.6%; Pred. No. 2.6; 7; Conservative 2; Mismatches 3; Mismatches 50.0%; Score 38; 46.7%; Pred. No. AAR56646 standard; peptide; 24 AA. English 94WO-US01025. 93US-0013414. 1 RVYDALNVLMAMNII 15 RIYDITNVLEGIGLI 61 (first entry) Local Similarity 46.7 tes 7; Conservative Claim 10; Page 75; 94pp; (ARIA-) ARIAD PHARM INC (updated) , Tao G, Green OM; WPI; 1994-264027/32. Query Match Best Local Similarity Matches 7; Conserv 24 AA; 76 AA; WO9417095-A1. 28-JAN-1994; 29-JAN-1993; 25-MAR-2003 23-MAR-1995 04-AUG-1994 Weigele M, AAR56646; Sequence Green J, Sequence Query Match Best Loc Matches 888888888888888 ઠ

(first entry)

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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human polypeptides and polymucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                            Human ORFX protein sequence SEQ ID NO:1490.
                         ABP00754 standard; Protein; 88 AA.
                                                                                                                                                                                                                                                                                               29-MAY-2001; 2001WO-US10836.
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                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                       2002-106308/14.
                                                                                                                                                                                                       myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABN16506
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29-AUG-2000;
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                                                                          25-JUN-2002
                                                  ABP00754;
      RESULT 33
                 4BP00754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Regulating plant growth and/or cellular DNA replication and/or cell cycle progression, differentiation and development using a plant E2F polypeptide -
                                                                                                                                                                      Wheat; transcription factor; TME2F; plant retinoblastoma; plant E2F; Rb protein; cell cycle regulation; plant growth regulation; DNA replication; differentiation; E2F-derived peptide; DNA binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.7%; Score 37; DB 21; Length 28;
46.7%; Pred. No. 3.2;
iive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ramirez Parra E;
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                AAY44493 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 26; 45pp; English.
                                                                                                                                                                                                                                                                                                       'label= Unknown
                                                                                                                                                                                                                                                                                                                            label= Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-EP03158.
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                                                                                                                                                     Wheat E2F derived peptide-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 46.77
Local 7, Conservative
                                                                                                                             (first entry)
RVYDALNVLMA 11
            3 RVYEELNILSA 13
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                                                                                                                                                                                                                                    Triticum monococcum.
                                                                                                                                                                                                                                                                                                                                         Misc-difference 25
                                                                                                                                                                                                                                                                                                                  Misc-difference 27
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                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                     Misc-difference
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11-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                            WO9958681-A2
                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-1999;
                                                                                                                               27-MAR-2000
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                                                                                                        AAY44493;
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2000US-206132P. 2000US-228716P.

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27522 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated (sorder in humans, and in the manufacture of a medicament for treating a disorder in humans, and in the manufacture of a medicament for treating a sequences can be used in gene therapy. ORFX sequences can be used in the therapy. ORFX sequences can be used in the creating a sequences can be used in gene therapy. ORFX sequences can be used in the creatment of cancer, hyperproliferative disorders, cirrhosis of liver, treatment of cancer, hyperproliferative disorders, isorders, pasenorrhage, osteoarthritis, neurodegenerative disorders, disorders pasted to organ cramplantation, cardiovascular diseases, disorders related to organ cramplantation, cardiovascular diseases, disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid disease, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut creating on triating disease. ORFX proteins are also creatision injury in various tissues and conditions resulting from the man and treatment of flung or liver fibrosis, and man and present and conditions resulting from the man and conditions anotation and conditions and conditions and conditions and conditio
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Disclosure; SEQ ID 1490; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 AA;
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1 RVYDALNVLMAMNII 15 |:|| ||| ::| 4 RIYDITNVLEGIXLI 18

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19-MAY-2000;
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22-AUG-2000;
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                                                                                    18-DEC-2001
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                                                                                                                                                                                                        cytostatic.
                                                        AAU22567;
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                                                                                                                                                                                                                                                                             Human; foetal protein; cytostatic; immunosuppressive; immunostimulant; noctropic; neuroprotective; thrombolytic; osteopathic; antiinflammatory; gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder; nervous system disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune disorders, growth disorders, thrombolytic disorders, nervous system disorders and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel foetal polypeptides encoded by polynucleotides comprising one of 477 sequences fully defined in the specification. The foetal polynucleotides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present sequence is a polypeptide encoded by a cDNA assembled using an expressed sequence tag (EST) found to be expressed in human foetal tissue cDNA libraries.
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                              Gaps
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Zhou P, Werhman T;
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DB 23; Length 88;
                             Indels
47.4%; Score 36; DB 42.9%; Pred. No. 23; ive 5; Mismatches
                                                                                                                                                                                                                                                   Human foetal protein, SEQ ID NO: 74.
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                                                                                                                                                            AAM06343 standard; Protein; 52
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15-SEP-2000; 2000US-0663870.
06-NOV-2000; 2000US-0707351.
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                                                        3 YDALNVLMAMNIIS 16
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30 YSSLNLAMAVQVIA 43
                                                                                                                                                                                                                      (first entry)
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                             6; Conservative
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Asundi V,
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Les 5; Conserv
            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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 Query Match
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                Best Loc
Matches
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Matches
                                                                                                                               RESULT 34
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MAU22667,

AM MAZ267,

AM MAZ267,

Movel human colon associated polypeptide #100.

Movel human colon septimen colon associated polypeptide #100.

Movel human colon associated polypeptide #100.

Movel human colon septimen colon associated polypeptide #100.

Movel human colon septimen colon sept
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08-NOV-2000; 2000US-0246610.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246613.
17-NOV-2000; 2000US-0246613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-CCT-2000; 2000US-0241808.
20-CCT-2000; 2000US-0241809.
20-CCT-2000; 2000US-0241809.
01-NOV-2000; 2000US-0246474.
08-NOV-2000; 2000US-0246474.
08-NOV-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246578.
08-NOV-2000; 2000US-0246528.
                                                                                                                                                                                                                                   14-SEP-2000; 2000US-0233064.

14-SEP-2000; 2000US-0233065.

21-SEP-2000; 2000US-0234274.

25-SEP-2000; 2000US-0234991.

26-SEP-2000; 2000US-0234991.

26-SEP-2000; 2000US-0234991.

27-SEP-2000; 2000US-0234991.

27-SEP-2000; 2000US-0234991.

29-SEP-2000; 2000US-0236361.

29-SEP-2000; 2000US-0236361.

29-SEP-2000; 2000US-0236361.

29-SEP-2000; 2000US-0236361.

29-SEP-2000; 2000US-0236361.

29-SEP-2000; 2000US-0236391.

29-CCT-2000; 2000US-0236391.

20-CCT-2000; 2000US-0237031.

20-CCT-2000; 2000US-0239935.

13-CCT-2000; 2000US-0239935.

13-CCT-2000; 2000US-0239935.

13-CCT-2000; 2000US-0239937.

20-CCT-2000; 2000US-024181.

20-CCT-2000; 2000US-024181.

20-CCT-2000; 2000US-024181.

20-CCT-2000; 2000US-024181.
08-SEP-2000; 2000US-0232080.
08-SEP-2000; 2000US-0232081.
12-SEP-2000; 2000US-023298.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232400.
14-SEP-2000; 2000US-0233400.
14-SEP-2000; 2000US-0233063.
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The present invention relates to the isolation of novel human colon associated polypeptides, and the cDNA (AAS39348-AAS39581) and genomic sequences encoding for them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders of the colon including colon cancer, congenital abnormalities of the colon including colon cancer, congenital abnormalities of the colon including colon cancer, congenital abnormalities inflammatory bowel disease (IBD), neoplastic cell disorders, colinic inflammation, diarrhoea and dysentery, malabsorption syndromes colonic inflammation, diarrhoea and dysentery, malabsorption syndromes (e.g. lactose incolerance), intestinal inflammatory disorders, colinic inflammation, diarrhoea and dysentery, malabsorption syndromes (e.g. lactose incolerance), intestinal obstruction and sigmoid diseases. The polymucleotides sequences of the invention can also be used in gene therapy. AAU22468-AAU22701 represent the novel human colon associated polymphighes of the invention.

Colonic The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO of the wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polypeptide for treating, preventing and or prognosing disorders related to the colon including colon cancers and also for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID No 344; 562pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders related to the colon includin
testing and detection e.g. diagnosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM;
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17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-02550160.
05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251980.
05-DEC-2000; 2000US-0251980.
06-DEC-2000; 2000US-0251860.
08-DEC-2000; 2000US-0251866.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-465567/50.
N-PSDB; AAS39447.
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Matches 8; Conserv
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WO200155314-A2

Homo

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(HUMA-) HUMAN GENOME SCI INC
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2000US-0179065.
2000US-0180628
2000US-018664.
2000US-0188350.
2000US-019874.
2000US-0198123.
2000US-0205515.
2000US-0205515.
2000US-0205515.
2000US-0205515.
                                                                              2000US-0216647.
2000US-0216880.
2000US-0217487.
2000US-0218290.
2000US-0228290.
2000US-022964.
2000US-0224518.
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2000US-0232401.
2000US-0233063.
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2000US-0233065
              17-JAN-2001; 2001WO-US01324
                                                                                                                                     2000US-0225266
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14-SEP-2000;
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21-SEP-2000;
                       31-JAN-2000;
04-FBB-2000;
02-MAR-2000;
16-MAR-2000;
11-MAR-2000;
19-MAY-2000;
19-MAY-2000;
19-MAY-2000;
19-MAY-2000;
19-MAY-2000;
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19-MAY-2000;
11-JUL-2000;
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26-JUL-2000;
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29-SEP-2000;
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25-SEP-2000;
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01-SEP-2000;
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-AUG-2000;
-AUG-2000;
-AUG-2000;
    02-AUG-2001
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29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-SEP-2000; 20-SE 7-NOV-2000; 7-NOV-2000; -DEC-2000; Ruben SM

Barash SC,

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6; Conservative
                                                              Similarity
                              67 AA;
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                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                               Sequence
                                                                                                                                                                                                 AAM89362;
                                                   Query Match
Best Local
                                                                           Matches
                                                                                                                                                      RESULT 38
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                                                                                           The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABPS-124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to acree for compounds able to interfere with the S. epidermidis lifections.
                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                     Gaps
                              Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4216.
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                                                                                                                                                                                                               Score 35; DB 22; Length 63;
Pred. No. 23;
                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                     Mismatches
                                                                              Claim 11; SEQ ID NO 1879; 986pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID 4216; 267pp; English
                                                                                                                                                                                                                                                                                                                                        ABP39371 standard; Protein; 67 AA.
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                                                                                                                                                                                                                  46.18;
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97US-064964P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis.
                                                                                                                                                                                                                                                             2 VYDALNVLMAMNII 15
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                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                       Conservative
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N-PSDB; ABN91916.
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   WPI; 2001-502630/55.
N-PSDB; AAK88303.
                                                                                                                                                                                                                          Local Similarity
hes 8; Conserv
                                                                                                                                                                                            63 AA;
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08-NOV-1997;
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                                                                                                                                                                                              Sequence
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specification, but was obtained in electronic format directly from the USPIO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
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                                                                                                                                   ö
                                                                                              23; Length 67;
                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune/haematopoietic antigen SEQ ID NO:16955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; gene therapy; vaccine; metastasis
                                                                                            Score 35; DB 2
Pred. No. 25;
6; Mismatches
                                                                                                                                                                                                                                                                                                          AAM89362 standard; Protein; 87 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2001; 2001WO-US01354
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2000US-0190076
                                                                                                                 40.04;
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2000US-0246475
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2000US-0249213
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017-NOV-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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17-NOV-2000;
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13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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08-NOV-2000;
08-NOV-2000;
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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic to AAK87694 represent human immune/haematopoietic antigen genomic represent sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 16955; 3071pp + Sequence Listing; English.
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Pred. No. 36;
1; Mismatches 4; Indels
                                                                                                                                                          2000US-0249299.
2000US-0249300.
2000US-0250160.
                                                                                                                                                                                                          2000US-0250391.
2000US-0251030.
2000US-0251988.
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483426/52.
N-PSDB; AAK62143.
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05-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
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AAB53284 standard; Protein; 90 AA.

RESULT 39

AAB53284

3 YDALNVLMAMNI 14

73 YDILNFLNAKNV

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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gymaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and renear and antibodies to the proteins are useful for the prevention, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymuclectides may be used in diagnostics and research, such as for chromosome identification, and as hybridiation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune gastrointestinal disorders, wounds, real disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAC98707 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                  vulnerary;
                                                                                              identification; cytostatic; cardioactive; neuroprotective; vulner. immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.
                                                                               cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 21; Length 90;
Pred. No. 38;
2; Mismatches 0; Indels
                                            Human colon cancer antigen protein sequence SEQ ID NO:824.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 1376; 2104pp; English.
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Best Local Similarity 75.v
6. Conservative
                (first entry)
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42 FDALNILM 49
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N-PSDB; AAC98041.
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                                                                                                                                                                                                                                Homo sapiens.
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                09-MAR-2001
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AAW71314 and AAW79337-39 represent Staphylococcus aureus WCHU (NCIMB 40771) proteins that have homology to Haemophilus influenzae haein lipoic acid synthetase (lipoate biosynthesis protein A (liph) homologue. The protein is used to generate antibodies and to screen for antimicrobials. The products are used to treat or prevent bacterial infections, particularly where caused by S. aureus but also against Helicobacter Pylori: Particular applications are to treat subjects before surgery or insertion of an in-dwalling device (alternatively the device itself is impregnated before placement). The nucleic acid sequence is used as sources of antisense sequences (for therapeutic use) or regulatory elements for controlling expression of bacterial genes, and for antibacterial screening. The protein can be also used as a vaccine.
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                                                                                                                                                                                                                                                                                                                                  - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                   lipoare biosynthesis protein A; lipA; treatment; prevention; bacterial infection; Helicobacter pylori; vaccine.
                                                                                                                                                                                                                                                                                                                               New nucleic acid from Staphylococcus aureus NCIMB 40771 - 1 for, e.g. diagnosis, prevention and treatment of bacterial infection(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 19; Length 44; Pred. No. 23; 0; Mismatches 2; Indela
        Haemophilus influenzae; haein lipoic acid synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 5' EST related polypeptide SEQ ID NO:1231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY65070 standard; Protein; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Pages 51; 114pp; English.
                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.78;
77.88;
                                                                                                                                                                                                 96US-0031469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 44.7
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 YDALETLWA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 YDALNVLMA 11
                                                                          Staphylococcus aureus
                                                                                                                                                                                                                                                                                                WPI; 1998-322718/28.
                                                                                                                                                                                                                                                                                                              N-PSDB; AAV59884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9953051-A2
                                                                                                                                                                     24-NOV-1997;
                                                                                                                                                                                                   25-NOV-1996;
                                                                                                      WO9823738-A2
                                                                                                                                       04-JUN-1998
                                                                                                                                                                                                                                                                Warren RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY65070;
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21-OCT-1999.

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coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).

The coding sequences and proteins of the present invention are useful for preventing, treating or amelicating a medical condition; and for the diagnosis and treatment of diseases and disorders. Diseases and disorders that can be diagnosed and treated include (auto)immune diseases and disorders (e.g. graft versus host disease and rheumatoid arthritis), inflammatory and allergic disorders (e.g. asthma), hyperproliferative disorders (e.g. cancers and leukemias), cardiovascular disorders (e.g. hart attacks and arrythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g. retinopathy and keloid scars), coular disorders (e.g. glancoma), nuroscipal disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi, viruses or parasites. They may also be useful for wound healing, epithelial cell proliferation, supporting cell cuture, tissue regeneration, birth control and as a food additive or preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to human secreted prostate cancer antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecule encoding human secreted prostate cancer antigens, useful for the diagnosis and treatment of disorders such cancer, leukemia and autoimmune disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes immunogenic protein #21506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dermatological; osteopathic; neuroprotectant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 2
Pred. No. 34;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 56; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU60610 standard; Protein; 60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.78;
50.08;
                                                                                                                                                                                                      HUMAN GENOME SCI INC
                                             21-JUL-1999; 99US-0144972.
13-AUG-1999; 99US-01486B1.
17-AUG-1999; 99US-0149173.
06-0CT-1999; 99US-0158004.
05-APR-2000; 2000US-0194689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2001; 2001WO-US12865.
20-JUL-2000; 2000WO-US19666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Bust Local Similarity 50.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RVYDALNVLMAM 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 RVYEYLNLLISV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes
                                                                                                                                                                                                                                                                                 Rosen CA, Birse C;
                                                                                                                                                                                                                                                                                                                                 WPI; 2001-138554/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200181581-A2
                                                                                                                                                                                                                              ROSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU60610;
                                                                                                                                                                                                   (HUMA-)
                                                                                                                                                                                                                                   ROSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU60610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY65438 represent the EST-related proteins. AAX6651 to
AAX65438 represent the EST-related proteins corresponding to AAZ42265 to
AAX465438 represent the EST-related proteins corresponding to AAZ42265 to
AAZ43052. The S. ESTS can be used for producing secreted human gene
products. They can be used to identify and isolate S' untranslated
regions (UTRs) and upstream regulatory regions which control the
ceptons (UTRs) and upstream regulatory regions which control the
coation, development stage, rate, and quantity of protein synthesis, as
well as stability of mRNA. The ESTS are also useful as probes for
chromosome mapping, and to obtain full length cDNA clones. The ESTS can
also be used in forensic procedures to identify individuals, or in
calso be used in forensic procedures to identify individuals and be used
in gene therapy protocols. The nucleic acids encoding signal peptides can be
used for directing extracellular secretion of a polypeptide
into a cell. The proteins encoded by the EST sequences may be useful in
the acell. The proteins encoded by the EST sequences may be useful in
the acell. The proteins encoded by the EST sequences may be useful in
the acell. The proteins encoded by the RST sequences may be useful in
the acell. The proteins encoded by the RST sequences may be useful in
the acell. The AAX42249 to AAX42264 and AAX426450 represent
therapeutic value, and the identification of the present invention.
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                                                                                                                                                                                                                                                                                                                            Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunosuppressive; nootropic; neuroprotective; antiviral; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; cancer; cytostatic; antiarthritic; antirheumatic; antiasthmatic; anticonvulsant; vasotropic; vulnerary; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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42.9%; Pred. No. 28;
ive 2; Mismatches 6; Indels
                                                                                                                                                                                                      Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted protein; prostate cancer antigen
                                                                                                                                                                                                   Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate cancer antigen #89.
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 724; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB80361 standard; Protein; 59 AA.
                        99WO-IB00712.
                                                                        98US-0057719
                                                                                                98US-0069047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 YDALNVLMAMNIIS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDPINTYMYYNVFS 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                 Dumas Milne Edwards J,
                                                                                                                                                                                                                                                   WPI; 2000-038446/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 AA;
                                                                                                                                                                                                                                                                                 N-PSDB; AAZ42684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200107476-A1
                                                                                                                                              (GEST ) GENSET
                     09-APR-1999;
                                                                        09-APR-1998;
                                                                                                28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB80361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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RESULT 42 AAB80361

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Gaps

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DB 22; Length 59; 1; Indels

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Wang PJ,
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                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU07882;
                                                                                                                                                                              brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU07882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
ð
                                                                                                                                                                                                                            Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in polypeptides. The proteins and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

The acnes is also involved in infections of bone, joints and the central carvin, however it is particularly involved in the inflammatory lesions system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The colypeptides may be used as antigens in the production of antibodies polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downrequlate expression and activity of P. acnes proteins and ctivity of P. acnes proteins and ctivity of P. acnes presence, for example, by cannot inked immunosorbent assay (ELISA).

Compresence of an acnes and assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human brain expressed single exon probe encoded protein SEQ ID NO: 30467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                     Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.7%; Score 34; DB 22; Length 60;
46.7%; Pred. No. 35;
ive 4; Mismatches 4; Indels
                                                                              Bhatia A;
                                                                              Mitcham JL, Wang SS,
Jen S, Carter D;
                                                                                                                                                                                                           Example 1; SEQ ID No 21805; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM58362 standard; Protein; 67 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000; 2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VYDALNVLMAMNIIS 16
  21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                              Persing DH, MJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 46.7.

Best Local 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||:||: | |
24 VYDSLNMGLGLRIHS
                                                                                                                     WPI; 2001-616774/71.
                                                       CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epilepsy; cancer.
                                                                                              L'maisonneuve J,
                                                                                                                                   N-PSDB; AAS59610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
                                                                                 Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 44
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                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel reproduction-specific protein, useful for treating disorders of reduced sperm count, enhancing/increasing sperm count and/or sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalian; reproductive-specific protein; male infertility;
spermatogenesis; sperm count disorder; anti infertility; reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO: 30467; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.7%; Score 34; DB
35.7%; Pred. No. 40;
ive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide sequence for mammalian Spg87.
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                                                                                                                                                                                                                                          Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU07882 standard; Protein; 80
                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2001; 2001WO-US07371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-2000; 2000US-0187518.
12-JAN-2001; 2001US-0261557.
26-MAY-2000; 2000US-0207456.
30-UIN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023659.
                                                                                                                                     04-OCT-2000; 2000GB-0024263.
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38 IITTINIIIAINII 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                                                                                             Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-570774/64.
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The present invention relates to the isolation of novel mammalian and human reproductive-specific proteins (AAU07859-AAU07899), and the nucleic acids encoding them. The nucleic acids encoding reproductive-specific proteins are useful for diagnosing infertility which is a result of reduced sperm count, reduced sperm motility, malch is a result of reduced sperm count, reduced sperm motility, and for useful as markers for spermacogonial cells, for identifying genes or proteins characteristic of male infertility, diagnosing or aiding in the diagnosis of infertility in men, and for contraception in which sperm production or sperm count is reduced or defective sperm is produced. Antibodies to reproductive-specific proteins are useful for determining the presence of these proteins in a sample obtained from a man being assessed for infertility, for identifying the expression of genes in particular cell type or particular developmental stage, for studies of spermatogenesis, and for immunofluorescence of germ cells or in Western blots for assessing the presence of the protein the antibody binds. The sequences of the invention are also useful for treating disorders of reduced sperm count, and for increasing sperm count and/or sperm activity. The nucleic acids of the invention are useful in gene therapy. AAU07882-AAU07882 represent the mammalian reproduction-specific proteins of the present invention. 80 AA; Sequence

Gaps ö Query Match 44.7%; Score 34; DB 22; Length 80; Best Local Similarity 50.0%; Pred. No. 51; Matches 7; Conservative 1; Mismatches 6; Indels

1 RVYDALNVLMAMNI 14

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31 KYYSVLNVAFACNI 44

Search completed: February 17, 2004, 10:53:42 Job time : 30.4158 secs

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Q8RYN3 Q96Y48 Q8EQ09

Q88q09 oceanobacii Q88q15 monkeypox vi Q8V214 camelpox vi Q8V214 camelpox vi Q84y29 listeria mo Q8fey1 escherichia Q8fey1 escherichia Q8fey1 escherichia Q8fey1 escheria in Q9fey2 versinia en Q57370 brachydanio Q9fey2 homo sapien Q8Alc3 homo sapien Q8Alc3 homo sapien Q8Alc3 hochnera ap Q8Alc3 buchnera ap Q97xm8 sulfolobus Q8yrs4 anabaena sp Q97xm8 sulfolobus Q8yrs4 anabaena sp Q9ypn3 versinia pe Q8yrs4 anabaena sp Q8yrs4 anabaena sp Q8yrs4 anabaena sp Q8yrs4 anabaena sp Q9ypn3 versinia pe Q8yrs4 tanabaena sp Q9ypn3 versinia pe Q8yrs4 tanabaena sp Q9ypn3 versinia pe Q8yrs6 listeria in Q8yrs6 listeria mo Q8yrs6 listeria mo Q8yrs6 listeria mo

Q8V415 Q8V214 Q8V214 Q8Y959 Q8FEY1 Q8VTS1 Q8VTS1 Q8VIG5 Q9RIG5 Q9RIQ0 Q9EXLC3 Q8XLC3 Q8YXM8 Q944637 Q8YXM8 Q9YXM8 Q9YXM8

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STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
MEDLINE=21267165; PubMed=11353084;
MEDLINE=21267165; PubMed=11353084;
MOSZET I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
"The complete genome sequence of the murine respiratory pathogen
Wycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
EMBL; AL445563; CAC13324.1; -.
MypuList; WYPU_1510; -.
Gomplete proteome.
SEQUENCE 78 AA; 9386 MW; 05018A7BF7D87E46 CRC64;
                                                                                                                                                                                                                                                                                                                      Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Transposase for insertion sequence element IS1138.
MYPU_1S10.
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Similarity 42.1%;
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O68162 staphylococ
O8kyl2 bacillus an
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q9F6Z5
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Q9JFT1
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Q8KYL2
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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78 AA.

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ALIGNMENTS

Q8VS57 Q8CNM6 Q9SD80 Q928K6 Q8Y4K6

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Gaps

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Score 39; DB 16; Length 78; Pred. No. 1.5e+02; 5; Mismatches 6; Indels

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SECURNCE FROM N.A.
STRAIN=KIMS / Biovar Mediaevalis;
STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=221379863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-HTEB1/ DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus ineyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                              Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Yersinia.
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Pred. No. 2.6e+02;
4; Mismatches 3; Indels
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EMBL, AP004604; BAC15302.1; -
Hypothetical protein; Complete Proteome.
SEQUENCE 64 AA; 7353 MM; EB13P6E557963693 CRC64;
                                                                                                                                                                                                                                                                                                     "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
EMBL, AE013714; AAM84690.1; -.
Hypothetical protein.
SEQUENCE 37 AA; 4466 MW; ECDE7F667857AB87 CRC64;
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Bacteria; Firmicutes; Bacillales; Oceanobacillus.
NCBI_TaxID=182710;
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Best Local Similarity 50.0%;
Matches 7; Conservative
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VLMTYGIVAEKKKE 62
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Matches 6; Conservative
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                ersinia pestis.
                                                                                  NCBI_TaxID=632;
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QBEL85
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MEDLINE=205079125; PubMed=11053400;
MEDLINE=205079125; PubMed=11053400;
Jarrand S., Lyon G.J., Figueiredo A.M.S., Gerard L., Vandenesch F.,
Etienne J., Muir T.W., Novick R.P.;
Exienne J., Muir T.W., Novick R.P.;
Tribitatin-producing strains define a fourth agr specificity group in Staphylococcus aureus.";
J. Bacteriol. 182:6517-6522(2000).
EMBL, FA288215; AAG03054.1;
EMBL, PR288215; AAG03054.1;
ENSP; PO1506; 1DTC.
EQUIENCE 26 AA; 3009 MW; 9F9EF3C5EFE4DFD2 CRC64;
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MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatau K.,
"Genome and virulence determinants of high virulence community-
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36.6%; Score 37; DB 2; Length 26;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 6; Indels
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                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
Bacteria, Firmicutes, Bacillales, Staphylococcus
                                                                                                                                      Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
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17 ISMAQDIISTISDLVKWI 34
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EMBL; AP004829; BAB95824.1; -.
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1 MAODIISTISDLVKWI 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.6%;
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Matches 8; Conservative
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                                                                                                Delta-hemolysin.
HLD OR MW1959.
                                                                                                                                                                                                                                                                                                                                                                       acquired MRSA.";
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QBCLL0
ID QBCLL
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DT 01-M
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OGP625
IO 0996
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Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                          Shankar N., Baghdayan A.S., Gilmore M.S.;
"Modulation of virtulence within a pathogenicity island in vancomycin-
resistant Enterococcus faecalis.";
Nature 417:746-750(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ectromelia virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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MEDLINE-20192152; PubMed=10725549;
Chen N., Buller R.M.L., Wall E.M., Upton C.;
"Analysis of host response modifier ORFs of ectromelia virus, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 12; Length 87; Pred. No. 3.4e+02; 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                           Length 77;
                                                                                                                                                                                  EMBL, AF454824; AAM75299.1; -.
InterPro; IPR001367; HTH DLXX.
InterPro; IPR01355; FG dep_ress; 1.
SEQUENCE 77 AA; 8884 MW; 00F76CDED10F5C47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      causative agent of mousepox.";
Virus Res. 66:155-173 (2000).
EMBL; AP012825; AAC995641; -
ERQUENCE 87 AA; 9879 MW; ECAC2FA1023BAACE CRC64;
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Last annotation update)
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Last annotation update)
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 Enterococcus faecalis (Streptococcus faecalis).
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46.7%; Pred. No. s...
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-0CT-2000 (TrEMBLrel. 15, Last anno
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SEQUENCE FROM N.A.
MEDLINE=22061258; PubMed=12066186;
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STRAIN=Brighton Red;
MEDLINE=83117629; PubMed=6961398;
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22 NVEDIMNEIDREKEEI 37
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13 LLAIQELSKRKKKLK 27
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Best Local Similarity 46.79
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7; Conservative
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Best Local Similarity 56.2
Matches 9; Conservative
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NCBI_TaxID=10243;
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                                    NCBI_TaxID=1351;
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                                                                   SEQUENCE FROM N.A.
STRAIN=Ankara;
Antoine G., Scheiflinger F., Falkner F.G., Dorner F.;
"The complete genomic sequence of the Modified Vaccinia Ankara (MVA)
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein, Complete proteome.
SEQUENCE 75 AA, 8592 MW; D243608FA8177F2C CRC64;
                                                                                                                                                                                   EMBL; U94848; AAB96552.1; -.
SEQUENÇE 74 AA; 8501 MW; 7152A06380829716 CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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EMBL; AE015551; AAN54141.1; -.
TIGR; SO1069; -.
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11 SVVVAISLMMSDIKKLRWL 29
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9 NVEDIMNEIDREKEEI 24
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21.1%;
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Best Local Similarity
                     Orthopoxvirus.
NCBI_TaxID=126794;
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95 AA; 10967 MW; 2044EF16E363F911 CRC64;
           SEQUENCE
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QBT0D7 .
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EMBL, AE001272; AAC56046.1; -. Hypothetical protein; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Brighton Red; MEDLINE=94378510; PubMed=8091665; MEDLINE=94378510; PubMed=8091665; Hu F.Q., Smith C.A., Pickup D.J.; "Cowpox virus contains two copies of an early gene encoding a soluble secreted form of the type II TNF receptor."; Virology 204:343-356(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1358;
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                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Brighton Red;
MEDLINE=91196263; PubMed=2014645;
Hu F.O., Pickup D.J.;
"Transcription of the terminal loop region of vaccinia virus DNA is initiated from the telomere sequences directing DNA resolution."; Virology 181:716-720(1991).
             Pickup D.J., Bastia D., Stone H.O., Joklik W.K.; "Sequence of terminal regions of cowpox virus DNA: arrangement of repeated and unique sequence elements."; Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116 (1982).
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                                                                                                                                  SEQUENCE FROM N.A..
STRAIN=Brighton Red;
MEDLIN=240, PubMed=2309453;
Pareons B.L., Pickup D.J.;
"Transcription of orthopoxvirus telomeres at late times during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Brighton Red;
Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF482758; AAM13644.1; -.
SEQUENCE 90 AA; 10260 MW; DOC313A190A0DC2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match . 36.6%; Score 37; DB 12; Length 90; Best Local Similarity 56.2%; Pred. No. 3.6e+02; Matches 9; Conservative 2; Mismatches 5; Indels
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Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
hypothetical 11.0 kDa protein.
Lactococcus lacits.
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MEDLINE=99000510; PubMed=9767571;
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25 NVEDIMNEIDREKEEI 40
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STRAIN=Brighton Red;
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                                               Gaps
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall G.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AX069386; AAL39531.1; -.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome.
SEQUENCE 97 AA; 11914 MW; D16C48E41F9FD7EA CRC64;
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Last annotation update)
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Last annotation update)
Score 37; DB 2; I
Pred. No. 3.7e+02;
0; Mismatches 6;
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MEDLINE=21886394; PubMed=11889109;
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nilarity 60.0%;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                  AONTFEKEKKEDKII 28
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son OR CG16901 OR CG17791.
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Best Local Similarity
Matches 6; Conserv
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                              Best Local Similarity
Matches 9, Conserv
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Q8EBS4

RESULT 14 Q8EBS4

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SEQUENCE FROM N.A.
STRAIN=A2012;
MEDLINE=2206136; PubMed=12004073;
Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
Keim P., Fraser C.M.;
"Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
Bacillus anthracis.";
[2]
SEQUENCE OF 2-26 FROM N.A.
SEQUENCE OF 2-26 FROM N.A.
STRAIN=ATCC 14990, and UW-3;
MEDLINE=9870; PubMed=9537521;
Otto M., Subszmuth R., Jung G., Goetz F.;
Structure of the pheromone peptide of the Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                          STRAIN=0869.12.80;
MEDLINE=9829499; PubMed=9631538;
Van Wamel W.J.B., Roseum G., Verhoef J.,
Vandenbroucke-Grauls C.M.J.E., Fluit A.C.;
"Cloning and characterization of an accessory gene regulator (agr)-
like locus from Staphylococcus epidermidis.";
FEMS Microbiol. Lett. 163:1-9(1998).
EMBL; APC121774; CAA11541.1; -.
EMBL; APO12132; AAC38296.1; -.
EMBL; AF066634; AAC21574.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 2; Length 20;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 2; Length 39;
Pred. No. 2.4e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                   Mehlin C., Headley C.M., Klebanoff S.J.;
"Phenol Soluble Modulin Gamma.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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EMBL, AE011190; AAM26055.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 39 AA, 4581 MW; 8D485CBCDCE3E177 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 AA; 2952 MW; 34688172E4DFCF19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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1 MMAADIISTIGDLVKWI 17
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                                                                                                              agr system.";
FEBS Lett. 424:89-94(1998).
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Best Local Similarity
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                                                                                                                                                                                    STRAIN=UW-3;
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Q8KYL2;
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Matches
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Tegmark K., Morfeldt E., Arvidson S.;
Regulation of agr-dependent virulence genes in Staphylococcus aureus
by RNAILI from coagulase-negative staphylococci.";
J. Bacteriol. 180:3181-3186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daudherty S., Deboy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Melblyum T.V., Smith H.O., Vuterback T.R., McDonald L.A., Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."
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                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
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                                                     Score 37; DB 5; Length 100;
Pred. No. 3.9e+02;
4; Mismatches 5; Indels
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FlyBase; FBgn0003498; sqd.
SEQUENCE 100 AA; 11589 MW; 657C4191AC93788A CRC64;
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SEQUENCE 52 AA; 5946 MW; E7B65973BA99240A CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
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EMBL; AE015778; AAN56422.1; -.
                                                                                                                                                                                                                                                                                              Created)
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MEDLINE=22297686; PubMed=12368813;
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50.0%;
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                                                       36.6%;
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Matches 9; Conservative
                                                                        Local Similarity 47.1
ses 8; Conservative
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01-MAR-2003
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01-MAR-2002 (TrEMBLrel. 20,
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Viruses; dsDNA viruses, no
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Best Local Similarity 44.4<sup>3</sup>
Matches 8; Conservative
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NCBI_TaxID=10244;
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01-MAR-2003 (
01-MAR-2003 (
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Q8V4T5;
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Q8V4T5
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RESULT 19
Q8EQ09
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STRAIN=JCM 10545 / 7;

PubMed=11572479;

Rawarabaysai Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato, Y.,

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

Oshima T., Kikuchi H.;
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Sulfolobus.
                                                                                                                                                                                                Oryza sativa (japonica cultivar-group).

Oryza sativa (japonica cultivar-group).

Sukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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STRAIN=cv. hipponbare;
SABAKI T., Matsunoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 17; Length 65; Pred. No. 3.8e+02; 2; Mismatches 4; Indels
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DNA Res. 8:123-140(2001).
ENBL; APO00999; BAB67429.1; -
Hypothetical protean; Complete proteome.
SEQUENCE 65 AA; 7748 MW; 178CB648B70EDCFB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 10; Length 62;
Pred. No. 3.6e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          clone:P0663E10.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP004317; BAB90729.1; -.
Gramene; QRRYN3; -.
SEQUENCE 62 AA; 7432 MW; 8A2F84AD87B913EA CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein STS241.
                                                                                                              Last sequence update)
Last annotation update)
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53.8%;
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
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1e8 7; Conservative
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                                                     PRELIMINARY;
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Best Local Similarity
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Shchelkunov S.N., Totmenin A.V., Safronov P.F., Gutorov V.V.,
Shazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,
Esposito J.J., Moss B., Sisler J.R., Jahrling P. B., Sandakhchiev L.S.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF380138; AAL40612.1;
SEQUENCE 74 AA; 8376 MW; CC9232CB8408A89 CRC64;
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STRAIN=HTEB31 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
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MEDLINE=21592287; PubMed=11734207;
MEDLINE=21592287; PubMed=11734207;
MEDLINE=21592287; PubMed=11734207;
Mickenvo S.N., Totmenin A.V., Babkin I.V., Gyarova E.A.,
Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss Isandakholev L.S.;
"Human monkeypox and smallpox viruses: genomic comparison.";
PEBS Lett. 509:66-70(2001).
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Pred. No. 4.3e+02;
7; Mismatches 4; Indels
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44.4%; Pred. No. 3.9e+02;
ive 3; Mismatches 7; Indels
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EMBL, AP004599; BAC13876.1; -
Hypothetical protein; Complete proteome.

SEQUENCE 66 AA, 7775 MW; 4456C54A0BF9D73D CRC64;
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                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical conserved protein.
                                                                                                                                                                                           Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Oceanobacillus.
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Best Local Similarity 35.3%;
Matches 6; Conservative
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Gubser C., Smith G.L.;
"The sequence of camelpox virus shows it is most closely related to
variola virus, the cause of smallpox.";
J. Gen. Virol. 83:855-872(2002).
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Vaccinia virus (strain Ankara).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
NCBI_TaxID=10245, 126794;
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Afonso C.L., Tulman B.R., Lu Z., Zsak L., Zaitsev V.L.,
Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;
"The genome of camelpox virus.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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Gubser C., Smith G.L.;
Gubser C., Smith G.L.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR438165 AAL73870.1;
EMBL, AY009089; AAG37659.1;
Hypothetical protein.
SEQUENCE 78 AA; 8808 MW; CC8B8471E95A3E6D CRC64;
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MEDLINE=62203625; PubMed=4891218;
Meda Y., Ito M., Tagaya I.;
"A specific surface antigen induced by poxvirus.";
virology 38:180-182(1969).
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Howard S.T., Smith G.L.; "Two early vaccinia virus genes encode polypeptides related to protein
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proteinase inhibitors.";
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transcriptional mapping.";
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MEDLINE=90111697; PubMed=2607336;
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STRAIN=WR;
MEDLINE=80052057; PubMed=501796;
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antigen induced by vaccinia virus.";
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MEDLINE=91259063; PubMed=2045793;
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MEDLINE=92041833; PubMed=1657913;
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MEDLINE=21537279; PubMed=11679669;

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terminal repeat proteins and a discontinuous ORF related to the tumor
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Buller R.M., VanSlyke J.;
"Vaccinia and cowpox viruses encode a novel secreted interleukin-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugimoto M.; Regulation of plaque mize and host range by a vaccinia virum gene regulation of plaque mize morteins."; virology 181:158-164(1991).
                                                                                                                       Kerr S.M., Smith G.L., "Vaccinia for virus replication: "Vaccinia virus DNA ligase is nonessential for virus replication: recovery of plasmids from virus-infected cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Firmicutes; Bacillales; Listeriaceae; Listeria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein lmo0475.
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35.6%; Score 36; DB 12;
Best Local Similarity 35.3%; Pred. No. 4.5e+02;
Matches 6; Conservative 7; Mismatches 4
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SECUENCE FROM N.A.
STRAIN=WR;
MEDLINE=91111981; PubMed=1989387;
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42 DVLLAQSVAVEEAKDVK 58
                                                                                                                                                                                                                                                                                       Virology 180:625-632(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NVLMAMNIISKEKKEIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding protein.";
Cell 71:145-152(1992).
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"Characterization of the prfA virulence gene cluster insertion site in non-hemolytic Listeria gpp.: Probing the evolution of the Listeria
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EMBL, AJ238284; CABS7394.1; ...
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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Bach S., Buchrieser C., Prentice M., Guiyoule A., Msadek T.,
Carniel E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.6%; Score 36; DB 2; Length 91; 40.0%; Pred. No. 5.1e+02; tive 6; Mismatches 3; Indels
                                                                                                                                                            Score 36; DB 2; Length 90;
Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virulence gene island";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF322004, AAL36598.1; -.
InterPro; IPR001236; ldh.
Pfam; PF02066; ldh_C; l.
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                                                                                                         033D966F56B0B413 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                     6; Mismatches
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1-MAY-2000 (TrEMBLrel. 13, Last sequence
01-UNY-2002 (TrEMBLrel. 21, Last annotat.
Hypothetical 7.4 kDa protein (Fragment).
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                                                                                                                                                            35.6%;
                                                                                                         90 AA; 9917 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LMAMNIISKEKKEIK 17
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59 IVEMNLNDKEKEOMK 73
                                                                                                                                                                                                                     6; Conservative
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InterPro; IPR001236; ldh.
Pfam; PF02866; ldh_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 6; Conserv
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                               Pfam; rrv...
Oxidoreductase.
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SEQUENCE
                                                                                                         SEQUENCE
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Q8VTS6;
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Matches
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Q8VTS6
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Matches
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"Characterization of the prfA virulence gene cluster insertion site in non-hemolytic Listeria spp.: Probing the evolution of the Listeria virulence gene island.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF322005; AAL36603.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388234; PubMed=12471157; Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                     Gaps
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                                                                                                                                                         Score 36; DB 16; Length 80;
Pred. No. 4.6e+02;
5; Mismatches 4; Indels
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NCBI_TaxID=1643;
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SEQUENCE 88 AA; 10092 MW; 76D61A2F2869094A CRC64;
                      EMBL, AL591975; CAC98554.1; -.
Listilist; LM000475; -.
Hypothetical protein; Complete proteome.
SEQUENCE 80 AA; 9128 MW; B3FCSC721686CFC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of uropathogenic Bscherichia coli.",
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL; AE016764; AAN81595.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Escherichia
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NVLMAMNIISKEKKEIKW 18
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                                                                                                                                                         35.6%;
40.0%;
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46 LATSIVNVKKKEYLW 60
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                                                                                                                                                                                                                                                                     4 MAMNIISKEKKEIKW 18
Science 294:849-852(2001).
                                                                                                                                                                                     Best Local Similarity 40.0
Matches 6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli 06.
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                                                                                                                                                               Query Match
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OBFET
1008FET
1008FET
AC QBFET
DT 01-MA
MEDLI
RX MEDLI
R
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Q8VTS1
D Q8VTS
AC Q8VTS
DT 01-MA
DT 01-MA
DT 01-MC
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Length 51;

Score 35; DB 4; I Pred. No. 4.4e+02;

1C8B9EEED80CDB59 CRC64;

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34.78;
70.0%;
5581 MW;
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                                                                                                                                                                                                                                       6 MNIISKEKKE 15
                                                                                                                                                                                                                                                                                                             37 MNOLGKEKKE 46
                                                                                                           Local Similarity
nes 7; Conserv
        51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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        SEQUENCE
                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBNOT8
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Q8XLC3
                                                                                                                                                                 Matches
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        SO
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                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Prince V.E., Joly L., Ekker M., Ho R.K.;
"Zebrafish hox genes: genomic organization and modified colinear
"Thression patterns in the trunk.";
Submitted (AUG-1997) to the EWBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                   Length 65;
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                                                                                                                                                                                                                                                                                                                                  2, Indels
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                                                                                                                                                                     65 AA; 7404 MW; 90E14C97C1216DF6 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FGF-2 activity-associated protein 3.
GAFA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Best Local Similarity 47.1%; Pred. No. 4.5e+02;
Matches 8; Conservative 6; Mismatches 2;
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PROSITE; PS50071; HOMEOBOX 2; 1.
                InterPro; IPR002178; PTS_EIIA_2.
Pfam; PF00359; PTS_EIIA_7; 1.
Hypothetical protein.
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14 NVMFIAIGVIAKEKEHI 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoxc9 protein (Fragment).
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nes 8; Conserv
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SEQUENCE
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Q96PS2;
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AC 096PS
AC 096PS
AC 096PS
DT 01-DE
DT 
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055370
1D 05737
AC 05737
AC 05737
DT 01-JU
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  Gарв
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STRAIN=13 / Type A;
Pubmed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shimizu T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 54;
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2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC030767; AAH30767.1; InterPro; IPR002453; Beta_tubulin. PROSITE; PS0022B TUBULIN_BAUTOREG; 1. Hypothetical protein. SEQUENCE 54 AA; 6227 MW; F4EF7945303F09BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, AP003189; BAB80825.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 57 AA; 6854 MW; B46DF46C56CE59DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Mypothetical protein CPE1119.
                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to hypothetical gene LOC133874.
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50.0%; Pred. No. 4.6e+02;
tive 3; Mismatches 5;
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  1; Mismatches
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37 VIKNINTISSELKKIK 52
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Best Local Similarity 50.03
Matches 8; Conservative
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RESULT 32 Q8C1Q0

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STRAINS—ATCC 35092 / DSM 1617 / P2;
STRAINS—ATCC 35092 / DSM 1617 / P2;
STRAINS—ATCC 35092 / DSM 1617 / P2;
She Qi, Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M. K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J;
The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                           Munson M.A., Baumann L., Baumann P.,
Munson M.A., Baumann L., Baumann P.,
Buchnera aphidicola (a prokaryotic endosymbiont of aphids) conta
putative 165 rRNA operon unlinked to the 23S rRNA-encoding gene;
sequence determination and promoter and terminator analysis.";
Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; L18928; AAA72379.1;
InterPro; IPR005148; N.
Pfam; PF03485; N.AR9; 1.
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                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
                             85 AA.
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01-OCT-2001 (TrEMBLrel. 18, Last seq
01-OCT-2001 (TrEMBLrel. 18, Last ann
Partial transpoasse ISC1190.
                                                                                  01, Created)
                             PRT;
                       Q44637
Q44677.
Q46577.
Q40077.
Q4007.
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58.3%;
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1 MNILSKLRNKIK 12
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                                                                                                                                                                                                                            Buchnera aphidicola.
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Small intestine;
MEDLINS=223546813; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs.";
Nature 420:563-573(2022).
BMBL; AKO08039; BAC25195.1; -.
SEQUENCE 81 AA; 9496 MW; OFBE651BC92082A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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"Isolation of novel full-length cDNA clones from macaque testis cDNA
                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypotherical 9.5 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Testis;
Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
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Pred. No. 6.6e+02;
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB070133; BAB63078.1; -.
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SEQUENCE 83 AA; 9450 MW; 7EC2FFA2706CA3F1 CRC64;
                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                       Created)
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53.8%;
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14 ILLAMLMADKEKK 26
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les 7; Conservative
7 NIISKEKKEIKW 18
                                   3 NIIKKLKNKILW 14
                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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Best Local
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Q95JP8 Q95JP8;

Matches

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Q954PB
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                          Yersinia pestis.
                                                                                                                                                                                                                                     Plasmid pYC
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                                                                       09RPN3;
                                            O9RPN3
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Q8E4H3
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RESULT 38
                      D9RPN3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Expression of Genes Involved in Anthocyanin Biosynthesis in Relation to Anthocyanin, Proanthocyanidin, and Flavonol Levels during Bilberry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, Ericales, Ericaceae, Vaccinioideae, Vaccinieae, Vaccinium. NCBI_TaxID=180763;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
BLANELINE-22264001; PubMed=12376640;
Jaakola L., Maatta K., Pirttila A.M., Torronen R., Karenlampi S.,
Hohtola A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21595285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
EMBL, AR003592; BAB75068.1; -. SEQUENCE G. AA, 6701 MW; B26CFA037642BC94 CRC64;
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Pred. No. 6.1e+02;
5; Mismatches 4; Indels 1
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34.7%; Score 35; DB 10; Length 94;
Best Local Similarity 31.2%; Pred. No. 7.6e+02;
Matches 5; Conservative 5; Mismatches 6; Indels
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Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 AA; 10548 MW; DDD96D7D62CF9923 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Asr3369.
                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anthocyanidin synthase (Fragment).
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                                                      94 AA
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                                                      PRT;
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Plant Physiol. 130:729-739(2002).
EMBL; AY123768; AAM96895.1;
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17 ILIAPNIEAIKERRNOKW 34
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76 ILHRGLVNKEKVRISW 91
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                                                      PRELIMINARY;
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nes 8; Conserv
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                                                                              Q8H247;
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Matches
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08YRS4
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STRAIN=NEM316 / Serctype III;
MEDLINE=2224508; PubMed=12354221;
MEDLINE=2224508; PubMed=12354221;
MEDLINE=2224508; BubMitaser C., Chevalier F., Frangeul L.,
Msader P., Rueniok C., Buchriaser C., Chevalier F., Frangeul L.,
Msadek I., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
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                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20153814; PubMed=10686133; MEDLINE=20153814; Dong X.Q., Lindler L.E., Chu M.C.; Complete DNA sequence and analysis of an emerging cryptic plasmid isolated from Yersinia pestis."; Plasmid 43:144-148[2000].
                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766850; CAD47087.1;
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Best Local Similarity 35.0%; Pred. No. 8.8e+02;
Matches 7; Conservative 8; Mismatches '4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.2%; Score 34.5; DB 2; Length 90; 40.0%; Pred. No. 8.8e+02; ive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Ribosomal protein; Complete proteome.
SEQUENCE 90 AA; 10282 MW; CDCA763D78007CBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 AA; 10070 MW; 80D1C30322A92D7C CRC64;
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90 A.A.
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01-MAR-2003 (TrEMBLrel. 23, Created)
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NVLMAMNIIS-KEKKEIKWI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VLMAMNIIS---KEKKEIKW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 VLMAISLLSGCGEETKSADW 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF152923; AAF05100.1; -. Plasmid.
                                                                                                                                                                                                                                                  Enterobacteriaceae; Yersinia
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OBDYW5

RESULT 40 Q8DYW5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Bevan M., Van Der Schueren J., Chuang Y.J., Voet M., Robben J.,
Volckaert G., Bancroft I., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 6.6e+02;
3; Mismatches 6; Indels
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                               Indels
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133421; CAB62616.1; -.
Hypothetical protein.
SEQUENCE 54 AA; 6091 MW; 8DB3B77A2F0FC3A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE016749; AA005233.1; -.
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Hypothetical 6.1 kDa protein.
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Pred. No. 3.3e+02;
2; Mismatches 6;
     Pred. No. 9.5e+02;
                                                                                                                                                                                                                                                                                25 AA.
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                            5; Mismatches
                                                                                   2 VLMAMNIISKE----KKEIKWIG 20
                                                                                                                     Created)
                                                                                                                                                                                                                                                                                PRT;
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50.0%;
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     33.3%;
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1 MVNNVVSIEKMKALW 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis
                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                PRELIMINARY;
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Best Local Similarity
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1282;
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Q8CNM6
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Weigel L.M., Anderson G.J., Tenover F.C.;
Submitted (Jul. 2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR397169; ALST340.1;
InterPro; IPR002205; DNA_topoisolV.
Pfam; PP00521; DNA_topoisolV.
ProDom; PD000742; DNA_topoisolV; 1.
ProDom; PD000742; DNA_topoisolV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Proteus.
NCBI_TaxID=584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002). TEMBI; AEO14254; AAN00229.1; -. TIGR; SAG1358; -.
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Pred. No. 8.8e+02;
8; Mismatches 4; Indels
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                                                                                                                                                                                                                                             Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 AA; 10282 MW; CDCA763D78007CBE CRC64;
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                                                                                                         Created)
Last sequence update)
Last annotation update)
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Last sequence update)
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                                                      90 AA
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                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=2603 V/R / Serotype V;
MEDLINE=22222988; PubMed=12200547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NVLMAMNIIS-KEKKEIKWI 19
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                                                                                                       ul-mAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, biharama)
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                                                      PRELIMINARY;
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                                                                                                                                                                                       Ribosomal protein S16. RPSP OR SAG1358.
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SEQUENCE 90 AA;
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                                                                                                                                                                                                                                                                                                       Streptococcus.
NCBI_TaxID=216466;
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08VS57

Matches

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RESULT 41
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Charbit A., Brini H., Garcia-del Portillo F., Garrido P.,
Charlan K.-D., Faini H., Garcia-del Portillo F., Garrido P.,
Charlan K.-D., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Charbiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Nordsiek G., Schlueter T., Simoes N., Tierrez A.,
Nacquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
Comparative genomics of Listeria species.";
Science 294:849-852(2001).
Listilist, LIN02556:
Na Hypothetical protein, Complete proteome.
SEQUENCE 54 AA, 6263 MW; 200858BFE484508E CRC64;
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Pred. No. 6.6e+02;
3; Mismatches 3; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein lmo2432.
LMO2432.
Lateria monocytogenes.
Bacteria, Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UJV-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical procein lin2526.
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                                                                                     54 AA
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STRAIN-EGD-e / Serovar 1/2a;
MEDLINE-21537279; PubMed=11679669;
                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / Serovar 6a;
PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.7%;
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Best Local Similarity 50...
6; Conservative
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42 LNIVDKKKPSIK 53
                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria innocua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8Y4K6
Q8Y4K6;
                                                                                     Q928K6
Q928K6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 45
089486
1D Q89486
AC Q89487
AC Q89487
DJ 01-MAD
RESULT 44
10928K
AC 0928K
AC 0928K
AC 0928K
DT 01-DB
DT 0
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 17, 2004, 10:50:13; Search time 12.0792 Seconds (without alignments) 159.230 Million cell updates/sec Run on:

US-09-900-147-4 101 1 NVLMAMNIISKEKKEIKWIG 20

Title: Perfect score: Sequence:

Scoring table:

283308 segs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

37673 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query Match	o Query Match Length DB	DB	ID	Description
-	39	38.6	78	7	G90530	hypothetical prote
7	37	36.6	74	7	T37447	K pro
e	37	36.6	95	7	T43125	
4	36	35.6	42	7	T07291	
S	36	35.6	44	~	A89995	
9	36	35.6	64	~	D69406 .	hypothetical prote
7	36	•	78	~	JQ1781	
80	36	ъ.	80	N	AD1134	hypothetical prote
6	36	35.6	88	7	B64888	
10	36	35.6	88	~	C64909	protein -
11	35	34.7	56		LESAD	sin
12	35	34.7	74		G69286	hypothetical prote
13	35	34.7	88		H90329	partial transposas
14	34.5	34.2	9		AB2227	hypothetical prote
15	34	33.7	25		A33058	•∺
16	34	33.7	54		T45629	hypothetical prote
17	34	33.7	54	C¥	AH1378	
18	34	33.7	54	N	A11747	
19	34	33.7	67	N	H97845	
20	34	33.7	67	~	AE3378	
21	34	33.7	72	~	S34404	0
22	34	33.7	79	~	AC1217	hypothetical prote
23	34	33.7	90	N	B81102	conserved hypothet
24	34	33.7	91	-	C64069	virulence-associat
25	34	33.7	95	~	F72864	AcOrf-117 protein
56	34	33.7	95	~	T41855	ACMNPV orfil7 - Bo
27	34		96	~	B84142	
28	34	33.7	97	~	C45681	cal
29	33.5	33.2	73	~	H71893	~

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0; Gaps

Query Match 36.6%; Score 37; DB 2; Length 74; Best Local Similarity 56.2%; Pred. No. 95; Matches 9; Conservative 2; Mismatches 5; Indels

molybdopterin conv	hypothetical prote	ribosomal protein	probable SSV1 viru	mammary transformi	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	cold shock-like pr	cold shock-like pr	B11R protein - vac	hypothetical prote	small nuclear ribo	hypothetical prote	BilR protein - vac
A64620	E84146	538633	B90196	I59337	T43096	T12860	F97798	98006Н	B71673	E97827	JQ1805	H90332	C90115	F81321	A42527
7	~	N	~	~	~	~	N	~	~	7	7	~	7	7	0
74	33	42	46	61	99	67	63	69	70	70	72	9/	82	87	88
33.2	32.7	32.7	32.7	32.7	32.7	32:7	32.7	32.7	32.7	32.7	32.7	32.7	32.7	32.7	32.7
33.5	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1
hypothetical protein MYPU 1510 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;species: Mycopiasma purmonis C;Date: 24-May-2001 #sequence revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: G90530 R:Chambaud, I.: Heilig, R.: Ferris, S.: Barbe, V.: Samson. D.: Galisson. F.: Moszer. I.:
Nucleic Acids Res. 29, 2145-2153, 2001 A:Title: The complete genome semience of the mirine respiratory pathogen Mycoplasma milmo
A; Reference number: A99512; MUID:21267165; PMID:11353084
Astrocessors Systems Astrocessors Astrocesso
Appendix 1.78 KURN A ALLEGE DER CLANOFEL BERN CHALLION A CORRECT CLANOFEL CLANOFEL CHALLION A CORRECT CLANOFEL CHALLION A CORECT CLANOFEL CHALLION A CORRECT CLANOFEL CHALLION A CORRECT CLANO
A; Lious-Itelements: ob: Antwarpsoo; Fib'giavospoa; FibN: CACLSSZ4.1; GSFDB: GNUOLSS A; Experimental source: strain UAB CTIP C:Genetics:
A;Gene: MYPU 1510 A;Genetic code: SGC3
Query Match 38.6%; Score 39; DB 2; Length 78; Best Local Similarity 42.1%; Pred. No. 49;
S
Qy 1 NVLMAMNISKEKKEIKWI 19 .
Db 10 NVKLILDHISKNKFDKEWI 28
RESULT 2
T37447
probable 8.5K protein - vaccinia virus (strain Ankara) C;Species: vaccinia virus
A;Variety: Btrain Ankara C.Date: 21_Tan_2000 #semmence revision 21_Tan_2000 #text chance 21_Tan_2000
C;Accession: T37447
R;Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F. submitted to the EMBL Data Library, March 1997
A; Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strair A; Reference number: 220877
A;Accession: T37447 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA A;Residues: 1-74 <ant></ant>
A;Cross-references: EMBL:U94848; PIDN:AAB96552.1 A;Experimental source: strain Ankara
C;Genetics: A;Note: MVA179R

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2 VLMAMNIISKEKKEIKWI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 ISMAQDIISTIGDLVKWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-78 < BLA>
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C; Species: chloroplast Chlorella vulgaris
C; Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C; Date: 17-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C; Date: 17-May-1707291
R; Wakasugi, T: Nagai, T:; Kapoor, M:; Sugita, M:; Ito, M:; Ito, S:; Tsudzuki, J:; Nakas
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A; Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo
A; Reference number: 215985; MulD:97303241; PMID:9159184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ogud
K.;
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T43125

T43125

T6 125

T7 125

T7 125

T7 125

T7 127

T8 127
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delta-hemolysin [imported] - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: A89995
R;Kuroda, M.; Ohte, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; (ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kalto, C.; Sekimizu, L.; Lancet 357, 1225-1240, 2001
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C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 95;
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Pred. No. 1.2e+02;
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A;Molecule type: DNA
A;Residues: 1-42 <WAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: T43125
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-95 < DOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-references: EMBL:AE001272; PIDN:AAC56046.1
A, Experimental source: strain DPC3147
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1 NVLMAMNIISKEKKEI 16
                                                5 AMNIISKEKKEIKWI 19
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Best Local Similarity
Matches 9; Conserva
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A.Genome: plasmid pMRC01
A.Note: ORF00054
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C,Keywords: chloroplast
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Richerk H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F., Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
Ajauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woses, C.R.; Venter, J.C.
Ajritle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor. Ajreference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AjAccession: D69406
AjStatus: preliminary; nucleic acid sequence not shown; translation not shown
AjMolecule type: DNA
AjRediues: 1-64 <KLE>
AjRediues: 1-64 <KLE>
AjCross-references: GB:AE001018; GB:AE000782; NID:g2689341; PIDN:AAB90006.1; PID:g264934:
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SalFGR 8.8K protein - vaccinia virus (strain WR and Ankara)
C;Sapecies: vaccinia virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Feb-2000
C;Accession: JOI781; D40897; T37429
C;Accession: JOI781; D40897; T37429
B;Smith, GL.; Chan, Y.S.; Howard, S.T.
J. Gen. Virol. 72, 1349-1376, 1991
A;Title: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right inv
A;Tetle: nucleotide sequence of 42kbp of vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-78 <SMI>
A;Cross-references: DDBJ:D11079; NID:g222717; PIDN:BAA01817.1; PID:d1002293; PID:g222732
R;Blasco, R.; Cole, N.B.; Moss, B.
J. Virol. 65, 4598-4608, 1991
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A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accasion: A8995
A;Acture: preliminary
A;Molecule type: DNA
A;Residues: 1-44 <KUR>
A;Cross-references: GB:BA000018; PID:g13701829; PIDN:BAB43122.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: hld
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: D69406
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Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
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Best Local Similarity 44.4%; Pred. No. 79;
Matches 8; Conservative 3; Mismatches
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Indels

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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: C64909
G;Batcher, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Rtle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: acid sequence not shown; translation not shown
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R;Janzon, L; Loefdahl, S; Arvidson, S.
Mol. Gen. Genet. 219, 480-485, 1989
A;Title: Identification and nucleotide sequence of the delta-lysin gene, hld, adjacent to
A;Reference number: JQ0386; MUID:90158509; PMID:2622452
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A; Residues: 'MMSCLILARFILIKEGVIS',1-26 <JAN>
A; Cross=rreferences: EMBL:X17301; NID:946585
A; Note: the authors translated the codon ATT for residue 9 as Val
A; Note: the authors suggest that Met in the first position indicated may serve as an alte
A; Note: the authors suggest that Met in the first position indicated may serve as an alte
A; Note: the Bubl. Data March March 1990
A; Reference number: S20793
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A;Residues: 1-88 <BLAT>
A;Cross-references: GB.>BE000252; GB:U00096; NID:G2167119; PIDN:AAC74617.1; PID:g1787826;
A;Experimental source: strain K-12, substrain MG1655
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A;Residues: 'MSCLILRIFILIKEGVIS',1-26 «KOR»
A;Cross.references: EMBL:X52543; GB:M32737; NID:g46505; PIDN:CAA36780.1; PID:g46507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 35.6%; Score 36; DB 2; Length 88; Similarity 44.4%; Pred. No. 1.6e+02; 8; Conservative 2; Mismatches 6; Indels
    44.4%; Pred. No. 1.6e+02;
tive 2; Mismatches 6;
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C, Keywords: blocked amino end; exotoxin; hemolysis
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                                                                                                                1 NVLMAMNIISKEKKEIKW 18
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                                                  Conservative
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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AD134
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C;Species: Listeria monocytogenes
C;Species: Listeria Li
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B64888

ynaE protein - Escherichia coli (strain K-12)
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: B64888
R;Blattner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278803
A;Accession: B64888
A,Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strail A;Reference number: 220877
A;Recession: T31429
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-78 <ANT>
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A;Experimental source: strain K-12, substrain MG1655
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Pred. No. 1.4e+02;
7; Mismatches 4; Indels
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Pred. No. 1.5e+02;
5; Mismatches 4;
                                                                                                                                                                                                                                              A,Cross-references: EMBL:U94848; PIDN:AAB96536.1
A,Experimental source: strain Ankara
C,Genetics:
A,Note: WVA156R
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42 DVLLAQSVAVEEAKDVK 58
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40.0%;
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Best Local Similarity 35.3%;
Matches 6; Conservative
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A,Molecule type: DNA
A,Residues: 1-80 <GLA>
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AB2227
C;Accession: AB2227
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Recession: AB2227
A;Molecule type: DNA
A;Residuea: preliminary
A;Residuea: L-60 «KUR»
A;Residuea: Complete AKIR»
A;Residuea: Complete AKIR»
A;Residuea: Data ARIR»
A;Residuea: Data ARIR»
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A;Residuea: Data ARIR»
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C;Date: 04-Peb-2000 #sequence_revision 04-Peb-2000 #text_change 04-Peb-2000
C;Accession: T45629
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Bar submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23009
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A,Status: preliminary
A,Rolecule type: protein
A,Rolecule type: Drotein
A,Rolecule type: 1-25 «MCK»
R,McKevitt, A.I.; Bjornson, G.L.; Mauracher, C.A.; Scheifele, D.W.
Infect. Immun. 58, 1473-1475, 1990
A,Title: Amino acid sequence of a deltalike toxin from Staphylococcus epidermidis.
A,Reference number: A37189; MUID:90216022; PMID:2323825
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:BA000019; PIDN:BAB75068.1; PID:g17132464; GSPDB:GN00179 A; Experimental source: strain PCC 7120 C; Genetics:
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C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 19-Jan-1996
C;Accession: A33058; A37189
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A;Reference number: A33058
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54 < BEV
A;Cross-references: EMBL:Ail33421
A;Experimental source: cultivar Columbia; BAC clone F13G24
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Pred. No. 1.9e+02;
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ed. No. 90;
Mismatches (
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Pred. No. 9
2; Mismatch
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Best Local Similarity 50.0%;
Matches 8; Conservative 2
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17 ILIAPNIEAIKERRNOKW
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A,Status: preliminary
A,Molecule type: protein
C,Stendues: 1-5,7-25 <MC2>
C,Superfamily: delta-hemolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 MAMNIISKEKKEIKWI
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Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A33058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: asr3369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 16
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G69286
hypothetical protein AF0295 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: G69286
C;Accession: G69286
R;Klank, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
I; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woses, C.K.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69280; MUID:98049343; PMID:9389475
A;Accession: G69286
A;Accaus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: L.T4 exLBS
A;Accassion: G69286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB: AE001084; GB: AE000782; NID: 92689407; PIDN: AAB90939.1; PID: 9265034
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A;Molecule type: DNA
A;Redidues: 1-88 <KUR>
A;Coss-references: GB:AE006641; NID:gl3814935; PIDN:AAK41895.1; GSPDB:GN00155
C;Genetics:
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C;Species: Nostoc sp. PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.7%; Score 35; DB 2; Length 74; illarity 52.9%; Pred. No. 2e+02; Conservative 1; Mismatches 7; Indels
                                                                                                                          Query Match

34.7%; Score 35; DB 1; Length 26;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 8; Conservative 2; Mismatches 6; Indels
                                                       F;1/Modified site: N-formylmethionine #status experimental
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Best Local Similarity 53.3
Matches 8; Conservative
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Matches 9; Conserv
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RESULT 14

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RibelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesscreroc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitenss A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: S34404
R;Tschauder, S.; Driessen, A.J.M.; Freudl, R.
Rol. Gen. Genet. 235, 147-152, 1992
A;Title: Cloning and molecular characterization of the secY genes from Bacillus lichenifc A;Reference number: S30115; MUID:93062802; PMID:1435726
A;Accession: S34404
                                                                                                                                                                                                                                                                 RiOgata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rot
Science 293, 2093-2098, 2001
                                                                                                                                                                                                                                                                                                              A,Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii
A,Reference number: A97700; MUID:21442074; PMID:11557893
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C;Genetics:
A;Gene: RC1168
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A,Experimental source: strain 16M
                                                                                                                                                                  hypothetical protein RC1168 [imported] - Rickettsia conorii (strain Malish 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Brucella melitensis
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C.Accession: AE3378
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C;Species: Bacillus licheniformis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
                                                                                                                                                                                           C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Accession: H97845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 2; Ler
Pred. No. 2.5e+02;
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50.0%; Pred. No. 2.5e+02;
ive 3; Mismatches 4;
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27.8%;
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       6 MNIISKEKKEIK 17
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42 LNIVDKKKPSIK
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: AE3378
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-67 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary A; Molecule type: DNA A; Residues: 1-67 < KUR>
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Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Cipacession: AH1378
Ridaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:NC_003210; PIDN:CAD00510.1; PID:g16411920; GSPDB:GN00177 A;Experimental source: strain EGD-e C;Genetics:
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A;Experimental source: strain Clip11262
C;Genetics:
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hypothetical protein lin2526 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: A11747
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Pred. No. 2e+02;
3; Mismatches 3; Indels
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                                                                                                                     DB 2; Length 54;
2e+02;
                                                                                                                                                                    6; Indels
                                                                                                                                                                    3; Mismatches
                                                                                                                     33.7%; Score 34; 40.0%; Pred. No. ;
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50.0%;
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1 MVNNVVSIEKMKALW 15
                                                                                                                                                                                                                    4 MAMNIISKEKKEIKW 18
                                                                                                                                                                    6; Conservative
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Matches 6; Conservative
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LNIVDKKKPNIK 53
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                                                                                                                                           Best Local Similarity
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54 <GLA>
C;Genetics:
A;Map position: 5
A;Introns: 29/3
A;Note: F13G24.240
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                                                                                                                       Query Match
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Virulonce-associated protein vapD homolog H10450 - Haemophilus influenzae (strain Rd KW2(C) Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: C64069
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kalley, J.M.; Weidman, J.D.; Prince, J.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, S.A.; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, S.A.; Aritle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Accession: C64069
A;Accession: C64069
A;Accession: C64069
A;Accession: C64069
A;Accession: C64069
A;Residues: 1-91 < TIGR>
A;Residues: 1-91 < TIGR>
A;Cross-references: GB:U32728; GB:L42023; NID:g1573425; PIDN:AAC22108:1; PID:g1573426; T1
C;Superfamily: virulence-associated protein vapD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: Protein - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C;Accession: F72864
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: F72864
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Gaps
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C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A;Variety: isolate T3
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Best Local Similarity 36.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.7%; Score 34; DB 1; Length 91; 36.8%; Pred. No. 3.5e+02; Live 4; Mismatches 4; Indels
8; Indela
6; Mismatches
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                                                               1 NVLMAMNIISKEKKEIKWIG 20
                                                                                                         56 HILKSYPEFAEETKYLNWIG 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.7%
Best Local Similarity 36.8%
Matches 7; Conservative
   6; Conservative
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A,Gene: AcOrf-117
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            Matches
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B81102
conserved hypothetical protein NWB1264 [imported] - Neisseria meningitidis (strain MC58 conserved hypothetical protein NWB1264 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B81102
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.X.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Tettence number: Aglo00; MUID:2017575; PMID:10710307
A;Reference number: Aglo00; MUID:2017575; PMID:10710307
A;Residues: 1-90 <TET>
A;Resperimental source: serogroup B, strain MC58
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AC1217
AC1217
AC1217
AC1217
AC1217
AC1217
AC1217
AC1217
C; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C; Accession: AC1217
C; Accession: AC1217
R; Glaser, P: Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C; Dones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
A, Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A, Actelence number: AB1077; MUID:21537279; PMID:11679669
A, Accession: AC1217
A) Status: preliminary
A, Status: preliminary
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A;Experimental source: strain EGD-e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 2; Length 79;
Pred. No. 3e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 36.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 5; Mismatches 7; Indels
                   A; Molecule type: DNA
A; Residues: 1-72 <TSC>
A; Cross-references: EMBL:X70087
C; Genetics:
A; Gene: rpl15
C; Superfamlly: Bscherichia coli ribosomal protein L15
C; Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                     2 VLMAMNIISKEKKEIKWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 LLLETGVISKLKSGVKILG 39
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30.0%;
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33 VNLSYSEKDEQKWL 46
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Best Local Similarity 42.9
Matches 6; Conservative
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Best Local Similarity
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A; Residues: 1-79 <GLA>
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A;Gene: lmo1139
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probable molybdopterin converting factor, chain 1 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
C;Date: J2-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 19-Jan-2001
C;Accession: H71893
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J Nature 397, J76-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathx A;Reference number: A71800; MUID: 99120557; PMID: 9921682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: GB:AE001505, GB:AE001439; NID:g4155295; PIDN:AAD06323.1; PID:g415530<sup>o</sup>
A,Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RiTomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D., Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

Alytuthors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185
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F;74/Modified site: 1-thioglycine (Gly) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molybdopterin converting factor, subunit 1 - Helicobacter pylori (strain 26695)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Helicobacter pylori
C;bate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 19-Jan-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.2%; Score 33.5; DB 2; Length 73; ilarity 38.1%; Pred. No. 3.3e+02; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 3.4e+02;
5; Mismatches 7;
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ilarity 38.1%;
Conservative
                                    6 MNIISKEKKEIK 17
                                                                  49 MNIVKRDRPEMK 60
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Best Local Similarity
Matches 8; Conserval
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les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-73 <ARN>
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Matches
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A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3938
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: C45681; J50560
R;Selon: C45681; J50500
J. Virol. 67, 2305-2316, 1993
A;Title: Analysis of five presumptive protein-coding sequences clustered between the pri
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A; Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus. A; Reference number: Z22020; MUID:99281911; PMID:10355780
A; Accession: T41855
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-95 < KAM>
A; Residues: 1-95 < KAM>
A; Residues: 1-95 < KAM>
A; Experimental source: isolate T3
C; Genetics:
A; Note: Orf_96
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A;Note: sequence extracted from NCBI backbone (NCBIN:128289; NCBIP:128292)
C;Genetics:
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42.1%; Pred. No. 3.7e+02;
tive 5; Mismatches 6; Indels
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C,Species: phage T4
                                                                                                                                                                                                                                                                                                   Score 34; DB 2; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                Query Match
33.7%; Score 34; DB
Best Local Similarity 36.8%; Pred. No. 3.6e
Matches 7; Conservative 7; Mismatches
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NVLLVPNAL--KKRDVKYI 22
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Best Local Similarity 42.1
Matches 8; Conservative
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A,Molecule type: DNA
A,Residues: 1-97 <SEL>
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Matches 6; Conserva
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A;Note: ORF00024
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83550; MUID:20512582; PMID:11058132
A;Accession: B48146
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-33 < CNA
A;Residues: 1-33 < CNA
A;Residues: 1-35 < CNA
A;Residues: 1-37 < CNA
A;Residues: 1-30 < CNA
A;Residu
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ribosomal protein L32, cytosolic - maize (fragment)
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Species: O6-Jan-1995 #sequence_revision O6-Jan-1995 #text_change 17-Oct-1997
C;Accession: S38633
R;Bates, E.B.M; Vergne, P.; Dumas, C.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38633
A;Reference number: S38633
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Pred. No. 2.4e+02;
4; Mismatches 4; Indels
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Pred. No. 1.7e+02;
4; Mismatches 4;
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Pred. No. 2.2e+02;
5; Mismatches 2;
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A;Residues: 1-42 <BAT>
A;Cross-references: EMBL:X75646
C;Superfamily: rat ribosomal protein L32
C;Keywords: protein biosynthesis; ribosome
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Best Local Similarity 37.9%;
Matches 11; Conservative
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Local Similarity 46.2%;
hes 6; Conservative
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6 IAHNVSTKKRKEI 18
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nes 6; Conserv
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1 NVLM--AMNIISKEKKE-

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hypothetical protein - Lactococcus lactis plasmid pMRC01
clspecies: Lactococcus lactis
clspecies: Lactococcus lactis
clspecies: Lactococcus lactis
clspecies: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
claccesion: T43096
Riccession: T43096
Alfile: Sequence and analysis of the 60 kb conjugative, bacteriocin-producing plasmid phanalysic number: 222314
Alfile: Sequence and analysis of the 60 kb conjugative, bacteriocin-producing plasmid phanalysic number: 222314
Alfile: Sequence and analysis of the 60 kb conjugative, bacteriocin-producing plasmid phanalysic number: 222314
Alfile: Sequence and Alfile: Conjugative, bacteriocin-producing plasmid phanalysic number: 220014
Alfile: Sequence and Alfile: Conjugative, bacteriocin-producing plasmid phanalysic number: 220014
Alfile: Sequence and Alfile: Conjugative, bacteriocin-producing plasmid phanalysic number: 220014
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C;Species: Bacillus subtilis phage SPBC2
C;Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C;Accession: T12860; H69918
F;Lazarevic, V; Duesternoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D. submitted to the EMBL Data Library, August 1997
A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophaga; A;Reference number: 217583
                                                                                                                                                                                                                                                                           mammary transforming protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 159337
R;Bera, T.K.; Guzman, R.C.; Miyamoto, S.; Panda, D.K.; Sasaki, M.; Hanyu, K.; Enami, J.;
R;Bera, T.K.; Guzman, R.C.; Miyamoto, S.; Panda, D.K.; Sasaki, M.; Hanyu, K.; Enami, J.;
R;Reference number: 159337; MUID:95024046; PMID:7937892
A;Accession: 159337
A;Accession: 15937
A;Accession: 
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C;Genetics:
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Pred. No. 3.6e+02;
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Similarity 31.6%; Pred. No. 3.3e+02;
6; Conservative 8; Mismatches 3;
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A;Molecule type: DNA
A;Residues: 1-67 <LAZ>
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16 NVLVKEGLNILSNSKKRQYLKLLRTIKYI 44
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55.6%;
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Best Local Similarity 55...
Si Conservative
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A, Accession: H90086
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-68 < DOU>
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R; Kunst, F; Ogasswara, N.; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V.; Berten C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Char, Ebrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krodh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell Y. M.; Ogawa, K.; Ogawa, K.; Ogawa, R.; Oudeaga, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portectelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Satonon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serolan, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serolan, A; Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Tosato, V.; Uchiyama, A; Title: The complete genome sequence of the Gram-Positive bacterium Bacillus subtilis. A; Fasciues: Lefy Residues: 1-67 <KUN>
A; Residues: 1-67 <KUN
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H90086
H90086
Hypothetical protein orf68 [imported] - Guillardia theta nucleomorph
C;Species nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
R;Douglas, S:; Zauner, S:; Fraunholz, M.; Beaton, M.; Penny, S:; Deng, L.T.; Mu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
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Pred. No. 3.6e+02;
6; Mismatches 1; Indels
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Best Local Similarity 41.7
Matches 5; Conservative
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Matches 5, Conservative
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IDVIEKENKELR 22
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A;Molecule type: DNA
A;Residues: 1-67 <KUR>
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C;Accession: E97827
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.B.; Barbe, V.; Samson, D.; Rot Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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A;Experimental source: strain Madrid E
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R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genuence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
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A;Cross-references: GB:AF165818; NID:g13794452; PIDN:AAK39827.1; GSPDB:GN00150 C;Genetics:
A;Gene: orf68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cold shock-like protein (cspA) RP670 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
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C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 17-May-2002
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cold shock-like protein [imported] - Rickettsia conorii (strain Malish 7)
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C;Superfamily: major cold shock protein; cold shock domain homology
F;7-67/Domain: cold shock domain homology <CSD>
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Pred. No. 3.7e+02;
3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                  Query Match 32.7%;
Best Local Similarity 50.0%;
Matches 7; Conservative
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A,Genome: nucleomorph
C,Keywords: nucleomorph
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A; Residues: 1-70 < AND>
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A,Molecule type: DNA
A,Residues: 1-70 <KUR>
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hypothetical protein Cj1164c [imported] - Campylobacter jejuni (atrain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: F81321
C;W.; Arrian, F81321
C;W.; Munian, M.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C;W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrelli
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
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A;Cross-references: GB:AJ010592; NID:g12580778; PIDN:CAC27096.1; GSPDB:GN00151
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C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 08-Apr-1994
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 08-Apr-1994
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 08-Apr-1994
B;Johnson, G.P.
Submitted to GenBank, June 1990
A;Reference number: A33172
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Pred. No. 4.8e+02;
3; Mismatches 5; Indele
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                                                                                                                                                                                                                                                                                                                                                      Length 82;
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50.0%; Pred. No. 4.7e+02;
tive 3; Mismatches 2;
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33.3%; Pred. No. 4.5e+02;
tive 6; Mismatches 4
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Job time : 14.0792 secs
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23 NVEDIINEIDREKEEI 38
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Best Local Similarity 50.0%;
Matches 8; Conservative
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Best Local Similarity 33.3x
Local Similarity 5, Conservative
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73 KKKKKESWLG 82
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Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                         C; Keywords: nucleomorph
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-87 <PAR>
                                                                                            C,Genetics:
A,Map position: 2
A,Genome: nucleomorph
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(290115

gmall nuclear ribonucleoprotein SM D2 [imported] - Guillardia theta nucleomorph
G19115

gmall nuclear ribonucleoprotein SM D2 [imported] - Guillardia theta
G19115

A10116
A20115
A2011 #Sequence_revision 10-May-2001 #text_change 24-May-2001
C20115
A30115
A30115
A30115
A30116
A30117
A30117
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A30118
A
                                                                                                                                                                                                                                                                                                             B11R protein - vaccinia virus (strain WR)
C;Species: vaccinia virus
C;Species: vaccinia virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
C;Accession: JQ1805
R;Smith, GL.; Chan, Y.S.; Howard, S.T.
J. Gen. Virol. 72, 1349-1376, 1991
A;Title: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right in A;Reference number: JQ1767; MUID:91259063; PMID:2045793
A;Accession: JQ1805
A;Moleonle reconstruction of the property of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-72 <SMI>
A;Cross-references: DDBJ:D11079; NID:g222717; PIDN:BAA01841.1; PID:d1002317; PID:g222756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SSO8760 [imported] - Sulfolobus solfataricus transposon ISC1491 C;Species: Sulfolobus solfataricus (C;Species: Sulfolobus solfataricus (C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: H90332 C;Accession: H90332 A;C; Kozers, F; Zivanovic, Y; Allard, G;; Awayez, M.J.; Chan R;She, Q; Singh, R.K.; Confalonieri, F; Zivanovic, Y; Allard, G;; Awayez, M.J.; Chan Jong, I; Jeffries, A.C.; Kozers, C.J.; Medina, N.; Peng, X; Thi-Ngoc, H.P.; Redder, Jenbmitted to GenBank, April 2001 Submitted Submit
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C, Genetics:
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32.7%; Score 33; DB 2; Length 72;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 8; Conservative 3; Mismatches 5; Indels
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32.7%; Score 33; DB 2; Length 76;
Best Local Similarity 37.5%; Pred. No. 4.1e+02;
Matches 6; Conservative 7; Mismatches 3; Indels
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A;Accession: H90332
A;Actatus: preliminary
A;Molecule type: DNA
A;Residues: 1-76 < KUR>
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'(gnz 6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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76
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seq length: 100
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Appl i
                            Sequence 5, Appl
Sequence 3, Appl
                                                                                                                    Sequence 45697
Sequence 9, A
                                              Sequence 1, Sequence 10,
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Sequence 16,
Sequence 6,
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Sequence 17
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          Description
                                                                                                                   US-09-864-761-45697
·US-09-900-147-9
                                                     US-10-214-188-10

US-09-900-147-15

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US-10-214-188-5
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Query
Match Length DB
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10-214-188- 10-029-386- 09-932-581- 10-338-294- 10-165-614-	US-10-214-188-8 US-10-214-188-6 US-09-932-581-6 US-10-38-294-6 US-10-165-614-3	US-09-764-812-344 US-09-925-299-824 US-09-925-229-824 US-10-036-542-148 US-09-864-761-43263	US-09-801-574-48 US-09-839-80-513 US-09-864-761-40202 US-09-864-761-40202 US-09-864-761-41902 US-10-044-359-2 US-10-044-359-2	US-10-U3-U3-U3-U3-U3-U3-U3-U3-U3-U3-U3-U3-U3-
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75 76 85 85	69 74 76 76	000000000000000000000000000000000000000	8 8 4 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	96 7 7 115 115 119 119
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ALIGNMENTS

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parence 5, Application US/09900147

Parent No. USZO020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: BARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 16

TYPE: PRIOR Artificial Sequence

FEATURE:

ORGANISM: Artificial Sequence

FEATURE:

OUTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-900-147-5

Query Match

Best Local Similarity 100.0%; Score 76; DB 10; Length 16;

Best Local Similarity 100.0%; Pred. No. 6.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps

ON 1 RYVDALNYLMANNIS 16

DD 1 RYVDALNYLMANNIS 16
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; Sequence 3, Application US/09900147; Patent No. US20020103121A1

RESULT 2 US-09-900-147-3

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Query Match
Best Local Similarity
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Sequence 1, Application US/09900147

Batent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFREENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT FILING DATE: 2001-07-09

PRIOR PILING DATE: EARLIER PILING DATE: 1999-05-27

PRIOR PILING DATE: BARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
                                            APPLICANT: Bandara, Leantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1999-15-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATCH OF NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-900-147-1
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Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
BERNARDS, RENE
HIJWANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 7.8e-07;
Matches 16; Conservative 0; Mismatches 0;
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RVYDALNVLMAMNIIS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 37
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NS-01-900-147-15

Sequence 15, Application US/09900147

Sequence 15, Application US/09900147

Sequence 15, Application US/09900147

Sequence 15, Application US/0900147

APPLICANT: Bandara, Lesantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT FILING DATE: 2001-07-09

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: BARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NOS: 18
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Best Local Similarity 100.0%; Score 76; DB 15; Length 74;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                  ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Pred. No. 2e-05;
                                                                                                                                                                                                                                                                                                               FILING DATE: 08-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
ADDRESSER: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-214-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 74 amino acids
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                                                                            STATE: VIRGINIA COUNTRY: U.S.A.
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Gaps

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Indels

2;

0; Mismatches

14; Conservative

Matches

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; Sequence 4, Application US/09900147
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  RESULT 8
US-09-900-147-11
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Fatent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REPERBENCE: 200-07-09

FRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935

FRIOR FILING DATE: BARLIER FILING DATE: 1999-02-27

FRIOR FILING DATE: EARLIER FILING DATE: 1999-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTIN OF 2.1

SEQ ID NO 6

LENGTH: 30
                                                                                                                                                 Sequence 16, Application US/09900147

Sequence 16, Application US/09900147

Sequence 16, Application US/09900147

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TILE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPERBNCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT APPLICATION NUMBER: EARLIER PAPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOUTHWARE: Patentin Ver. 2.1
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1 RVYDALNVLMAMNIIS 16
                                          3 RAYDALNALMAMNIIS 18
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                  US-09-900-147-16
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US-09-900-147-6
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LENGTH: 19
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Sequence 17, Application US/09900147

Patent No. US2002013121A1

GENERAL INFORMATION:

APPLICANT: Larangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 2001-07-09

PRIOR FILING DATE: 2001-07-09

PRIOR PLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935

PRIOR PLILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 17

LENGTH: 19
                                                                   APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
LENGTH: 14
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US-09-900-147-17
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Pred. No. 7.2e-05;
0; Mismatches 0;
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84.2%; Score 64; DB 10;

Best Local Similarity 87.5%; Pred. No. 0.0001;

Matches 14; Conservative 0; Mismatches 2
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100.0%; Pred. No.
Sequence 11, Application US/09900147
Patent No. US20020103121A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
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TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT PILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
PRIOR PILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PALENTIN VET. 2.1
SSEQ ID NO 9
LENGTH: 11
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-900-147-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.92
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.07
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.75
OTHER INFORMATION: EXT HUMAN HIT: BEB80658.1, EVALUE 2.00e-51
OTHER INFORMATION: SWISSPROT HIT: Q61501, EVALUE 5.00e-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.5%; Score 46; DB 9; Length 96; 43.8%; Pred. No. 0.98; 2; IndelB tive 7; Mismatches 2; IndelB
                PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PILICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARR: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 45697
APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAP TO AC021804.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09900147
Patent No. US20020103121A1
GENERAL INFORMATION:
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APPLICANT: Bandara, Lasantha R
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S RIYDIVNVLESLHLVS 20
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Best Local Similarity 43.8<sup>3</sup>
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
FRATURE:
OTHER INFORMATION: EXPRE
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| Sequence 45697, Application US/09864761
| Patent No. US200200049763A1
| GRNERAL INFORMATION:
| APPLICANT: Penn, Sharron G. APPLICANT: Rank David M. APPLICANT: Harael, David M. APPLICANT: Harael, David M. APPLICANT: Chen, Wensheng GROME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FOR STRICK PILLING DATE: 2000-05-23 |
| PRICR PRILIANG DATE: 2000-05-24 |
| PRICR PILLING DATE: 2000-06-26 |
| PRICR PILLING DATE: 2000-06-26 |
| PRICR PILLING DATE: 2000-06-27 |
| PRICR PILLING DATE: 2001-06-27 |
| PRICR PILLING DATE: 2001-06-27 |
| PRICR PILLING DATE: 2001-01-30 |
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                             GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: EARLIER PILING DATE: 1999-027
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
PRIOR PILING DATE: BARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 4
LENTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-900-147-4
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100.0%; Pred. No. 0.16;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 60.5
Best Local Similarity 100.
Matches 10; Conservative
             Patent No. US20020103121A1
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US-09-864-761-45697
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Gaps

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Query Match' 5 51.3%; Score 39; DB 15; Length 74; Best Local Similarity 43.8%; Pred. No. 13; Matches 7; Conservative 4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                         BERNARDS, RENE
HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 51.3%; Score 39; DB 15; Best Local Similarity 46.7%; Pred. No. 13; Matches 7; Conservative 4; Mismatches 4
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FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Mug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
  SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10214188
Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEPHONE: (703) 816-4001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-214-188-9; Application US/10214188; Sequence 9, Application US/0214188; Publication No. US20030022260A1; GENERAL INFORMATION:
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                                                                                                                                                                         1 RVYDALNVLMAMNIIS 16
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47 RIYDITNVLEGIQLIA 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON
       ;
US-10-214-188-5
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                                        APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR FILING DATE: EARLIER PILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTING DATE: 1996-12-20
SOFTWARE: PATENTING DATE: 2,1
SEQ ID NO : 2,1
SEQ ID NO : 2,1
                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-900-147-2
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LA TRANGUE, NICHOLAS B.
BERNARDS, RENE
HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13.AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10214188 Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
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                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
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APPLICANT: Andrews, William H.
APPLICANT: Foster, Christopher A.
APPLICANT: Foster, Christopher A.
APPLICANT: Fraser, Stephanie
APPLICANT: Fraser, Stephanie
TITLE OF INVENTION: WETHOOS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT)
TITLE OF INVENTION: TOOS
CURRENT APPLICATION NUMBER: US/09/932,581
PRIOR FILING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/227,865
PRIOR APPLICATION NUMBER: 60/227,865
PRIOR APPLICATION NUMBER: 60/230,174
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APPLICANT: Andrews, William H.
APPLICANT: Fraser, Christopher A.
APPLICANT: Fraser, Stephanie
APPLICANT: Fraser, Stephanie
APPLICANT: Fraser, Stephanie
APPLICANT: Fraser, Stephanie
APPLICANT: Mohammadpour, Hamid
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILER REFERENCE: SIER-005
CURRENT APPLICATION NUMBER: 06/227,865
PRIOR APPLICATION NUMBER: 60/227,865
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-00-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 85
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Pred. No. 15;
4; Mismatches 5; Indels
                                                                                                                                                                                                                     51.3%; Score 39; DB 12; Length 76; 43.8%; Pred. No. 13; cive 4; Mismatches 5; Indels
CTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.4

OTHER INFORMATION: SWISSPROT HIT: Q01094, EVALUE 1.00e-36
US-10-029-386-29071
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Publication No. US20030171326A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 5, Application US/09932581; Publication No. US20030050264A1; GENERAL INFORMATION:
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57 RIYDITNVLEGIQLIA 72
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Best Local Similarity 43.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         51.RIYDITNVLEGIQLIA 66
                                                                                                                                                                                                                                   Query Match 51.3<sup>1</sup>
Best Local Similarity 43.8<sup>1</sup>
Matches 7; Conservative
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 18
US-09-932-581-5
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Sequence 29071, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR UTITLE OF INVERTION: EXPERSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARR: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 29071
LENGTH: 76
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                                                                                                                                                                                                       STREET: LIOU NORTH GLEBE KOAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 1-4UG-1997
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERRATION NUMBER: 32,955
REFERRATION NUMBER: 32,955
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION: OR SEQ ID NO: 9:
INFORMATION: OR SEQ ID NO: 9:
INFORMATION: OR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 15; Length 75; Pred. No. 13; 4; Mismatches 4; Indels
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL
                   BERNARDS, RENE
HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
                                                                                                                                                         ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
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SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-214-188-9
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LENGTH: 75 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.3%;
46.7%;
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                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.7
Matches 7; Conservative
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ORGANISM: Homo sapiens
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US-10-029-386-29071
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APPLICATION NUMBER: US/10/214,188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 816-4100
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                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RVYDALNVLMAMNII 15
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                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER-OIL
CURRENT APPLICATION NUMBER: US/10/165,614
CURRENT FILING DATE: 2002-06-25
PRIOR PILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRAESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10214188
Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: LA THANUE, NICHOLAS B.
HIJMANS, RELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/238,345
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 85
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10165614
Publication No. US20020193289A1
GENERAL INFORMATION:
                                                                                                                                                                                                                     51.3%;
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57 RIYDITNVLEGIQLIA 72
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57 RIYDITNVLEGIQLIA 72
                                                                                                                                                                                                  Query Match
Best Local Similarity 43.8
Trans 7; Conservative
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                         TYPE: PRT
ORGANISM: human
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US-10-214-188-8
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US-10-165-614-2
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LENGTH: 85
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ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 69;
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BERNARDS, RENE
HIJVANS, BLEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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                                                    PRIOR APPLICATION DAIAN

PAPPLICATION NUMBER: US/08/894,139

FILING DATE: 13-AUG-1997

ATTORNEY AGENT INFORMATION:
NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REPRENCE/DOCKET NUMBER: 620-22

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                      TYPE: anino acids
TYPE: anino acid
STRANDEDNESS: cUnknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-214-188-8
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TELEPHONE: (703) 816-4000
FILING DATE: 08-Aug-2002
CLASSIFICATION: <Unknown>
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 76
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47 RIYDITNVLEGIGLI 61
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Best Local Similarity 46.7
Matches 7; Conservative
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Best Local Similarity 46.77
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                      ; TYPE: PRT
; ORGANISM: human
US-10-338-294-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
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; Sequence 6, Application US/10338294
; Publication No. US20030171326A1
; GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Fraser, Christopher A.
APPLICANT: Fraser, Stephanie
APPLICANT: Fraser, Stephanie
APPLICANT: Mohammadpour, Hamid
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REPERENCE: SIER-005
CURRENT APPLICATION NUMBER: US/10/338,294
CURRENT FILING DATE: 2003-01-07
; PRIOR PILING DATE: 2000-08-24
; PRIOR PILING DATE: 2000-08-24
; PRIOR PILING DATE: 2000-09-01
; PRIOR PILING DATE: 2000-09-01
; PRIOR PILING DATE: 2000-09-01
; PRIOR PILING DATE: 2000-10-05
; PRIOR PILING DATE: 2000-10-05
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APPLICANT: FOSTEY, CITISTOPHER A.
APPLICANT: FOSTEY, CITISTOPHER A.
APPLICANT: FOSTEY, STEPHANIE
APPLICANT: FOSTEY, STEPHANIE
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REPERENCE: SIRE-005
CURRENT APPLICATION NUMBER: US/09/932,581
CURRENT PILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/227,865
PRIOR PILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-4
PRIOR FILING DATE: 2000-01
PRIOR FILING DATE: 2000-10-05
NUMBER: 60/238,345
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 6
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                                                                                                                 50.0%; Score 38; DB 15; Length 74;
46.7%; Pred. No. 19;
tive 3; Mismatches 5; Indels
           TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09932581; Publication No. US20030050264A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Andrews, William H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RVYDALNVLMAMNII 15
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47 RIYDITNVLEGIGLI 61
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47 RIYDITNVLEGIQLI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.71
Matches 7; Conservative
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ORGANISM: human
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US-09-932-581-6
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US-10-214-188-6
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; Sequence 3, Application US/10165614
; Publication No. US20020193289A1
; GENERAL INFORMATION:
    APPLICANT: Andrews, William H.
    TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
    TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT)
; FILE REPERENCE: SIER-018
; CURRENT APPLICATION NUMBER: US/10/165,614
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION UNMBER: 60/296,992
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PASLEGG for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (3) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (29)
CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-872-344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 314, Application US/09764872;
Sequence 314, Application US/0050231A1;
GENERAL INFORMATION:
JAPLICANT: Rosen et al.
TITLE OF INVENTION: Uncleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: NUMBER: US/09/764,872;
CURRENT FPLING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper;
NUMBER OF SEQ ID NOS: 957;
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 344
                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%; Score 38; DB 14; Length 76; 46.7%; Pred. No. 20; tive 3; Mismatches 5; Indel8
50.0%; Score 38; DB 12; Length 76; 46.7%; Pred. No. 20;
                                                     5; Indels
                                                           3; Mismatches
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APPLICATION NUMBER: PCT/US01/00666 FILING DAFE: 201-01-30 APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                                                                                                                                                                  Sequence 148, Application US/10036542
Publication No. US20030083481A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.78;
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM; Homo sapiens
US-10-036-542-148
                                                               : | | | | : | |
42 FDALNILM 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-864-761-43263
                                                                                                                                                                       US-10-036-542-148
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LOCATION: (36)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-824
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                                                                                                                                                                                                                                             Sequence 824, Application US/09925299
; Sequence 824, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 824, Application US/09925299
Fublication No. US20030040617A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: PT/US00/05883
FRIOR APPLICATION NUMBER: PT/US00/05883
FRIOR FILING DATE: 2000-08-08
FRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 824
  46.1%; Score 35; DB 11; Length 63; larity 57.1%; Pred. No. 53; Conservative 1; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.1%; Score 35; DB 11; Length 90; Best Local Similarity 75.0%; Pred. No. 80; Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.1%; Score 35; DB 9; Length 90; 75.0%; Pred. No. 80;
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                                                                                                       2 VYDALNVLMAMNII 15
                                                                                                                                 8 VYFLENFEMEKNEI 21
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
Query Match
Best Local Similarity
'Local 8; Conserve
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42 FDALNILM 49
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Best Local Similarity
Matches 6; Conserv
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US-09-925-299-824
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US-09-925-299-824
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 69/32,366
PRIOR FILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-27
| GENERAL INFORMATION: 35 Human Prostate and Prostate Cancer Associated Proteins | TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins | FILE REFERENCE: PA002P1 | CURRENT APPLICATION NUMBER: US/10/036,542 | CURRENT APPLICATION NUMBER: US/10/07 | PRIOR APPLICATION NUMBER: PCT/US00/19666 | PRIOR FILING DATE: 2000-01-07 | PRIOR FILING DATE: 1999-07-21 | PRIOR FILING DATE: 1999-07-21 | PRIOR FILING DATE: 1999-08-13 | PRIOR FILING DATE: 1999-08-13 | PRIOR FILING DATE: 1999-08-13 | PRIOR FILING DATE: 1999-06-13 | PRIOR FILING DATE: 1999-10-06 | PRIOR FILING DATE: 1999-10-06 | PRIOR FILING DATE: 1999-10-06 | PRIOR FILING DATE: 2000-04-05 | PRI
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Pred. No. 74;
5; Mismatches 1; Indels
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Prokaryotic Polynucleotides,
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44.7%; Score 34; DB 9; Length 88;
Best Local Similarity 56.2%; Pred. No. 1.2e+02;
Matches 9; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: No. US20020082234Alel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/936,165
ATTING DATE: «Unknown»
ATTING DATE: «Unknown»
ATTING Gimmi, Edward R
REFERENCE/DOCKET NUMBER: 98/91
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 513:
US-09-939-980-513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-864-761-40202

'Sequence 40202, Application US/09864761

'Patent No. US20020048763A1

'GENERAL INFORMATION:
                                                                              Sequence 513, Application US/09939980 Patent No. US20020082234A1 GENERAL INFORMATION:
                                                                                                                                                                APPLICANT Black, Michael
Burnham, Martin
Hodgson, John
Knowles, David
Lonetto, Michael
Nicholas, Richard
Pratt, Julie
Reichard, Richard
Rosenberg, Martin
Mard, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
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SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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48 MYDAXMDNVLVPINII 63
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                                                        US-09-939-980-513
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Pred. No. 1.1e+02;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 9; Length 67; Pred. No. 86;
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PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PTLING DATE: 2001-01-30
PRIOR PTLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-30
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Peijing Jeremy
APPLICANT: Wang, Peijing Jeremy
APPLICANT: Wang, Peijing Jeremy
APPLICANT: Page, David C.
TITLE OF INVENTION: Reproduction-Specific Genes
FILE REFREENCE: 0399, 2007-002
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,518
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 80
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Sequence 48, Application US/09801574
Patent No. US20020081592A1
GENERAL INFORMATION:
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Best Local Similarity 35.7%;
Matches 5; Conservative
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Matches 7; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT

ORGANISM: Mus musculus
US-09-801-574-48
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica.*L.
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/804,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 59;
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Pred. No. 1.1e+02;
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2010-11-30
PRIOR PILING DATE: 2011-01-30
PRIOR PILING DATE: 2011-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                             APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2002-01-11
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PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
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APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR APPLICATION NUMBER: 60/140,227
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 59
TYPE: PRT
CRGANISM: Hottentotta judaica
US-10-044-359-10
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Patent No. US20020048763A1
GENERAL INFORMATION:
              Sequence 10, Application US/10044359
Publication No. US20020160454A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 33.3%;
Matches 5; Conservative
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5 RLYAIILIVLVMNVI 19
                                                                                                                    APPLICANT: Herrman, Rafael
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I: Chen, Wensheng
INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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N: EXPRESSED IN PLACENTA, SIGNAL = 1.4

N: EXPRESSED IN HEART, SIGNAL = 1.7

N: EXPRESSED IN BRAIN, SIGNAL = 5.2

N: EXPRESSED IN BRAIN, SIGNAL = 1.8

N: EXPRESSED IN PETAL LIVER, SIGNAL = 1.8

N: EXPRESSED IN HELA, SIGNAL = 1.8

N: EXPRESSED IN HELA, SIGNAL = 1.6

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.8

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.8

N: EXPRESSED IN BONE MARROW SIGNAL = 1.8

N: SYLISPROT HIT: P54938, EVALUE 7.00e-17
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                                                                                                                 FILING APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
RRIOR APPLICATION NUMBER: US 60/180,312
RRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 06/23,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-04
PRIOR PLING DATE: 2000-09-13
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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Best Local Similarity 63.0
Transport 17 Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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OTHER INFORMATION:
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FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00661

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RESULT 34 US-10-044-359-10

PRIOR FILING DATE: 2001-01-30

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GENERAL INTOGRAPION: 207 Human Secreted Proteins TITLE OF INVENTION: 207 Human Secreted Proteins TITLE OF INVENTION: 207 Human Secreted Proteins FILLE REFERENCE: P2000-02-2 CURRENT FILING DATE: 2001-08-2 PRIOR PILING DATE: 2001-02-21 PRIOR PILING DATE: 2001-02-21 PRIOR PILING DATE: 2001-02-24 PRIOR PILING DATE: 2001-02-24 PRIOR PILING DATE: 2000-03-24 PRIOR PILING DATE: 2000-03-24 PRIOR PILING DATE: 1000-03-29 PRIOR PILING DATE: 1000-03-29 PRIOR PILING DATE: 1995-06-04 PRIOR PILING DATE: 1995-06-04 PRIOR PILING DATE: 1995-06-04 PRIOR PILING DATE: 1997-06-06 PRIOR PILING
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APPLICATION NUMBER: 60/048,949
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,916
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,970
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FILING DATE: 1997-06-06
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EXPRESSED IN BRAIN, SIGNAL = 5.6
EXPRESSED IN PLACENTA, SIGNAL = 7.9
EXPRESSED IN BONE MARROW, SIGNAL = 7.9
EXPRESSED IN LUNG, SIGNAL = 1.9
EXPRESSED IN HELA, SIGNAL = 5.9
EST HUMAN HIT: AU119666.1, EVALUE 6.00e-35
SWIĞSPROT HIT: P08670, EVALUE 6.00e-36
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42.1%; Score 32; DB 14; Length 58
Best Local Similarity 33.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 9; Length 73;
Pred. No. 1.4e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXPRESSED IN ADULT LIVER, SIGNAL = 3.9
EXPRESSED IN FETAL LIVER, SIGNAL = 4.7
EXPRESSED IN HEART, SIGNAL = 6.2
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-21
PRIOR FILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOCTUMBER: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 41902
LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10044359; Sequence 2, Application US/10044359; Publication No. US200201604541
GENERAL INFORMATION:
APPLICANT: Herrman, Rafael
APPLICANT: Heerman, Rafael
APPLICANT: Lee, Jian-Ming
TILE OF INVENTION: SCORPION TOXINS
FILE REPERBNCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2002-01-11
PRIOR PILING DATE: 2000-06-22
PRIOR FILING DATE: 1909-06-22
PRIOR FILING DATE: 1909-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: MICROSOft Office 97
SEQ ID NO 2
LENGTH: 58
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US-09-933-767-812
; Sequence 812, Application US/09933767
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ORGANISM: Hottentotta judaica
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3 RIFTIILIVFALNII 17
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Best Local Similarity 63.6.
Best Local Similarity 7, Conservative
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DLLNVKMALDI 59
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ORGANISM: Homo sapiens
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US-09-864-761-41902
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FILING DATE: 2001-12-20
APPLICATION NUMBER: 09/205,258
FILING DATE: 1998-12-04
APPLICATION NUMBER: PCT/US98/11422
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/048,885
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (16)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-933-767-812
                DR FILING DATE: 1997-06-06

DR APPLICATION NUMBER: 60/048,883

PFILING DATE: 1997-06-06

DR APPLICATION NUMBER: 60/048,897

PRILING DATE: 1997-06-06

DR APPLICATION NUMBER: 60/048,999

PRILING DATE: 1997-06-06

DR APPLICATION NUMBER: 60/048,963

PRILING DATE: 1997-06-06

DR APPLICATION NUMBER: 60/048,977

PRILING DATE: 1997-06-06

DR APPLICATION NUMBER: 60/048,877

PRILING DATE: 1997-06-06

DR APPLICATION NUMBER: 60/048,878

DR FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,922
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1245
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                    R APPLICATION NUMBER: 60/070, 923
R FILING DATE: 1997-12-18
R APPLICATION NUMBER: 60/073, 160
R PILING DATE: 1998-01-30
R APPLICATION NUMBER: 60/073, 159
R FILING DATE: 1998-01-30
                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/068,064
FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/068,053
FILING DATE: 1997-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/073,165
FILING DATE: 1998-01-30
APPLICATION NUMBER: 60/073,164
FILING DATE: 1998-01-30
APPLICATION NUMBER: 60/085,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1998-05-18
APPLICATION WINBER: 60/085,921
ALING DATE: 1998-05-18
APPLICATION NUMBER: 60/085,923
  APPLICATION NUMBER: 60/048,974
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
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R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,882
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,899
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,993
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,993
R APPLICATION NUMBER: 60/048,990
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R PELLING DATE: 1997-06-06
R PELLING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,915
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,019
R FILING DATE: 1997-06-06
RILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,375
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,881
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048, 896
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,876
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APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,875
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APPLICATION NUMBER: 60/048,901
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,884
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APPLICATION NUMBER: 60/048,894
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APPLICATION NUMBER: 60/
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3; Indels

5; Mismatches

Query Match
Best Local Similarity 38.5%;
Matches 5; Conservative

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US-10-023-282-812; Sequence 812, Application US/10023282; Publication No. US20030092893A1; GENERAL INFORMATION:

Score 32; DB 12; Length 97; Pred. No. 3e+02;

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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: LA Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REPRESENCE: 200-67

CURRENT PILING DATE: 2001-07-09

CURRENT PILING DATE: 2001-07-09

PRIOR PELIANG DATE: BARLIER APPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: BARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: BARLIER FILING DATE: 1999-05-27

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTIN VET. 2.1
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Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: MAP TO AL031280.6
CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98
CTHER INFORMATION: SWISSPROT HIT: P25502, EVALUE 6.40e+00
US-09-864-761-46653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7;
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                    PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 46653
LENGTH: 99
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APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPB: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMB GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMB GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL POR FILE REPRENENCE: Acomica-x.1

GURRENT APPLICANTON: HUMBER: US/09/664,761

CURRENT PELLIAN DATE: 2001-05-23

PRIOR PELLOR TON NUMBER: US 60/180,312

PRIOR PELLOR TON NUMBER: US 60/207,456

PRIOR PELLOR TON NUMBER: US 60/207,456

PRIOR PELLOR TON NUMBER: US 60/206,666

PRIOR PELLOR DATE: 2000-09-20

PRIOR PELLOR TON NUMBER: BC 24266

PRIOR PELLOR TON NUMBER: PCT/US01/00666

PRIOR PELLOR PELLOR UNMBER: PCT/US01/00666

PRIOR PELLOR PELLOR NUMBER: PCT/US01/00666

PRIOR PELLOR PELLOR POLICE: 2001-01-30

PRIOR PELLOR PELLOR NUMBER: PCT/US01/00666

PRIOR PELLOR PELLOR NUMBER: PCT/US01/00666

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PRIOR PELLOR PELLOR POLICE: 2001-01-30

PRIOR PELLOR PELLOR POLICE: 2001-01-30

PRIOR PELLOR PELLOR POLICE: 2001-01-30
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-023-282-812
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EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,978
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-16
EARLIER FILING DATE: 1997-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-15
SEARLIER FILING DATE: 1998-07-15
SEARLIER FILING DATE: 1998-07-15
SOFTWARE: PARENTIN VON: 1227
SOFTWARE: PARENTIN VON: 2.0
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66 YDAIAVFLCIHIV 78
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                         APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY6
FILE REFERENCE: DOO44 CIP
CURRENT APPLICATION NUMBER: US/10/262,272A
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: U.S. 09/966,422
PRIOR APPLICATION NUMBER: U.S. 09/966,422
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.2
SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; COTHER INFORMATION: peptide US-09-962-756-1214
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Pred. No. 53;
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  1; Indels
  1; Mismatches
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US-10-262-272A-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1214, Application US/09962756 Publication No. US20030195147A1 GENERAL INFORMATION:
                                                                                                                                                                      US-10-262-272A-70
Sequence 70, Application US/10262272A
Publication No. US20030170671A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 75.0%;
Matches 6; Conservative
  6; Conservative
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8 YDALDTLM 15
                                         3 YDALNVLM 10
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Best Local Similarity
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TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY6, EXPRESSED HIG
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY6, EXPRESSED HIG
TITLE OF INVENTION: SMALL HINESTINE
FILE REPERENCE: D0040NP/3053-4119US3
CURRENT APPLICATION NUMBER: US/09/966,422B
CURRENT APPLICATION NUMBER: 00/235,602
PRIOR APPLICATION NUMBER: 60/235,602
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
RIOR FILING DATE: 2001-07-19
SEQ ID NOS: 81
SOFTWARE: PACENTIN VERSION 3.0
SEQ ID NOS: 81
                                                                  GENERAL INFOGRATION:
APPLICANT: FEDER, J.N.
APPLICANT: MINNIER, G.
APPLICANT: HAWKEN, D.R.
APPLICANT: HAWKEN, D.R.
APPLICANT: HAWKEN, D.R.
APPLICANT: HAWKEN, D.R.
APPLICANT: CACACE, A.
APPLICANT: BARBER, L.
APPLICANT: BARBER: 2001-09-26
CURRENT APPLICATION NUMBER: 60/235,833
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 55
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.8%; Score 31; DB 11; Length 15; Best Local Similarity 75.0%; Pred. No. 53; Matches 6; Conservative 1; Mismatches 1; Indels
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Pred. No. 53;
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; OTHER INFORMATION: Synthetic Polypeptide
US-09-966-422B-70
             Sequence 55, Application US/09966459A Publication No. US20030022237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 70, Application US/09966422B Publication No. US20030044892A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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8 YDALDTLM 15
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Best Local Similarity
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US-10-253-471-1214

Sequence 1214, Application US/10253471

Sequence 1214, Application US/10253471

BUBLication No. US20030236190A1

GENERAL INFORMATION:

TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS

FILE REFERRINCE: 1878-4057

CURRENT APPLICATION NUMBER: US/10/253,471

CURRENT FILING DATE: 2002-09-24

PRIOR PELING DATE: 2001-09-29

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 1998-09/146,127

PRIOR PILING DATE: 1998-09/146,127

PRIOR PILING DATE: 1998-0-02

NUMBER OF SEQ ID NOS: 2227

SEQ ID NO 1214

LENGTH: 19

LENGTH: 19

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Gaps
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ORGANISM: Artificial Sequence
FEATUME:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-253-471-1214
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40.8%; Score 31; DB 12; Length 19;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 3; Indels
3; Indels
    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 YDALNVLMAMNI 14
    6; Conservative
                                      3 YDALNVLMAMNI 14
                                                               6 YDAIDRLLRMRI 17
    Matches
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Search completed: February 17, 2004, 11:02:21 Job time: 23.4455 secs

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Sequence 5, Appli Sequence 13, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 15, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 12, Appli Sequence 13, Appli Sequence 5, Appli Sequence 6, Appli Sequence 14, Appli Appli Sequence 14, Appli Appli Appli Sequence 14, Appli Appli Sequence 14, Appli App
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                                                                                                                                                                                   February 17, 2004, 10:50:13; Search time 11.5644 Seconds (without alignments) 58.540 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-428-131-13
US-09-308-935-3
US-09-308-935-3
US-09-308-935-1
US-09-308-935-15
US-09-308-935-15
US-09-308-935-15
US-09-308-935-16
US-09-308-935-17
US-08-428-1311-12
US-08-428-1311-12
US-08-428-1311-12
US-08-428-1311-12
US-08-428-1311-12
US-08-428-1311-12
US-08-428-1319-5
US-08-894-139-9
US-08-894-139-9
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Maximum Match 100% Listing first 45 summaries
                                                                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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seq length: 100
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Perfect score:
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                              Run on:
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No.
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Sequence 7, Appli
Sequence 1, Appli
Sequence 2, Appli
Patent No. 5258287
Sequence 8, Appli
Sequence 455, App
Patent No. 5258287
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 513, App
Sequence 30, Appl
Sequence 30, Appl
Patent No. 5248606
Sequence 812, Appl
                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09308935

Patent No. 6268334

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION:
PETILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/308,935

CURRENT APPLICATION NUMBER: US/09/308,935

CURRENT APPLICATION NUMBER: L957-12-22

EARLIER PILING DATE: 1997-12-22

EARLIER PILING DATE: 1997-12-22

NUMBER OF FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOSTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 76; DB 3; Length 16; 100.0%; Pred. No. 6.7e-08; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABOUT 2
US-08-428-131-13
Sequence 13, Application US/08428131
Sequence 13, Application US/08428131
Sequence 13, Application US/08428131
SENERAL INFORMATION:
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
CITY: ALINGTON
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2221-4714
COMPUTER READABLE FORM: /
                                                                                                                                                                                  US-09-107-532A-5706
US-09-235-451-16
US-09-235-451-17
US-08-604-965E-9
                                                  US-09-205-258-812
US-09-308-935-7
US-08-604-965E-7
US-08-604-965E-1
US-08-604-965E-2
525828-4
US-09-217-293-8
US-09-205-258-455
  US-08-936-165A-513
US-08-378-761A-30
US-08-485-286-30
                                                                                                                                                                                                                                                                 ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 16; Conservative
     JS-09-308-935-5
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LENGTH: 16
     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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US-09-308-935-1
; Sequence 1, Application US/09308935
; Patent No. 6268934
; GENERAL INFORMATION:
   APPLICANT: La Thangue, Nicholas B
   APPLICANT: Bandara, Lasantha R
   TITLE OF INVENTION: Peptide antagonists of DP transcription factors
   TITLE OF INVENTION: Peptide antagonists of DP transcription factors
   TITLE OF INVENTION: Peptide antagonists of DP transcription factors
   CURRENT APPLICATION NUMBER: US/09/308,935
   CURRENT FILING DATE: 1999-05-27
   EARLIER FILING DATE: 1997-12-22
   EARLIER FILING DATE: 1997-12-22
   EARLIER FILING DATE: 1996-12-20
   NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                         NS-09-308-935-3

// Sequence 3, Application US/09308935

// Sequence 3, Application US/09308935

// Sequence 3, Application US/09308935

// Sequence 3, Application US/0830835

// SERNEMAL INFORMATION:

// APPLICANT: La Thangue, Nicholas B

// APPLICANT: La Thangue, Nicholas B

// TILE REFERENCE: 620-67

// TILE REFERENCE: 620-67

// TILE REFERENCE: 620-67

// SEALIER APPLICATION NUMBER: US/09/308,935

// CURRENT FILING DATE: 1999-05-27

// SEALIER PILING DATE: 1997-12-22

// SEALIER PILING DATE: 1997-12-22

// NUMBER OF SEQ ID NOS: 18

// SEQ ID NO 3

// LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-3
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Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19;
                                                                   Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                     0; Indels
                                                                   100.0%; Score 76; DB 3; L
100.0%; Pred. No. 7.2e-08;
:ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RVYDALNVLMAMNIIS 16
                                                                                                                                                                              1 RVYDALNVLMAMNIIS 16
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                                                                                                                                                                                                      2 RVYDALNVLMAMNIIS 17
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SEQ ID NO 1
                                                                                             Best Local Similarity 100.
Matches 16; Conservative
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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US-09-078-596-13
                                                                           Query Match
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
                                                                        CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: U5/08/428,131

FILING DATE: 23-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGANT INFORMATION:

NAME: Arthur R. Crawford

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 117-181

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1000

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 76; DB 2; Length 17; 100.0%; Pred. No. 7.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-078-596-13
Sequence 13, Application US/09078596
Sequence 13, Application US/09078596
Sequence 13, Application US/09078596
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIPPICATION:
PRIOR APPLICATION NUMBER: US/08/428,131
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-UNI-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REGISTRATION NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
...... amino acid
     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RVYDALNVLMAMNIIS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100. Matches 16; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
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Gaps
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                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: REALBLE FORDAGE COMPUTER: REALBLE FORDAGE COMPUTER: BM PC COMPATIBLE COMPUTER: BM PC COMPATIBLE COMPUTER: BM PC COMPATIBLE COMPUTER: BM PC-DOS/MS-DOS SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/894,139 FILING DATE: 13-AUG-1997 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARY J. REGISTRATION NUMBER: 620-22 TELECOMMUNICATION INFORMATION: MARCH COMMUNICATION INFORMATION: MARCH COMMUNICATION INFORMATION: MARCH COMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: LA THANGUE, RENE
APPLICANT: HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
NUMBER OF SEQUENCES: 25
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08894139 Patent No. 6448376
  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 RVYDALNVLMAMNIIS 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            CIT.
STATE: Virgin.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
PTLING DATE: 23-JUN-1995
PTLING DATE: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
0; Indels
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Patent No. 6150116

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas Barrie

TITLE OF INVENTION: Transcription Factor DP-1

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSE: Nixon & Vanderhye

STREET: 1100 No. 6150116th Glebe Road, 8th Floor

CITY: Arlington

STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arlington
                                                                                                                                                                                          Sequence 11, Application US/08428131
Patent No. 5863757
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
CORRESPONDENCE ADDRESS:
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 76;
Best Local Similarity 100.0%; Pred. No. Matches 16; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APFLICATION NOTION:
FILING DATE: 23-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ATTOR C. CTAMFORD
NAME: ATTOR C. CTAMFORD
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                           1 RVYDALNVLMAMNIIS 16
                                                                       6 RVYDALNVLMAMNIIS 21
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 amino acids
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-428-131-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 22201-4714
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US-09-078-596-11
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Matches
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1 RUYDALNVLMAMN 13
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; Sequence 15, Application US/09308935
; Patent No. 626834
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas B
; APPLICANT: La Thangue, Nicholas B
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; TITLE OF INVENTION: Poptide antagonists of DP transcription factors
; CURRENT APPLICATION NUMBER: US/09/308,935
; CURRENT FILING DATE: 1997-12-27
; EARLIER PILING DATE: 1997-12-20
; EARLIER FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 15
; LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: GB 9626589.7
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide
US-09-308-935-16
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                                                                                                                               Gapa
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                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 87.5%; Pred. No. 2.5e-06;
Matches 14; Conservative 0; Mismarchae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09308935
Parent No. 6268334
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RVYDALNVLMAMNIIS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RAYDALNALMAMNIIS 18
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                                                                                                                                                                                                     48 RVYDALNVLMAMNIIS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-139-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-09-308-935-16
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US-09-308-935-15
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89.5%; Score 68; DB 3; Length 19;

Query Match

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GENERAL INFORMATION:
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT APPLICATION NUMBER: PCT/GB97/03506
EARLIER FILING DATE: 1999-05-27
EARLIER FILING DATE: 1999-12-20
SAFLIER FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
EENGTH: 14
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                        Gape
                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/108,935
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: PT/GB97/03506
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: GB 9626589.7
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-308-935-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-6
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84.2%; Score 64; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

88.2%; Score 67; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels
                        1; Indels
Best Local Similarity 93.8%; Pred. No. 2.5e-06; Matches 15; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09308935 Patent No. 6268334
                                                                                                                                                                                                                                                            Sequence 6, Application US/09308935
Patent No. 6268334
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                              3 RVYAALNVLMAMNIIS 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YDALNVLMAMNIIS 14
                                                                               1 RVYDALNVLMAMNIIS
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RESULT 16
US-09-308-935-2
; Sequence 2, Application US/09308935
; Sequence 2, Application US/09308935
; Patent No. 626834
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas B
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; TITLE OF INVENTION: 1999-02.7
; EARLIER APPLICATION NUMBER: DCT/GB97/03506
; EARLIER APPLICATION NUMBER: GB 9626589.7
; EARLIER APPLICATION NUMBER: DS 97.12-20
; SEQ ID NOS: 18
; SEQ ID NO 2
; LENGTH: 9
; Sequence 9, Application US/09308935
; Patent No. 626834
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas B
; APPLICANT: Bandara, Lasantha R
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; FILE REPRENCE: 620-67
; CURRENT FILING DATE: 1999-05-27
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: PCT/GB97/03506
; EARLIER APPLICATION NUMBER: 999-12-22
; EARLIER PILING DATE: 1996-12-20
; CONTREST FILING DATE: 1996-12-20
; CONTREST FILING DATE: 1996-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.9%; Score 44; DB 3; Length 11; Best Local Similarity 100.0%; Pred. No. 0.036; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.3%; Score 42; DB 3; Length 9; Best Local Similarity 100.0%; Pred. No. 2.5e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-428-131-14
; Sequence 14, Application US/08428131
; Patent No. 5863757
; GENEAL INFORMATION:
; APPLICANT: La Thangue, Nicholas Barrie
; TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
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; Sequence 4, Application US/09308935
; Patent No. 626834
; GENERAL INPORMATION:
    APPLICANT: La Thangue, Nicholas B
; APPLICANT: Bandara, Lasantha R
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; TITLE REFERENCE: 620-67
; CURRENT APPLICATION NUMBER: US/09/308,935
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: PCT/GB97/03506
; EARLIER PTLING DATE: 1997-12-22
; EARLIER PTLING DATE: 1996-12-20
; MUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; TYPE: PRT
                                                                                                                                                                                                                                JOHNSTON IN COURTY IN CALCULAGE

APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
ITILE OF INVENTION: Peptide antagonists of DP transcription factors
ITILE OF INVENTION: Peptide antagonists of DP transcription factors
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1990-05-27
EARLIER PILING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-22
BARLIER FILING DATE: 1997-12-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide US-09-308-935-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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84.2%; Score 64; DB 3; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.5%; Score 46; DB 3; Length 20; 100.0%; Pred. No. 0.031; Live 0; Mismatches 0; Indels
                                                                                           RESULT 13
US-09-308-935-17
Sequence 17, Application US/09308935;
Patent No. 6268334;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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              2 RVYDALNVLMAMN 14
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Matches 10; Conservative
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US-09-308-935-4
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US-09-308-935-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 NO. CITY: Arlington
STATE: 1200 NO. CITY: Arlington
STATE: Virginal
COUNTRY: U.S.A.
ZIP: 222014714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-UN-1995
ILLASIFICATION NUMBER: 25.327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 73;
                                                                                                                                                                                                                                                                              DB 3; Length 17;
                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08428131
Sequence 12, Application US/08428131
Patent No. S863757
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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Pred. No. 3;
4; Mismatches
                                                                                                                                                                                                                                                                                Score 39; DB 3; Pred. No. 0.51;
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US-09-078-596-12
; Sequence 12, Application US/09078596
TELECOMMUNICATION INFORMATION:
                                          TELEFACE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.3%;
ilarity 43.8%;
Conservative
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                                                                                                                                                                                                                                                                                     Query Match 51.3%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 1 RVYDALNVLMAMNIIS 16
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                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-078-596-14
                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                               amino acid
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                                                                                                   STREET: ALTON NO. 2003/37/LL GLEEN COUNTRY:
CITY: Artington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENAPPLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: STATEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
CLASSIFICATION: S14
ATTORNAY AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703) 816-4000
TELEFAX: (703) 816-4100
TELEFAX: 17 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 2; Length 17;
Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/078,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COMPUTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
                 NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
CARRESEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 18
US-09-078-596-14
; Sequence 14, Application US/09078596
; Parent No. 6150116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 43.8%;
Matches 7; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RVYDALNVLMAMNIIS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-131-14
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08894139
Fatent No. 6448376
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: HUMANS, ELEANORE M.
TITLE OF INVERTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                  CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY 32,955
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
LENGTH: 74 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RVYDALNVLMAMNIIS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 RIYDITNVLEGIQLIA 62
      13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-894-139-7
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-139-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-894-139-7
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Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                               COMPTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
                                                                                                                               ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08894139
Patent No. 6448376
GENERAL INFORMATION:
APPLICANT: BERNARDS, RENE
APPLICANT: HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
Patent No. 6150116
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
ATTORNEY, AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMOUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ABLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 43.8%;
Matches 7; Conservative
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9 RIYDITNVLEGIQLIA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-078-596-12
                                                                                                                                                                  CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 21
US-08-894-139-5
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Sequence 6, Application US/08894139

Patent No. 6448376

GENERAL INFORMATION:

APPLICANT: BERNARDS, REINE
APPLICANT: HIJMANS, ELEANORE M.

TITLE OF INFORMATION: TRANSCRIPTION FACTOR E2F-5

NUMBER OF SEQUENCES: 25

CORRESPONDENCE SISS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIKGINIA
COMPUTER: PLOPY disk
MEDIUM TYPE: FLOPY disk
COMPUTER: PLOPY disk
COMPUTER: PLANBELE FORM:
MEDIUM TYPE: PLOPY disk
COMPUTER: PLANBER: US/08/89-DOS
SOFTWARE: PALENTION SAGENER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELEPRONE: (703) 816-4000
TELEFRAX: (703) 816-4000
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFCATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARN J:
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 32,955
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 8:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
THORE AND ACCOUNTY OF A SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RVYDALNVLMAMNII 15
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 RIYDITNVLEGIGLÍ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-894-139-8
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US-08-894-139-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.

ZIP: ALLINGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,139

FILING DATE: 13-AUG-1997

CLASSIFICATION: S36

ATTORNEY/AGRAT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 20,955

REFERENCE/DOCKET NUMBER: 20,925

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 9:

SEQUENCE CHARACTERSOTICS:

LENGTH: 75 amino acids

TYPE: ATRANDEDNESS:

FORMATION OF 15 and 15 and
                                                                                                                                                                                                                                           Sequence 9, Application US/08894139
; Sequence 9, Application US/08894139
; Patent No. 6448376
; GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: BERNARDS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STRATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: BERNARDS, RENE
APPLICANT: HIJMANS, ELERNORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100:NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
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; Sequence 8, Application US/08894139
; Patent No. 6448376
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                                                        1 RVYDALNVLMAMNII 15
                                                                                            |:|| ||| :::|
47 RIYDITNVLEGIHLI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.7°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-894-139-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                RESULT 23
US-08-894-139-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSEDE: SmithKline Beecham Corporation STRRET: 709 Sweedland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                             Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ for Windows Version 2.0
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 1;
Pred. No. 21;
4; Mismatches
               REGISTRATION NUMBER: 29,655
REFERENÇE/DOCKET NUMBER: NIH101.001DV1
TELECOMONUMICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ 1D NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 513, Application US/08936165A Patent No. 6348582 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T: Lonetto, Michael
T: Nicholas, Richard
T: Pratt, Julie
T: Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 513:
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                                                                                                                                                                                                                                                                                                                                                                               44.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hodgson, John
Knowles, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Black, Michael APPLICANT: Burnham, Marti
      Israelsen, Ned A.
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gimmi, Edward R
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO FRAGMENT TYPE: internal US-08-194-338-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                               Sequence No. 6380370

SEGUENCAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WILL OF INFORMATION:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
GENERAL APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
FRIOR FELLING DATE: 1998-08-13
FRIOR FILING DATE: 1997-11-08
FRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4216
LENGTH: 67
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                                                                                                         Gaps
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                                                             Score 38; DB 4; Length 74;
Pred. No. 4.6;
3; Mismatches 5; Indels
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Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08194338

Sequence 14, Application US/08194338

Patent NO. 5474898

GENERAL INFORMATION:

APPLICANT: Venter, John C.

APPLICANT: McCombie, William R.

TITLE OF INVENTION: OCTOPAMINE RECEPTOR

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, olson and Bear

STREET: 620 Newport Center Drive, Sixteenth Floor

CITY: Newport Beach

STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,336
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4216
                                                             Query Match 50.0%;
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40.0%;
Matches 6; Conservative
                                                                                                                                                                      1 RVYDALNVLMAMNII 15
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11 LYSKLNILMSIIILN 25
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ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
; MOLECULE TYPE: peptide US-08-894-139-6
                                                                                                                                                                                                                                                                        US-09-134-001C-4216
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US-08-194-338-14
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APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TROTHY D
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREST:
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5248606-16
Pacent No. 5248606
Pacent No. 5248606
Pacent No. 3000000
Paticant: Walsh, Terence A.; Hey, Timothy D.; Morgan, Tille B.R.
PITLE B.R.
TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND ACTIVE PORMS OF MALZE RIBOSOME INACTIVATIN
NUMBER OF SEQUENCES: 49
CURRENT APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 11-JUN-1990
                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US

ZIF: 46268 E COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BORUCKI, NUDREA T
REGIETRATION NUMBER: 33621
REFERENCE/DOCKET NUMBER: 3827
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 amino acide
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-485-286-30
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11 KTYDSLNVI 19
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5248606-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30. Application US/08378761A
Sequence 30. Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOWE-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                           Query Match

44.7%; Score 34; DB 4; Length 88;
Best Local Similarity 56.2%; Pred. No. 32;
Matches 9; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ed. No. 16;
Mismatches
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Pred. No.
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US-08-465-286-30
Sequence 30, Application US/08485286
; Patent No. 5646026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INPORMATION:
NAME: BORUCKI, ANDRER T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 3827.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.1%;
illarity 55.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                2 VYDAL -- NVLMAMNII 15
                                                                                                                                                                                                                                                                                                                                                       : 25 amino acids
amino acid
                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-378-761A-30
                                                                                                                                                 single
                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : ||:||:
11 KTYDSLNVI 19
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Matches 5; Conserv
                                                                                                                              TYPE: amino acid STRANDEDNESS: siz
                                                                                                                                                                                                              US-08-936-165A-513
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 29
US-08-378-761A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Gaps

APPLICATION NUMBER: 60/048,883

11 KTYDSLNVI 19

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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007Pl
                                  CURRENT APPLICATION NUMBER: US/09/205,258 CURRENT FILING DATE: 1998-12-04
RESULT 32
US-09-205-258-812
; Sequence 812, Application US/09205258
; Patent No. 6525174
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LOCATION: (16)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-205-258-812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT PILING DATE: 1999-05-27
EARLIER PILING DATE: 1999-12-22
EARLIER PILING DATE: 1997-12-20
EARLIER PILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.0%; Pred. No. 2.5e+05; 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 4
Pred. No. 83;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-07-12-18
EARLIER FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09308935 Patent No. 6268334 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 38.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 812
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 YDALNVLMAMNII 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 YDAIAVFLCIHIV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-308-935-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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APPLICANT: Kobayani, Fumie
APPLICANT: Yamaguchi, Kyoji
APPLICANT: Yamaguchi, Fumie
APPLICANT: Washida, Nachiro
APPLICANT: Satake, Nachiro
APPLICANT: Marinaga, Toomonori
APPLICANT: Higashio, Kanji
TITLE OF INVENTION: Basic Osteoblast Growth FactorII(boGF-
TITLE OF INVENTION: 11)
NUMBER OF SEQUENCES: 20
CORRESPONDENCES: 20
CORRESPONDENCES: Burgess, Ryan and Wayne
ADDRESSE: Burgess, Ryan and Wayne
STREET: 370 Lexington Avenue, Suite 2105
CITY: NEW YORK
STATE: NEW YORK
STATE: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08604965E Patent No. 6046033 GENERAL INFORMATION: APPLICANT: Goto, Magaaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goto, Masaaki
Tsuda, Eisuke
Yano, Kazuki
Kobayashi, Eumie
Yamaguchi, Kyoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
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Ueda, Masatsugu
Higashio, Kanji
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Feuda, Eisuke
Yano, Kazuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-604-965E-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: 811
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-604-965E-2
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APPLICANT: Washida, Nacus-
APPLICANT: Satake, Toshiko
APPLICANT: Satake, Toshiko
APPLICANT: Morinaga, Tomonori
APPLICANT: Mostanga, Tomonori
APPLICANT: Higashio, Kanji
TITLE OF INVENTION: Basic Osteoblast Growth FactorII(boGF-
TITLE OF INVENTION: II)
NUMBER OF SEQUENCES: 20
CORRESPONDENCES: 20
CORRESPONDENCES: 20
CITY: NEW YORK
STREET: 370 Lexington Avenue, Suite 2105
CITY: NEW YORK
STREET: WAY YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10017
ZIP: 10017
ZIP: 1017
ZIP: 1017
ZIP: 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM

COMPUTER READABLE FORM

COMPUTER: 5 1/4 inch diskette

COMPUTER: 9 1/4 inch diskette

COMPUTER: 9 2/4 inch diskette

COMPUTER: 9 1/4 inch diskette

COMPUTER: 9 1/4 inch diskette

COMPUTER: 9 1/4 inch diskette

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/604,965E

FILING DATE: US/08/604,965E

FILING DATE: JUNE 27, 1994

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 1,906

REFERENCE/DOCKET NUMBER: 1,906

REFERENCE/DOCKET NUMBER: 1,906

REFERENCE/DOCKET NUMBER: 1,906

TELECOMMUTCATION INFORMATION:

TELECOMMUTCATION INFORMATION:

TELEPHONE: 212-633-8150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-604-965E-1; Sequence 1, Application US/08604965E; Patent No. 6046033
                                                                                                                               US-08-604-965E-7; Sequence 7, Application US/08604965E; Patent No. 6046033
                                                                                                                                                                                                               Goto, Magaaki
Tauda, Elsuke
Yano, Kazuki
Kobayashi, Fumie
Yamaguchi, Kyoji
Washida, Naohiro
Satake, Toshiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 423794
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 DALNVLMAMNIIS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
;
TOPOLOGY: linear
US-08-604-965E-7
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                    ALNVLMA 11
                                         1 ALNVLMA 7
                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Goto, 1
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APPLICANT:
APPLICANT:
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Score 31; DB 3; Length 25; Pred. No. 25; 4; Indels 3; Mismatches 4; Indels
COUNTRY: UNITED CONTRY:

ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: 5 1/4 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,965E
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01270
FILING DATE: June 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WAYNE, Milton 17,906
REGISTRATION NUMBER: 17,906
REGISTRATION STATEMER: 17,906
REGISTRATION NUMBER: 17,906
REGISTRATI
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Sequence 8, Application US/09217293
Patent No. 6337181
GENERAL INFORMATION:
APPLICANT: Stewart, Jeffrey J
TITLE OF INVENTION: QUASISPECIES
FILLE REPERENCE: Stewart, US/09/217,293
CURRENT APPLICATION NUMBER: US/09/217,293
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
LENGTH: 43
                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Influenza A virus
FEATURE:
ORGANISM: Influenza A virus
FEATURE:
OTHER INFORMATION: Xaa1 is HY; Xaa2 is KE; Xaa3 is SRk; Xaa4 is DE;
OTHER INFORMATION: Capital letters indicate advantageous variants and
OTHER INFORMATION: lowercase letters indicate possibly advantageous
OTHER INFORMATION: variants (see detailed description)
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; Sequence 7, Application US/08740644
; Patent No. 60384710;
; GENERAL INFORMATION:
APPLICANT: Timothy F. Murphy
; TITLE OF INVENTION: Peptide Expression And Delivery Syst
NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB 4; Length 43; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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COUNTRY: United States
ZDIP: 14203-2391
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM Compatible
OORPWIER: IBM Compatible
OORPWIER: Wordperfect for Windows 3.1
SOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/08/740,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: October 31, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,168
FILING DATE: No. 603877ember 2, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 11520.0065
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (716) 856-4000
TELEPAX: (716) 849-0349
INFORMÁTION FOR SEO ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n
Similarity 63.6%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 YDALNVLMAMN 13
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Best Local Similarity
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION:
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Basic Osteoblast Growth FactorII(bOGF-II)
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Fatent No. 5258287

Fatent No. 5258287

TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53

NUMBER OF SEQUENCES: 58

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/171,623

FILING DATE: 22-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.8%; Score 31; DB 3; Length 40; 46.2%; Pred. No. 43; tive 3; Mismatches 4; Indels
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46.2%; Pred. No. 46;
tive 3; Mismatches 4; Indels
                                                                                                       ADDRESSEE: Burgess, Ryan and Wayne
STREET: 370 Lexington Avenue, Suite 2105
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIPTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01270
FILING DATE: JUNe 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Wayne, Milton J.
REGISTATION NUMBER: 17,906
REFERENCE/DOCKET NUMBER: U-Wp-5212
TELECOMMUNICATION INPORMATION:
TELEPHONE: 212-683-8150
TELEFAX: 212-532-4285
                                                                                                                                                                                                         ZIP: 10017
COMPUTER READBLE FORM:
MEDIUM TYPE: 5 1/4 inch diskette
COMPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: DOS
SOFTWARE: WONDERFECT 5.1
CURRENT APPLICATION NATA:
                                                                                                                                           CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.2°
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14 DTLNHLKFLNVLS 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 423794
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | || | :|::|
13 DTLNHLKFLNVLS 25
                 TITLE OF INVENTION: Basi
TITLE OF INVENTION: II)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURGESS, Ry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
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US-09-217-293-8
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SEQ ID NO:4: 5258287-4

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APPLICANT: BAXTER, ROBERT C., WOOD, WILLIAM I.
TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION
OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53
NUMBER OF SEQUENCES: 58
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/171,623
FILING DATE: 22-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.8%; Score 31; DB 6; Length 60;
46.2%; Pred. No. 71;
tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 37.5%; Pred. No. 63;
Matches 6; Conservative 5; Mismatches 5; Indels
                                                                                                         BARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILLING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER PILLING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,977
EARLIER PILLING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,973
EARLIER FILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-01-15
EARLIER FILLING DATE: 1997-15-18
EARLIER FILLING DATE: 1998-07-15
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US-09-107-532A-5706
; Sequence 5706, Application US/09107532A
                                                PPLICATION NUMBER: 60/049,374
                                                                                 ILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RVYDALNVLMAMNIIS 16
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35 RVYPAMHFTLCVHIYS 50
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DTLNHLKFLNVLS 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-455
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Best Local Similarity
Matches 6; Conserv
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5258287-1
;Patent No. 5258287
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; LENGTH: 60
5258287-1
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                                                                                                                             Score 31; DB 3; Length 46;
Pred, No. 51;
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007 P21
CURRENT PAPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: OC/048,885
EARLIER PAPLICATION NUMBER: 60/049,375
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PRILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
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EARLIER PILING DATE: 1997-06-06
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EARLIER PILING DATE: 1990-06-06
EA
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REPLING DAKE: 1997-06-06

RE APPLICATION NUMBER: 60/048, 994

REPLING DAKE: 1997-06-06

RE APPLICATION NUMBER: 60/048, 964

REPLING DATE: 1997-06-06

REPLING DATE: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 455, Application US/09205258 partent No. 6525174
                                                                                                                                              Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative
; ORIGINAL SOURCE:
; ORGANISM: H. influenzae
US-08-740-644-7
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7 YDANNIIVAI 16
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APPLICANT: Caterina, Michael J.
TITLE OF INVENTION: NOTEL ALID SEQUENCES ENCODING
TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
FILE REPERENCE: 9076/084CIP
CURRENT APPLICATION NUMBER: 60/072,151
PRIOR PLILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR PLILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Ucda, Masatsugu
APPLICANT: Higashio, Kanji
TITLE OF INVENTION: Basic Osteoblast Growth Factorii(bOGF-
TITLE OF INVENTION: II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
40.8%; Score 31; DB 4; Length 75;
Best Local Similarity 23.1%; Pred. No. 93;
Matches 3; Conservative 7; Mismatches 3; Indels
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                                                                                                                                                                                                                              Score 31; DB 4
Pred. No. 93;
7; Mismatches
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                                           NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 9, Application US/08604965E; Patent No. 6046033; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-235-451-17; Sequence 17, Application US/09235451; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goto, Masaaki
Tsuda, Estsuke
Yano, Kazuki
Kobayashi, Fumie
Yamaguchi, Kyoji
Washida, Naohiro
Satake, Toshiko
                                                                                                                                                                                                                              Query Match
Best Local Similarity 23.1%;
Matches 3; Conservative
                        PRIOR FILING DATE: 1997-08-20
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US-09-235-451-17
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                                                                                                                                    ; TYPE: PRT
; ORGANISM: Caliphora
US-09-235-451-16
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APPLICANT:
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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APPLICANT: Caterina, Michael J.
APPLICANT: Caterina, Michael J.
APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: UNCLEIC ACID SEQUENCES ENCODING
TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/235,451
CURRENT PILING DATE: 1999-01-22
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-22
PRIOR PLING DATE: 1998-01-22
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                                                                                                                                  NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION UNDERE: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION UNDERE: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
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LOCATION: (B) LOCATION 1...63

SEQUENCE DESCRIPTION: SEQ ID NO: 5706:

US-09-107-532A-5706
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                                                                                                                                                                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 16, Application US/09235451; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 5706:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 63 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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40 RVYDFLEIL 48
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Query Match

40.8%; Score 31; DB 3; Length 85;
Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 4; Indels
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: 5 1/4 inch diskette
CONPUTER: PC'S LIMITED SYSTEM 200
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: WORDPERFECT 5.1
CLASSIFICATION NUMBER: US/08/604,965E
FILING DATE: June 27, 1994
ATTORNEY/ASTEN INFORMATION:
PILING DATE: June 27, 1994
ATTORNEY/ASTEN INFORMATION:
PREJETRACION NUMBER: 17,906
REGISTRATION NUMBER: 17,906
REGISTRATION NUMBER: 17,906
REGISTRATION NUMBER: 17,906
REGISTRATION NUMBER: 17,906
REJERBENCE/DOCKET NUMBER: 17,906
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Search completed: February 17, 2004, 10:59:41 Job time : 12.5644 secs

4 DALNVLMAMNIIS 16 | || | :|::| 13 DTLNHLKFLNVLS 25

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us-09-900-147-5.rspt

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Run on:

Sequence:

Minimum DB Maximum DB

Database

Searched:

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SEQUENCE FROM N.A.
STRAIN=UA159 / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar P., Lai H., White J., Roe B.A., Perretti J.J.;
"Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 16; Length 68;
Pred. No. 1.1e+02;
; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
EMBL, AE014994; AAN5277.1; Arpothetical protein; Complete proteome.
SEQUENCE 68 AA; 7604 MW; EEF4578026865773 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                        Q8U278
Q8U178
Q8DK14
Q9RG90
Q9RG90
Q9X3B0
Q9X3A5
Q9DFF6
Q9DFF6
Q9BE4Q0
                                                                                                                                                                           Q8HA80
Q99UH5
Q8NWX8
Q9PGG
Q8ZV98
Q9KDN1
Q8F678
Q9HKS3
Q8GFW0
Q91FVZ
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Q9AC63
Q98215
Q8RUQ9
Q8S3M1
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53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus mutans
                                                                                                                                                                           40.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1309;
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Best Local 6
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                                                                                          February 17, 2004, 10:50:12; Search time 22.6535 Seconds (without alignments) 182.261 Million cell updates/sec
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              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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QBC8H4
Q99VZ5
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Q94Q82
Q484Q82
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P92249
P92261
Q95Z682
Q99RD1
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Q97A1Z
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
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sp_bacteriap:*
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Gaps

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Result No. 35AFAB2F9FF612AC CRC64;

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74 AA; 8228 MW;
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01-МAR-2001
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Q9HQ82
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MEDLINE=2131952; PubMed=11418146;

MEDLINE=2131952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Ranehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=223546683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK047089; BAC32957.1; -.
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MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Maba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SAV0618 (Hypothetical protein WW0582).
SAV0618 OR SA0575 OR WW0582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 11; Length 80; Pred. No. 1.3e+02; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 AA; 9655 MW; D03C342182DC4BD2 CRC64;
                 Q8C8H4;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Unknown EST (Fragment).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus (strain Mus0 / ATCC 700699), Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain MW2). Staphylococcus aureus (strain MW2). Staphylococcus aureus; Bacillales; Staphylococcus. NCBI_TaxID=158878, 158879, 196620;
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EMBL; AP003359; BAB56780.1; -.
EMBL; AP004313; BAB41807.1; -.
EMBL; AP040434; BAB94447.1; -.
Hypothetical protein; Complete proteome.
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Best Local Similarity 50.v
6; Conservative
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18 IYNALKLFMEMN 29
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MEDLINE=20504483; PubMed=11016950;
MEDLINE=20504483; PubMed=20504483;
MEDLINE=20504483; PubMed=20504483;
MEDLINE=20504483;
MEDLINE=2050
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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MEDLINE=21175748; PubMed=11279525;
MEDLINE=21175748; PubMed=11279525;
Mang P.J., McCarrey J.R., Yang F., Page D.C.;
Man abundance of X-linked genee expressed in spermatogonia.";
Nat. Genet. 27:422-426 (2001).
EMBL, AF285583; AAK1952.1; -.
MGD; MGI1890547; Text8.
SEQUENCE 80 AA, 9115 MW; F5CB6CE95F8EC2B1 CRC64;
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Length 74;
                                                                                    2; Indels
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Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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Last annotation update)
Score 34; DB 16;
Pred. No. 1.8e+02;
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    50.08;
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Best Local Similarity 50.03
Matches 7; Conservative
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                                                   Best Local Similarity 50.0
Matches 6; Conservative
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35 DSMNALVDLNII 46
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01-MAY-1999
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"Mitochondrial sequence characterisation of Austrailan commercial and feral honeybee strains (Hymenoptera: Apidae: Apis mellifera Linnaeus), in the context of the species worldwide.";

J. Aust. Entomol. Soc. 0:0-0(1997).

-!- FUNCTION: SUBGNITS I, II AND III FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME C + 2 H(2)0.

-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBGNIT 3 FAMILY. EMBL, U72265; AAB41167.1; - InterPro; IPR000298; CytC_oxdse_III.
                                                                                                                                                                                                                                                                    Alonso J.C., Luder G., Stiege A.C., Chai S., Weise F., Trautner T.A., "Analysis of the complete nucleotide sequence and functional organization of Bacillus subtilis bacteriophage SPP1.";
Submitted (WAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X97918; CAA66519.1; -...
InterPro; IRR006479; Hodin SPP1.
Fram: PF04688; Phage holin; 1.
TIGRFAMS; TIGR01522; holin SPP1; 1.
SEQUENCE 82 AA; 9391 MW; 558F709ADSE0D3AO CRC64;
                                Gaps
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
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01-MAY-1997 (TTEMBLrel. 03, Created)
01-MAY-1997 (TTEMBLrel. 03, Last sequence update)
01-0CT-2002 (TTEMBLrel. 22, Last annotation update)
Cytochrome oxidase subunit III (BC 1.9.3.1) (Cytochrome c oxidase
COII:
Apis mellifera (Honeybee).
                                                                                                                                                                                                    Bacteriophage SPP1.
Tituees, deDNA viruses, and RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
NCBI_TaxID=10724;
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          Length 66;
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Pred. No. 3.1e+02;
                                4; Indels
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
         Score 33; DB 17;
Pred. No. 2.5e+02;
43.4%; Scor.
50.0%; Pred. No. 4...
4; Mismatches
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50.0%;
                                                    1 RVYDALNVLMAMNIIS 16
                                                                         20 RVFDALLVLGPVVIVA 35
        Query Match
Best Local Similarity 50.0
Matches 8; Conservative
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nes 6; Conservative
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KOULIADOS S., Crozier R.H.;

KOULIADOS S., Crozier R.H.;

Mitochondrial sequence characterisation of Austrailan commercial and feral honeybee strains (Hymenoptera: Apidae: Apis mellifera Linnaeus), in the context of the species worldwide.";

J. Aust. Entomol. Soc. 0:-0(1997).

-!- FUNCTION: SUBUNITS I, II AND III FORM THE FUNCTIONAL CORE OF THE EXTRM COMPLEX (BY SIMILARITY).

-!- CATALYNIC ATIVITY: 4 PERROCYTOCHROME C + 0(2) = 4 FERRICYTOCHROME C + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C + 2 H(2)O.

1 - SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.

EMBL, V12271, AAB41169.1, -.

Interpro; IPR001298; CytC_oxdse_III.

Ffam; PF00510; COX3; 1.

ProDom; PD000382; CytC_oxdse_III; 1.

PROSITE; PS50253; COX3; 1.

Oxidoreductase; Transmembrane; Mitochondrion.
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Poeptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.
NCBI_TaxID=7460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Last sequence update)
, Last annotation update)
III (EC 1.9.3.1) (Cytochrome c oxidase
                                                                                                                                                                                                                         . 0
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Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                              Length 55;
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                                                                                                                                                                            42.1%; Score 32; DB 8; Length 55; illarity 26.7%; Pred. No. 3.1e+02; Conservative 7; Mismatches 4; Indels
                                                                                                                            55 AA; 6506 MW; 650A864ED7C2FC0C CRC64;
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Last annotation update)
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Pfam; PF00510; COX3; 1.
ProDom; PD003182; CYCC oxdse_III; 1.
PROSTIE; PS550253; COX3; 1.
Oxidoreductase; Transmembrane; Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 AA; 6488 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 10, (TrEMBLrel. 10, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| :::: | :|
34 IYSSISMFMILNFIN 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VYDALNVLMAMNIIS 16
                                                                                                                                                                                                                                                                                2 VYDALNVLMAMNIIS 16
                                                                                                                                                                                                                                                                                                                                34 IYSSISMFMILNFIN 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide III) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apis mellifera (Honeybee).
Mitochondrion.
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01-DEC-2001 (TrEMBLrel. 15
Exonuclease I (Fragment).
Bradyrhizobium japonicum.
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ses 4; Conserv
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71 AA

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01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2000 (TrEMBLrel. 15, Last annotation update)
                                          PRT;
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35 RIYDNMNISSQLVVI 49
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                                            PRELIMINARY;
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SEQUENCE FROM N.A.
SETAINSMUSO, and N315,
MEDLINE-21311952; PubMed=11418146;
MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashira A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
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                                                              Mayer R.M., "Analysis of a DNA fragment present in Bradyrhizobium japonicum 110 Fix+ derivatives but missing in a Fix- derivative."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF101073; AAD17890.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.; "Genome and virulence determinants of high virulence community-
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SAV2504 (Hypothetical protein WW2422).
SAV2504 OR SA2292 OR WW2422.
                                                                                                                                                                                                                             Length 61;
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SEQUENCE 66 AA, 8016 MW, 8B6BB4B3627F791C CRC64;
                                                                                                                                                                                    SEQUENCE 61 AA; 6729 MW; FF29A9A1891C986A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain MW2).

Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                       42.1%; Score 32; DB 2; I
46.2%; Pred. No. 3.5e+02;
iive 5; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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EMBL, AP003365; BABS866.1; -
EMBL, AP003137; BAB83595.1; -
EMBL, AP004830; BAB96287.1; -
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25 DALSLVMAADAVS 37
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                                                                                                                                                                                                                                                 Local Similarity 46.2
nes 6; Conservative
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                                    SEQUENCE FROM N.A.
NCBI_TaxID=375;
                                                          STRAIN=USDA110;
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Matches
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Q99RD1
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RVYDDLNTI 55

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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Brioks S., Buehler E., Chiou J., Choi E., Kin C., Altafi H., Bei B., Chin C., Chiou J., Choi B., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu S., Mukharsky N., Lee J., Lenz C., Li J., Liu A., Liu S., Mukharsky N., Than P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vayeberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J., Thank M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J., Ekker J., Ekk
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A Yao C.W., Huang C.J.;
Yao C.W., Huang C.J.;
Tiuviatilis)...;
Tiuviatilis)...;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
R RHSP; 0129677, 2RGF.
R InterPro; IPR000463; Fatty acid BP.
R InterPro; IPR000159; RA_domain...
R PROSITE; PS0214; FABP; 1.
R PROSITE; PS0214; FABP; 1.
T NON TER.
1 1 1
C SEQUENCE 78 AA; 9109 MW; 5EDA65DB7C297A16 CRC64;
                  Eukaryota; Viridiplantae; Sreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Botinopterygii, Neopterygii; Teleostei; Buteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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Best Local Similarity 33.3%; Pred. No. 4e+02;
Matches 5; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                 Ecker J.R.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Guanine nucleotide dissociation stimulator (Fragment)
Arabidopsis thaliana (Mouse-ear cress).
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                             6 LNVLMAMNIIS
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Matches
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                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL; AP001514; BAB05915.; Hypothetical protein; Complete proteome.

SEQUENCE 35 AA; 3960 MW; 9F851AF909DB2388 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                       Length 78;
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Pred. No. 3e+02;
                                                                                                                 5; Indels
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NCBL_TaxID=86665;
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SEQUENCE 66 AA; 7786 MW; 7237A16A61E309FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000)
EMBL; AP000995; BAB60342.1;
                                   Score 32; DB 13;
Pred. No. 4.4e+02;
L; Mismatches 5;
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MEDLINE=20570466; PubMed=11121031;
                                   42.1%;
53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein BH2196
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01-OCT-2000
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Score 31; DB 17; Length 66;

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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21595285; PubMed=11759840; Kaneko T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing
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                        Indels
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC007583; A4H07583.1; -.
InterPro; IFR01014; Ribosomal L23.
Pfam; PP00276; Ribosomal L23; I.
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PR051TE; PS00050; RIBOSOMAL_L23; 1.
Hypothetical protein.
SEQUENCE 70 AA; 7923 MW; ACIC466548F343C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome.
SEQUENCE 68 AA; 7648 MW; 8876D5D9FFCC4B14 CRC64;
                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
ASL4328.
54.5%; Pred. No. 5.7e+02; tive 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003596; BAB76027.1; -.
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Pred. No. 6e+02;
2; Mismatches
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MEDLINE=95138034; PubMed=7836307;
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MEDLINE-20112991; PubMed=10644495;

Carlyon J.A., Roberts D.M., Marconi R.T.;

Carlyon J.A., Roberts D.M., Marconi R.T.;

"Evolutionary and molecular analyses of the Borrelia bdr super gene family: Delineation of distinct sub-families and demonstration of the genus wide conservation of putative functional domains, structural properties and repeat motifs.";

Microb. Pathog. 28:89-105(100).

EMBL; AR143465; AAR19121.1;

InterPro: IPRO04874; Borrelia rep.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 8.0 Kba proctain.
Lactobacillus bacteriophage phi adh.
Viruses; dsDNa viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                               Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=140;
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pram; PF03183; Borrella rep; 4. SEQUENCE 72 AA; 8090 MW; 4C20FFCC4487F35A CRC64;
                                                                                                                        Created)
Last sequence update)
Last annotation update)
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Local Similarity 25.0%; Pred. No. 6.2e+02;
Leg 4; Conservative 9; Mismatched
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34 RLFSTVSILLSRSLIS 49
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
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         YDALNVLMAMNII 15
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58 YDALDVANKIGII 70
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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
                                                                                                                                         MEDLINE=93231538; PubMed=8472961; Fremaux C., De Antoni G., Raya R., Klaenhammer T.; "Genetic organization and sequence of the region encoding integrative functions from Lactobacillus gasseri temperate bacteriophage phi-
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Engel G., Altermann E., Klein J., Henrich B.;
Engel G., altermann E., Klein J., Henrich B.;
Estructure of a genome region of the Lactobacillus gasseri temperate
phage phi adh covering a repressor gene and cognate promoters.";
Gene 210:67-70(1998).
Henrich B., Binishofer B., Blaesi U.;
"Primary structure and functional analysis of the lysis genes of Lactobacillus gasseri bacteriophage phi-adh.";
J. Bacteriol. 177:723-732(1995).
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Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE010209; AAL81085.1; -.
HYPothetical protein; Complete proteome.
SEQUENCE 72 AA; 8246 MW; CA74EC8FB8371720 CRC64;
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Pred. No. 6.2e+02;
9; Mismatches 1; Indels
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Pred. No. 6.2e+02;
2; Mismatches 3; Indels
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InterPro; IPR000209; Peptidase S8.
INTERPRO; IPR00136; SUBTILASE_ASP; 1.
Hypothetical protein.
SEQUENCE 72 AA; 8045 MW; 773F8886575C889A CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein PF0961.
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01-MAR-2003 (TEMBLrel. 23,
01-MAR-2003 (TEMBLrel. 23,
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| RLPNSINILIALSV 45
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Best Local Similarity 58.3.
Rest Local 7, Conservative
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VKDALKELVALN 17
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88 AA

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PRT;
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25.0%;
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                               01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
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                 Q9RG90,
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nida Y.,
                                           Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
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DNA Res. 9:123-130(2002).
EMBL, AP005371; BAC08427.1; -.
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83 AA; 9075 MW; ACSD08F38ACB34SC CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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56.2%; Pred. No. 7.1e+02;
iive 2; Mismatches 3;
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Pred. No. 7.1e+02;
1; Mismatches 4;
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EMBL; AE015517; AAN53799.1; -.
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Conserved hypothetical protein.
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58.3%;
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Best Local Similarity 58.3.
7; Conservative
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                             Shewanella oneidensis
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Best Local Similarity
Matches 9; Conserv
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Q9RG90
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Carylon J.A., Roberts D.M., Theisen M., Sadler C., Marconi R.T., "Molecular and immunological analyses of the B. turicatae Bdr protein family: a polymorphic, linear plasmid carried, paralogous gene
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Carlyon J.A., Roberts D.M., Marconi R.T.;
"Evolutionary and molecular analyses of the Borralia bdr super gene
"Evolutionary and molecular analyses of the Borralia bdr super gene
genus wide conservation of distinct sub-families and demonstration of the
properties and repeat motifie.";
properties and repeat motifie.";
Microb. Pathog. 28:89-105(2000).
EMBL; AF143462; AAF19119:1;
                                                                                              Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=140;
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Pred. No. 7.5e+02;
9; Mismatches 3; Indels
              Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Created)
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Vallaeys T., Fulthorpe R.R., Lau P., Wright A.D.; "Vallaeys T.," Fulthorpe R.R., Lau P., Wright A.D.; "Comparison of tfdB sequences from bacterial isolates degrading 2,4-dichlorophenoxyacetic acid and 2,4-dichlorophenol."; Abstr. Gen. Meet. Am. Soc. Microbiol. 97:Q403-Q403 (1997).
                                                                                                                                                          Vallacys T., Courde L., McGowan C., Wright A.D., Fulthorpe R.R.;
"Phylogenetic analyses indicate independent recruitment of diverse gene cassettes during assemblage of the 2,4-D catabolic pathway.";
EMBL, APO68274; AAD24417.1;
InterPro; IFR002203; HMG-Coda red.
InterPro; IFR002203; MMG-Coda red.
InterPro; IFR002293; MAD2417.1;
PROMITE; PS01494; FAD binding 3; 1.
PROSTITE; PS00066; HMG COda REDUCTASE 1; 1.
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Best Local Similarity 53.3
Matches 8; Conservative
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Q99UC6
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Vallaeys T., Fulthorpe R.R., Lau P., Wright A.D.;
Vallaeys T., Fulthorpe R.R., Lau P., Wright A.D.;
"Comparison of tidB sequences from bacterial isolates degrading 2,4-dichlorophenol.";
dichlorophenoxyacetic acid and 2,4-dichlorophenol.";
Abstr. Gen. Meet. Am. Soc. Microbiol. 97:0403-0403(1997).
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Achromobacter.
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"Phylogenetic analyses indicate independant recruitment of diverse gene cassettes during assemblage of the 2,4-D catabolic pathway.";
FEMS Microbiol. Ecol. 28:33-382(1999).
InterPro; IPR002202; HMG-CoA red.
InterPro; IPR002202; HMG-CoA red.
Pfam; PP01494; PAD binding 3; L.
PROSITE; PS00066; HMG_COA_REDUCTASE_1; 1.
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Alcaligenaceae, Alcaligenes.
NCBI_TaxID=87548;
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                                                                                       Score 31; DB 2; Length 90;
Pred. No. 7.7e+02;
9; Mismatches 3; Indels
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                                                 C92CFFF19025846B CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAX-2003 (TrEMBLrel. 23, Last annotation update)
2,4-dichlorophenol hydroxylase (Fragment).
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    InterPro; IPR004874; Borrelia rep. Pfam; PF03183; Borrelia rep; 5. SEQUENCE 90 AA; 10131 MW; C92CF
                                                                                                                                                                                                                                                                                                                                                 PRT:
                                                                                               40.8%;
                                                                                                                                                                                           1 RVYDALNVLMAMNIIS 16
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34 RLFSTVSILLSRSLIS 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 53.3
                                                                              Query Match
Best Local Similarity 25.v.
Then 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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SEQUENCE FROM N.A.
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099X3B
OD 01-NO
DT 01-NO
DI 0
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40.8%; Score 31; DB 2; Length 94; 53.3%; Pred. No. 8e+02; tive 1; Mismatches 6; Indels

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                                                                                                                                                                                                                                                        Olymar.2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
60S ribosomal protein (Fragment).
61D conchiperygii; Neopterygii; Teleostei; Euteleostei;
61D rotacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
61D rotacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
61D rotacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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Pred. No. 8.1e+02;
2; Mismatches 4; Indel8
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Q99UC6;
01-JUN-2001 (TrEMBLrel: 17,
1 RVYDALNVLMAMNII 15
                                                           RLYAAPNDLMGENTI 25
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84 YDALDVANKIGII 96
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nes 7; Conservative
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emergence.";
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Q8P2F3;
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Ruroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N. K., Sawano T., Imoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogaaswara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus

aureus."
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STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MW2;
MRDLINE=22040717; PubMed=12044378;
MRDLINE=22040717; PubMed=12044378;
MBDLINE=22040717; PubMed=12044378;
MBDLINE=22040717; PubMed=12044378;
Magai Y., Takeuchi F., Kuroda M., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766850; CAD47009.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SAV1352 (Hypothetical protein MW1239).
SAV1352 OR SAIBS OR MW1239.
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Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lancet 359:1819-1827(2002).

EMBL; AP003362; BAB57514.1; -.

EMBL; AP004826; BAB51041.1; -.

EMBL; AP004826; BAB55104.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 98 AA; 11496 MW; 216697709B904141 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                         Staphylococcus aureus (strain Muso / ATCC 700699), Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain MW2).

Bacteria: Firmicutes; Bacillales; Staphylococcus.

NCBI_TaxID=158878, 158879, 196620;
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62 YDDLNVVVA 70
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acquired MRSA.";
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical phage protein spyM18_0380 (Hypothetical phage associated
protein SpyM3 0720).
SPYM18_0380 OR SPYM3_0720.
                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S. pyogenes; STRAIN=MGAS315 / Serotype M3; MEDLINE=22133808; PubMed=1212206; Berees S.B., Folve M.D., Berees S.B., Folve M.D., Liu M.-Y., Smoot J.C., Del B., Hoff J.S., Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Schlitevert P.M., Musser J.M.; Genome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=S.pyogenes; STRAIN=MGAS8232 / Serotype M18; MEDLINE=21927593; PubMed=11917108; Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S. Sylva G.L., Sturdevant D.E., Yalcklefs S.M., Porcella S.F., Barkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.; Required and comparative microarray analysis of serotype M18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever
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40.0%; Pred. No. 8.5e+02;
tive 4; Mismatches 5; Indels
                                                                         Score 31; DB 16; Length 99;
Pred. No. 8.4e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes (serotype M18), and
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                       99 AA; 11302 MW; BB3CBBFC1AB03CS3 CRC64;
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Last sequence update)
Last annotation update)
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EMBL; AE009981; AAL97130.1; -.
EMBL; AE014151; AAM79327.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 outbreaks.";
Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002)
                                                                                                                                                                                                                                                                                                                                                                                         100 AA.
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Hypothetical protein; Complete proteome. SEQUENCE 99 AA; 11302 MW; B83CB8FC1A
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Q8HA80;
Q8HA80;
Q1-MAR-2003 (TrEMBLrel. 23, C3)
O1-MAR-2003 (TrEMBLrel. 23, L6)
O1-MAR-2003 (TrEMBLrel. 23, L6)
Hypothetical protein.
                                                                              40.8%;
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MYDKLNMYELNNILA 82
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78 YIALNLLILLGIL 90
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                                                                                                                                      6; Conservative
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                                                                                                            dest Local Similarity
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Length 29;

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MEDLINE-20150912; PubMed-10688204; MEDLINE-20150912; PubMed-10688204; MEDLINE-20150912; PubMed-10688204; Mether J. W. Wingall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Fellwell T., Holroyd S., Jasham D., Chillingworth T., Davies R.M., Fellwell T., Holroyd S., Jasham D., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.; Trevals hypervariable sequences "; Nature 403:665-668(2000).

BALL, ALISOPG: CABAJ3017.1; --
BALL, ALISOPG: CABAJ3017.1; --
BERL, ALISOPG: CABAJ30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
                                                                                   SEQUENCE FROM N.A.
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Takeuchi F., Kuroda M., Naimi T., Kuroda H., Cui L.,
Yamamoco K., Hiramateu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 16; Length 35;
Pred. No. 4.6e+02;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 16; Length 29
Pred. No. 3.8e+02;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                      Lancet 359:1819-1827(2002)
EMBL; AP004826; BAB95046.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 29 AA; 3563 MW; 3E9E043A4272B619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein PAE2389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBL_TaxID=196620,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VYDALNV-----LMAMNI 14
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01-0CT-2000 (TEMBLES 115, Last seq
01-DEC-2001 (TEMBLES 119, Last anno
Hypothetical protein Cj0747.
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        acquired MRSA.";
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Q9PPG6
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SPECIES=S.aureus (strain MuSO), and S.aureus (strain N315);
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                         Bacteriophage T5.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
T5-like viruses.
T5-like viruses.
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Pred. No. 3.8e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                            01-JUN-2001 (TremBirel. 17, Last sequence update)
01-MAR-2002 (TremBirel. 20, Last sequence update)
Hypothetical protein SAV1299.
SAV1299 OR SA139.1 OR SAS038
Staphylococcus aureus (strain Mu50 / ATCC 700699), and
Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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EMBL, AP003131; BAB42393.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 29 AA, 3562 MW, 3E9E043A4662B619 CRC64;
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Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last seq
01-0CT-2002 (TrEMBLrel. 22, Last ann
Hypothetical protein MW1181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RVYDALNV-LMAMNI 14
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Best Local Similarity 55.6
Matches 5; Conservative
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7 LYDTLNTEL 15
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Best Local Similarity
7; Conserva
                                                                                                                                                                            SEQUENCE FROM N.A. Mikoulinskaia G.V.
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01-JUN-2001
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RESULT 31
C99UHS
DD Q99UH
AC Q99UH
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Gaps

14;

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RESULT 32

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MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

A Ng W.V., Kennedy S.R., Baliga N.S., Thorsson V., Sbrogna J., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., A lam M., Freitas T., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., A Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S., T. "Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;
"Complete nucleotide sequence of Staphylococcus aureus E-1 EDINA
plasmid.";
  STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 17; Length 60;
Pred. No. 7.8e+02;
2; Mismatches 4; Indels
                                                                                                                                              39.5%; Score 30; DB 16; Length 59; ilarity 41.7%; Pred. No. 7.7e+02; Conservative 4; Mismatches 3; Indels
                        Ren S.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halobacteríum sp. (strain NRC-1).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
                                                            EMBL; AE011323; AAN48630.1; -. Hypothetical protein; Complete proteome. SEQUENCE 59 AA; 7098 MW; 5EC5757B6E80868D CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Last annotation update)
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NCBI_TaxID=1280;
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23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VYDALNVLMAMNI 14
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5 YDSINVSHSRNL 16
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SEQUENCE 60 AA:
                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=E-1;
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01-MAR-2001
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Matches
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BYBL, AP001511; BABC4699-11; --
HYPOCHALICAL protein; Complete proteome.

SEQUENCE 59 AA; 6857 MW; 8FE49D9F98915E77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
VCBI_TaxID=173;
                                                                                                                                                                       "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.",
                                                                                                                               Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus halodurans.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
EMBL; AE009873; AAL64158.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 58 AA; 6342 MW; 110191142AD83792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein BH1180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                        Score 30; DB 17;
Pred. No. 7.5e+02;
3; Mismatches 6
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                                                                                STRAIN=IM2 / ATCC 51768 / DSM 7523;
PubMed=11792869;
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Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
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Horikoshi K.;
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Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the repetitive DNA element in
the genome of insect iridescent virus type 6.";
Virology 167:485-496(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-87321126; PubMed-2820141; Schnitzler P., Soltau J.B., Fischer M., Reisner H., Scholz J., Schnitzler P., Soltau J.B., Fischer M., Reisner H., Scholz J., Delius H., Darai G.; "Molecular cloning and physical mapping of the genome of insect iridescent virus type 6: further evidence for circular permutation of the viral genome."; Virology 160:66-74(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of origins of DNA replication within the of insect iridescent virus type 6.";
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Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
"Insect iridescent virus type 6 induced toxic degenerative hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=92196996; PubMed=1549908;
Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
                                                                                                                                              Gaps
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"DNA analysis of insect iridescent virus 6: evidence for circular
permutation and terminal redundancy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
Viruses; dsDNA viruses, no RNA stage; Iridovirudae; Iridovirus
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Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
                                                                                                     Score 30; DB 2; Length 64; Pred. No. 8.3e+02;
                                                                                                                                            1; Indels
  the EMBL/GenBank/DDBJ databases.
                                                                59BF2A1EEAE9A7F9 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                      64 AA
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MEDLINE=93118242; Pubmed=1475907;
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DNA sequences of the genome
Virus Genes 6:19-32(1992).
                                                                                                          39.5%;
45.5%;
        Submitted (JAN-2001) to the EMBL; AP003089; BAC54531.1; Plasmid.
                                                              64 AA; 7316 MW;
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                                                                                      Query Match
Best Local Similarity 45...
5; Conservative
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41 YPSLDILIAMS 51
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Jakob N.J., Muller K., Bahr U., Darai G.,
"Analysis of the First Complete DNA Sequence of an Invertebrate
Iridovirus: Coding Strategy of the Genome of Chilo Iridescent Virus.";
Virology 286:182-196(2001).
                                                                                                                                                                                                                                                                                                                                Delius H., Darai C.;
"Identification of genes encoding zinc finger proteins, non-histone
chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
in the genome of Chilo iridescent virus.";
Nucleic Acids Res. 22:158-166(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94353641; PubMed=8073636; Sonin E.V., Darai G.; Schnitzler P., Koonin E.V., Darai G.; Schnitzler P., Koonin E.V., Darai G.; Schnitzler B., Koonin E.V., Darai G.; Chilo iridescent virus encodes a putative helicase belonging to a distinct family within the 'DEAD/H' superfamily: implications for the evolution of large DNA virues."; Virus Genes 8:151-158(1994).
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MEDIATNE=4929906; PubMed=8021587;
MEDIATNE=4929906; Somteag K.C., Muller M., Janssen W., Bugert J.J.,
Koonin E.V., Darai G.;
"Insect iridescent virus type 6 encodes a polypeptide related to the
"Insect iridescent virus type 6 encodes a polypeptide related to the
Jargest subunit of eukaryctic RNA polymerase II.";
J. Gen. Virol. 75:1557-1567(1994).
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MEDILINE-98141699; PubMed=9482589;
MEDILINE-98141699; PubMed=9482589;
Bahr U., Tidona C.A., Darai G.;
"The DNA sequence of Chilo iridescent virus between the genome coordinates of 101 and 0.391; similarities in coding strategy between linsect and vertebrate iridoviruses.";
Virus Genes 15:235-245(1997).
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Muller K., Tidona C.A., Bahr U., Darai G.;
"Identification of a thymidylate synthase gene within the genome of
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MEDLINE-2513160; PubMed=7698884;

Sonntag K.C., Schnitzler P., Janssen W., Darai G.;

Midentification of the primary structure and the coding capacity indentification of the primary structure and the coding capacity indentification of the primary structure and the coding capacity indentification of insect iridescent virus type 6 between the genome coordinates 0.310 and 0.347 (7990 bp).";

Intervirology 37:287-297(1994).
"Identification of the gene encoding the major capsid protein insect iridescent virus type 6 by polymerase chain reaction."; J. Gen. Virol. 74:873-879(1993).
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MEDLINE=94167241; PubMed=8121799;
Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
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Jakob N.J., Mueller K., Bahr U., Darai G.;
Submitred (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF30771 AAR82091.1;
SEQUENCE 64 AA; 7741 MW; 42CB68481A85F957 CRC64;
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"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
101-MAR-2001 (TrEMBLrel. 16, Last annotation update)
11-Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
12-Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
13-Marmalia; Butheria; Primates; Craniata; Vertebrata; Euteleostomi;
13-Marmalia; Butheria; Primates; Catarrhini; Cercopithecidae;
13-Marmalia; Cercopithecidae;
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Xanthomonadaceae; Xylella.
WCBI _TaxID=2371;
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Pred. No. 9.2e+02;
4; Mismatches 5; Indels
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EMBL; AB047839; BAB12265.1; -.
Hypothetical protein
SEQUENCE 71 AA; 8296 MW; 1A50C4AE703A69C7 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Xf1305.
                                                                                8.3e+02;
                                      39.5%; Score 30; DB 12;
45.5%; Pred. No. 8.3e+02;
tive 5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=9a5c;
MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.5%;
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                                                                                                                          Conservative
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31 AIDILVLLNII 41
Query Match
Best Local Similarity
-Log 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissum=Cerebellum;
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09GMS
AC 09GMS
AC 09GMS
DT 01-MA
DT 01-MA
DT 01-MA
DE HYPOLI
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OGSPDS AC

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Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Moon D.H.; Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nhani A. 'Ar., Nabrega F.G., Nunes L.R., Oliveira M.A.,
A coliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A coliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A coliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A coliveira G.G., Rodrigues V., de Rosa A.J.M.,
A ca Silva A.C.R., da Silva F.W., Sawasaki H.E.,
A da Silva A.C.R., da Silva F.W., Silva F.W., Silva F.W.,
A coliveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.P.,
A coliveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.P.,
A coliveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.P.,
A coliveira J.F., Meidanis J., Setubal J.C.,
The genome sequence of the plant pathogen Xylella fastidiosa.";
RMBL; AB003963; AAF84114.1;
RMBL; AB003963; AAF84114.1;
RMBL; AB003963; AAR84114.1;
RMBL; AB003965; AAR84114.1;
RMCC 7; AA, 7462 MW; 1855A508694610B5 CRC64;
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Pred. No. 1e+03;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 16; Length 72;
Pred. No. 9.3e+02;
0; Mismatches 3; Indels
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Staphylococcus
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SEQUENCE 79 AA; 9192 MW; D019DADDAACE5D52 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus (strain N315). Plasmid pN315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lancet 357:1225-1240(2001).
EMBL; AP003139; BAB43897.1; -.
InterPro; IPR001387; HTH_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.5%;
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45.5%;
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nes 6, Conservative
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les 5; Conservative
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41 YPSLDILIAMS
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                                        Q8S3M1,
RESULT 45
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Tal A., Rubin B.;

Tal A., Rubin B.;

"A point mutation in the ACCase gene is responsible for the resistance to ACCase inhibiting herbicides in Lolium rigidum.";

Submitted (FRB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF482471; AAL87701.1; -.

EMBL; AF482473; AAL87703.1; -.

EMBL; AF482470; Carboxyl_trans.

Figur, PF01039; Carboxyl_trans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eukaryota, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Poeae, Lolium.
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                                                                                                                              MC047L.
Molluscum contagiosum virus subtype 1 (MCVI).
Viruses, dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Viruseipoxvirus.
NCBI_TaxID=10280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Senkevich T.G., Bugert J.J., Sisler J.R., Koonin B.V., Darai G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=96325459; PubMed=8670425;
Senkevich T.G., Bugert J.J., Sieler J.R., Koonin B.V., Darai G.
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Pred. No. 1.2e+03;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 12; Length 82;
Pred. No. 1.1e+03;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U60315; AAC55175.1; -:
InterPro; IRR06803; Pox.15.
Pfam; PF04713; Pox.15; 1.
SEQUENCE 82 AA; 8606 MW; 740DE5C73803B4A8 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Acetyl-CoA carboxylase (Fragment).
Lolium rigidum.
                              Created)
Last sequence update)
Last annotation update)
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Local Similarity 50.0%;
les 6; Conservative
                              01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 42.9
Matches 6; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                      Moss B.;
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Matches
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76 YSALNKLIGREVYS 89

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TO GRSSM1 PRELIMINARY; PRT; 92 AA.

DE 0863M1 PRELIMINARY; PRT; 92 AA.

DT 01-JUN-2002 (TEMBLE-1. 21, Last sequence update)

DT 01-JUN-2002 (TEMBLE-1. 21, Last sequence update)

DT 01-MAR-2003 (TEMBLE-1. 23, Last sequence update)

DE Acetyl-CoA carboxylase (Pragment).

OC Suclium rigidum.

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poale
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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 17, 2004, 10:50:13; Search time 5.06931 Seconds (without alignments) 148.428 Million cell updates/sec Run on:

US-09-900-147-5 76 1 RVYDALNVLMAMNIIS 16

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

13973 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Length	DB	QI.	cripti
	33			-	E2F1 RAT	009139 rattus norv
7	30	39.5	26	Н	SCP2_MESMA	O9njp7 mesobuthus
٣	30		2	-	SCP3_MESMA	Q9u8d1 mesobuthus
4	30	9.	6	н	YFRC PROVU	P20927 proteus vul
ស	29	æ.	7	-	YORA_TTV1	P19285 thermoprote
9	29		0	ч	NULM_DASNO	021333 dasypus nov
7	28	36.8	4	٦	RETS_BOVIN	_
89	28	•	7	ч	VI05_VACCC	P20500 vaccinia vi
σ	28	٠	7	٦	VI05_VACCV	P12924 vaccinia vi
10	28	•	7	٦	VI05_VARV	
11	28	ė	80	ч	PSBE_NEPOL	Q9tky1 nephroselmi
12	27	•	4	Н	ATP8_CANPA	
13	27	•	S	П	YC18 PORPU	porphyra
14	27	٠	σ	7	ILG1 CAEEL	
15	27	35.5	σ	-	VAPD_HAEIN	_
16	27	•	σ	Н	PLIE_AQUAE	-
17	27	•	σ	-	VAPD_ACTAC	_
18		•	σ.	-	NULM BALMU	
19	26.5	34.9	7	٦	ACPH_UREPA	•
20	26	•	4	Н	YCX9_CYAPA	
21	26	34.2	ß	-		
22	26	•	9	Н	ATPL_STRMU	P95783 streptococc
23	26	34.2	ø	-	YIFL ECOLI	_
24	26	•	9	Н	Y010 TROWT	'n
25	26	•	æ	Н	PSK6 ARATH	
26	26	•	æ	Н		_
27	26	•	۵	Н	TRP6_BOVIN	Q9myw0 bos taurus
28	56	٠	۵	Н	VDMA BPT3	P10309 bacteriopha
29	26	•	ω	٦	VDMA_BPT7	P03693 bacteriopha
30	56	•	o	П	EF1B_AERPE	Q9y904 aeropyrum p
31	26	34.2		٦		
32	26	34.2	92	7	ıı	-
33	56	34.2	92	~	YCHH ECOLI	P31807 escherichia

zjz9 helicobacte 4976 balaenopter	P34771 astasia lon P50370 chlamydomon 004395 bacteriopha	0102 ectothiorho 7966 methanococc	u8d2 mesobuthus 9103 saccharomyc	P76118 escherichia 292h14 rickettsia	P08950 rana pipien
09 P2	P. P. S.	9 S	60 6	P7	PO
CSS3_HELPJ NULM_BALPH	RK23_ASTLO YC12_CHLRE VG9_RPNF	LHAI ECTHL Y546 METJA	SCP1_MESMA	YNCH ECOLI DBHL RICCN	RANA_RANPI
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9 6 9 8	9 W 4	52 56	57 70	80	82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20530297; PubMed=11076505;
Xu Y.Q., Wu J.H., Pei J.M., Shi Y.Y., Ji Y.H., Tong Q.C.;
"Solution structure of BmP02, a new potassium channel blocker from the
"Solution structure of DmP02, a new potassium channel blocker from the
venom of the Chinese scorpion Buthus martensi Karsch.";
Biochemistry 39:13669-13675[2000].
-! FUNCTION: Blocks potassium channels.
-! SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

TISSUE-Venom gland;
MEDINE=99402983; PubMed=10471839;
MEDINE=99402983; PubMed=10471839;
MAUS.Y., Li W.-X., Zeng X.-C., Jiang D.-H., Mao X., Liu H.;
"Molecular cloning and sequencing of two 'short chain' and two 'long 'molecular cloning and sequencing of two 'short chain' and two 'long chain' K(+) channel-blocking peptides from the Chinese scorpion Buthus
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SULP TREAD SURVEY, PES491,
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
Neurotoxin BmP02 precursor (Potassium ion channel blocker P02P).
Mesobuthus martenali (Manchurian scorpion) (Buthus martensii).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthidae; Mesobuthus.
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Potassium channel inhibitor; Signal; 3D-structure.
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(Rel. 41, Last sequence update)
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RLFTLVLIVLAMNVM 17
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28 RIYDITNVL 36
         1 RVYDALNVL 9
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Matches 4; Conserv
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28-FEB-2003
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Q9U8D1;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@leb.ch).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Venom gland;
MEDLINE=99313193; PubMed=10386622;
Mu J.J., Dai L., Lan Z.D., Chi C.-W.;
"Genomic organization of three neurotoxins active on small conductance ca2+-activated potassium channels from the scorpion Buthus martensi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Venom gland;
MEDLINE=59402983; PubMed=10471839;
MEDLINE=59402983; PubMed=10471839;
Zhu S.-Y., Li W.-X., Zeng X.-C., Jiang D.-H., Mao X., Liu H.;
"Molecular cloning and sequencing of two 'short chain' and two 'long 'molecular cloning and sequencing of two 'short chain' and two 'long chain' K(+) channel-blocking peptides from the Chinese scorpion Buthus
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28-FEB-2003 (Rel. 41, Last annotation update)
Neurotoxin BmP03 precursor (Potassium ion channel blocker P03).
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chellcerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEBS Lett. 457:509-514(1999).
-1- FUNCTION: Blocks small conductance Calcium-activated potassium
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Enterobacteriaceae; Proteus.
NCBI_TaxID=585;
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-i- TISSUE SPECIFICITY: Expressed by the venom gland.
-i- SIMILARITY: BELONGS TO THE SCORPION LEIUROTOXIN FAMILY.
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                            NCBI_TaxID=34649;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-97357423; PubMed-9214749;
Arnason U., Gullberg A., Janke A.;
"Phylogenetic analyses of mitochondrial DNA suggest a sister group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Sukaryota Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Edentata, Dasypodidae, Dasypus.
NCBI_TaxID=9361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21173623; PubMed=11274389;
Folli C., Calderone V., Ottonello S., Bolchi A., Zanotti G.,
Stoppini M., Berni R.;
"Identification, retinoid binding and X-ray analysis of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relationship between Xenarthra (Edentata) and Ferungulates.";
Mol. Biol. Evol. 14:762-768(1997).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Retinol-binding protein III, cellular (CRBP-III) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.2%; Score 29; DB 1; Length 98; 55.6%; Pred. No. 2.2e+02; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y11832; CAA72524.1; -.
PIR; T1449; T1449.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
Pfam; PF00420; oxidored q2; 1.
Probom; PD000359; Oxidored q2; 1.
Probom; PD001359; Oxidored d2; 1.
SEQUENCE 98 AA; 10840 MW; D0FF9BC309048774 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 NADH-ubiquinone oxidoreductase chain 41 (EC 1.6.5.3).
MTND4L OR ND4L OR NADH4L.
                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dasypus novemcinctus (Nine-banded armadillo)
                                                                                                                                                                                                           98 AA
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    32 VYVAITVTLTLNL 44
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hes 5; Conservative
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TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LNVLMAMNI 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion
                                                                                                                                                           NULM DASNO
AC 02133;
DT NULL DASNO
AC 02133;
DT 15-JUL-1998
DE 15-JUL-1998
DE NADH-Ubiquin
GN MTND4L OR ND
OS MItochondrio
OC Bukaryota; M
OC C Bukaryota; M
OC This SUDINES978
CC This SWISS-P
CC This SWISS-
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                      Cole S.T.;
"Nucleotide sequence and comparative analysis of the frd operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                    encoding the fumarate reductase of Proteus vulgaris. Extensive sequence divergence of the membrane anchors and absence of an frd-linked ampC cephalosporinase gene.";

Bur. J. Blochem. 167-181-488(1987).
-!- SIMILARITY: BELONGS TO THE HUPP/HYPC PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 1; Length 70;
Pred. No. 1.5e+02;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.5%; Score 30; DB 1; Length 96; 66.7%; Pred. No. 1.4e+02; ative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neumann H.;
Submitted (MAR-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermoproteus tenax virus 1 (strain KRA1) (TTV1).
Viruses; dsDNA viruses, no RNA stage; Lipothrixviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 protein. -
96 AA; 10300 MW; BC094F1F37956EE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 AA; 8125 MW; F88F0A8E46323EDC CRC64;
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
Hypothetical 8.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterProj ENRO1109; HupF HypC.
Pfam; PF01455; HupF HypC; 1.
PIRSF, PRSF005618; HupF HypC; 1.
PRINTS; PR00445; HUPFHYPC; 1.
PRODING, PD003112; HupF HypC; 1.
TICRFAMS; TIGR00074; hypC; 1.
Hypothetical protein.
MEDLINE=88004470; PubMed=3308458;
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Best Local Similarity 66.7-
6; Conservative
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Best Local Similarity 38.5
Matches 5; Conservative
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67 ETLNALMAM 75
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NCBI_TaxID=10480;
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P19285;
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YORA TTV1 RESULT 5

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Gaps

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Length 98;

3 DAITVLTAIGI 13

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Late protein.
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                                                                                                                                                                    VACCV
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                                                                                                                                                                                                 P12924;
                                                                                       VIOS_VACCV
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                                                                                                                                                                        SOW WHAN THE TRANSPORT OF THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91021027; PubMed=2219722;
Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
retinol-binding protein.";

Proc. Natl. Acad. Sci. U.S.A. 98:3710-3715(2001).

-!- FUNCTION: Intracellular transport of retinol.

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- TISSUE SPECIFICITY: Kidney.

-!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF THANSPORTERS.

RANSPORTERS.

RINGEPPO: IPRO00463; Fatty acid BP.

RINGEPPO: IPRO00463; Fatty acid BP.

RINGEPPO: IPRO00566; Lipocln. CytrABP.

R Pfam; PF00061; lipocalin; l..

R Pfam; PF00061; lipocalin; l..

R Pfam; PR0061; lipocalin; l..
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Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 1; Length 79;
Pred. No. 2.7e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB 1; Length 42;
Pred. No. 1.4e+02;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 AA; 4892 MW; ACB4F1399FDD7F09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete DNA sequence of vaccinia virus.";
Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.8%;
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InterPro; IPR006803; Pox I5.
Pfam; PF04713; Pox I5; 1.
Late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 AA; 8762 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.8%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.3.
T; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 ALNVNMALRKIA 33
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Best Local Similarity
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SEQUENCE
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P20500;
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                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDIATE=8815015; bubmed=2835495;
Schmitt J.F.C., Stunnenberg H.G.;
"Sequence and transcriptional analysis of the vaccinia virus HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variola virus.
Viruses, dabna viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
VCBI_TaxID=10255;
                                                                                                                                Vaccinia virus (strain WR).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sandakhchiev L.S.; "Analysis of the nucleotide sequence of a 43 kbp segment of the genome of variola virus India-1967 strain."; Virus Res. 30:239-258(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 1; Length 79;
Pred. No. 2.7e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 AA; 8744 MW; 37F4826B71CF04C3 CRC64;
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(Rel. 27, Last sequence update)
(Rel. 33, Last annotation update)
                                 01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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79 AA.
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SEQUENCE FROM N.A.
STRAIN=India-1967 / Isolate Ind3;
  PRT;
                                                                                                                                                                                                                                                                                                                 I fragment.";
J. Virol. 62:1889-1897(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J03399; AAB59807.1; -. PIR; E29889; WZVZI5.
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Pfam; PF04713; Pox_I5; 1.
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Best Local Similarity 54.5
Matches 6; Conservative
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    STANDARD;
                                                                                                                                                                                Orthopoxvirus.
NCBI_TaxID=10254;
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01-0CT-1993 (
01-FEB-1996 (
Protein 15.
15L OR K5L.
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Matches
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      SETT TENDERS OF THE T
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MEDLINE=93190624; PubMed=8383392; Shchelkunov S.N., Blinov V.M., Totmenin A.V., Marennikova S.S., Kolykhalov A.N., Frolov I.V., Chizhikov V.E., Gytoxov V.V., Gabhikov P.V., Belanov E.F., Belavin P.A., Resenchuk S.M., Andzhaparidze O.G., Sandakhchiev L.S.; "Mucleotide sequence analysis of variola virus HindIII M, L, I genome
                                                                                                                                                                                                          STRAIN=India-1967 / Isolate Ind3;
MEDLINE=93202281; PubMed=8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
"Genes of variola and vaccinia viruses necessary to overcome the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Potential virulence determinants in terminal regions of variola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cytochrome b559 alpha subunit (PSII reaction center subunit V).
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0
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Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 1; Length 79;
Pred. No. 2.7e+02;
2; Mismatches 3; Indels
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Bukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
Chlorodendrales; Chlorodendraceae; Nephroselmis.
NCBI_TaxID=31312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIGURENCE 79 AA; B778 MW; AD4E703B701B5C86 CRC64;
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MEDLINE=99398694; PubMed=10468594;
                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Bangladesh-1975;
MEDLINE=94088747; PubMed=8264798;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X67119; CAA47559.1; -. EMBL; X69198; CAA49000.1; -. EMBL; L22579; AA66807.1; -. PIR; C36843; C36843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.8%;
                                                                                                                                                                                                                                                                                                 protective mechanisms.";
FEBS Lett. 319:80-83(1993).
                                                                                                                                                Virus Res. 27:25-35(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    smallpox virus genome.";
Nature 366:748-751(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                          COMPLETE GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter C.J.;
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PSBE_NEPOL
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IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
B267F4441B857D23 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Photosystem II; Heme; Electron transport; Transmembrane; Chloroplast. DOMAIN 1 18 STROMAL (POTENTIAL).
                        olivacea: insights into the architecture of ancestral chloroplast
                                                                                                          -i- FUNCTION: This b-type cytochrome is tightly associated with the reaction center of photosystem II and possibly is part of the water-oxidation complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI TaxID=5480;
                                                                                                                                                                                               -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.-!- SIMILARITY: Belongs to the psbE / psbF family.
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01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 1; Length 83;
Pred. No. 2.8e+02;
4; Mismatches 6; Indels
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                                                                                     Sci. U.S.A. 96:10248-10253(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_00642; ; ; 1.
InterPro; IRR006216; CYL b559.
InterPro; IRR006216; CYL b559 alpha.
Pfam; PF00283; cytochr_b559; 1.
Pfam; PF00284; cytochr_b559; 1.
TIGRNAS; TIGR0132; cyt_b559 alpha; 1.
PROSITE; PS00537; CYTOCHROME_B559; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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MEDLINE=90332440; PubMed=2143015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF137379; AAD54835.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida parapsilosis (Yeast).
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33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 AA; 9404 MW;
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66 ITDRFNALQQMDILT 80
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nes 5; Conservative
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                                                                                     Proc. Natl. Acad.
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Haemophilus influenzae.
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VAPD_HAEIN
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 Porphyra purpurea.
Chloroplast.
Bukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Avonport; seth M: Strain J:; Strain J:; Munholland J:; Runholland J:; Complex incleotide sequence of the Porphyra purpurea chloroplast
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                                                                                  EMBL; X52115; CAA36361.1; -. PIR; S10465; PWCK8P. Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.5%; Score 27; DB 1; Length 58; 41.7%; Pred. No. 2.9e+02; Live 3; Mismatches 4; Indels
                                                                                                                                                        Score 27; DB 1; Length 48; Pred. No. 2.4e+02; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S73287; S73287.
Pfam; PF04485; nblA; 1.
Chloroplast; Hypothetical protein.
SEQUENCE 58 AA; 6923 MW; 304D4D9EDD0D2371 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Mol. Biol. Rep. 13:333-335(1995).
-!- SIMILARITY: SOME, TO SYNECHOCOCCUS PCC 7942 NBLA.
                                                                                                                        12 32 POTENTIAL.
48 AA; 5492 MW; 0F7876341CAF0747 CRC64;
                                                                                                                                                                                                                                                                                                              01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Hypothetical 6.9 kDa protein ycf18 (ORFS8).
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(Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                        58 AA
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Best Local Similarity 41.7
Matches 5; Conservative
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DPLNLEQAQNLL 34
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nes 6, Conserv
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Q18060;
15-JUL-1998 (
15-JUL-1998 (
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ILG1_CAEEL
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Matches
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PROBABLE INSULIN-LIKE PEPTIDE GAMMA-TYPE
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                                                                                            Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
zв-гкВ-2003 (Rel. 41, Last annotation update)
Probable insulin-like peptide gamma-type 1 precursor (Ceinsulin-3).
INS-11 OR C17C3.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY TO INSULIN.
MEDLINE=98217375; PubMed=9548970;
MEDLINE=98217375; PubMed=9548970;
Duret L., Guex N., Peitzed M.; Pairoch A.;
New insulin-like proteins with atypical disulfide bond pattern characterized in Caenorhabditis elegans by comparative sequence analysis and homology modeling.";
Genome Res. 8:348-353(1998).
-! SUBCELLULAR LOCATION: Secreted (Potential).
-! SUBCELLULAR LOCATION: Secreted (Potential).
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                                                                                                                                                                                                                                                                       mRNA for a putative insulin-like peptide of Caenorhabditis
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                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
16-UUL-2001 (Rel. 40, Last annotation update)
Virulence-associated protein D.
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4; Mismatches
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A-CHAIN-LIKE
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InterPro; IPR004825; Ins/IGF/relax.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB032258; BAA84470.1; -.
EMBL; U41279; AAK31418.1; -.
PIR; T37327; T37327.
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KIFKALNVM 48
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-Bristol N2;
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                                                                                                                                                                                NCBI_TaxID=6239;
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Nature 392:353-358(1998).
-!- SIMILARITY: BELONGS TO THE FLIE FAMILY.
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                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                             Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; R. "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                  "Two-dimensional map of the proteome of Haemophilus influenzae.";
Electrophoresis 21:411-429(2000).
-!- SIMILARITY: BELONGS TO THE VAPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                     MEDLINE=20137488; PubMed=10675023;
Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
Gray C., Pountoulakis M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
35.5%; Score 27; DB 1; Length 91;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
Matches 5; Conservative 2; Mismatches 5; Indels
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Flagellar hook-basal body complex protein file.
FLIE OR AQ 1182.1 OR AQ 1182A.
Bacteria: Aquificae; Aquificales; Aquificaceae; Aquifex.
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Pfam; PF04605; VapD_N; 1.
Virulence; Complete proteome.
SEQUENCE 91 AA; 10543 MW; 70B23CDE28E083E7 CRC64;
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                                                          SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed=7542800;
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                                                                                                                                                                                                                                                                          Science 269:496-512(1995).
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                              NCBI_TaxID=727;
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AC 067242;
DT 30-MAY-2000
DT 30-MAY-2000
DT 16-OCT-2001
DE Plagellar ho
GN FLIE OR AQ 1
OS AQUIÉEX aeol
OX BACTETA; AG
OX NCBI_TAXID=6
RN [1]
RP SEQUENCE FRO
RC STRAIN=VF5;
RX MEDINE=9819
RA Graham D.E.,
RA Graham D.E.,
RA Feldman R.A.
RT aeolicus.,
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"Transcriptional analysis of rolling circle replicating plasmid
pyT736-1: evidence for replication control by antisense RNA.";
J. Bacteriol. 177:444-4480 (1995).
-: SIMILARITY: BELONGS TO THE VAPD FAMILY.
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Pasteurellaceae, Actinobacillus.
NCBI_TaxID=714;
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Pred. No. 4.9e+02;
1; Mismatches 5; Indels
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SEQUENCE 93 AA; 10764 MW; 6180AEA1C8FB9C39 CRC64;
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Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Virulence-associated protein D homolog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=95362676; PubMed=7543479;
                                                                                                                                                                                                                                                    EMBL; AE000727; AAC07208.1; -.
                                                                                                                                                                                                                                                                             PIR; G70401; G70401.
InterPro; IPR001624; F11E.
Pfam; PF02049; F11E; 1.
PRINTS; PR01006; PLGHOOKFLIE.
TIGRPAMB; TIGR00205; F11E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.5%;
62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::| | | | ::
80 KLLEAYNELMKMQV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RVYDALNVLMAMNI 14
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Plasmid; Virulence.
SEQUENCE 95 AA: 11190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actinomycetemcomitans)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VYDALNVL 9
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                        CX9_CYAPA
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 20
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                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                               MEDINE 914(1923): PubMed=8308901;
Arnason U., Gullberg A.;
Arnason U., Gullberg A.;
"Comparison between the complete mtDNA sequences of the blue and the fin whale, two species that can hybridize in nature.";
J. Mol. Evol. 37:312-322(1993).
-i- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Carrier of the growing fatty acid chain in fatty acid
                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti,
Balaenopteridae, Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria, Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27; DB 1; Length 98; Pred. No. 5.2e+02; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase, NAD, Ubiquinone, Mitochondrion.
SEQUENCE 98 AA, 10747 MW, 9F770651FE65ED1B CRC64;
                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
MIND4L OR ND4L OR NADH4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 AA.
                                        98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acyl carrier protein homolog (ACP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20500219; PubMed=11048724;
                                                                                                                       Balaenoptera musculus (Blue whale)
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S41828; S41828.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.5%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                        STANDARD;
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Matches 5; Conserv
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MNVLMAFSM
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI_TaxID=9771;
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15-SEP-2003
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                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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STRAMS-UTEX LB 555. / Pringsheim; schalowski C.B., Annarella M.,
STRAMI=UTEX LB 555. / Pringsheim; Michalowski C.B., Annarella M.,
Parley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
the complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
(In) Schoak H.B.A., Herrmann R., Jeon K.W., Mueller N.B.,
Schwemmler W. (eds.);
Bukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bryant D.A.; "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa."; Plant Mol. Biol. Rep. 13:327-332(1995).
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 5.7 kDa protein in PSBM-PSBX intergenic region (ORF48).
                                                             to a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00550; pp-binding; 1.
PROSITE; PS50075; ACP DOWAIN; 1.
PROSITE; PS00012; PHOSPHOPANIETHEINE; 1.
Hypothetical protein; Fatty acid biosynthesis; Phosphopantetheine;
Complete proteome.
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STRAIN=UTEX LB 555 / Pringsheim;
Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHOPANTETHEINE (BY SIMILARITY). 3CDB655FBFA968C6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26.5; DB 1; Length 77; pred. No. 4.9e+02; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eûkaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE002149; AAF30918.1; -.
Interpro; IPR006163; Pp_bind.
Interpro; IPR006162; Ppantne_attach.
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ilarity 38.1%;
Conservative
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77 AA; 8750 MW;
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Best Local Similarity
Best Conserve
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SPECIES=E.coli; STRAIN=K12;
SPECIES=E.coli; STRAIN=K12;
SPECIES=E.coli; STRAIN=K12;
SINDER STRAIN=K12;
SINDER STRAIN=K12;
SINDER STRAIN 
                                                                                                                                                                                                                               Gaps
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MEDIATE=90008815; PubMed=2477362;
Tanaka Y., Tsujimura A., Fujita N., Isono S., Isono K.;
"Cloning and analysis of an Escherichia coli operon containing the rpmF gene for ribosomal protein L32 and the gene for a 30-kilodalton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Protecobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334, 602, 601, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927; MEDLINE=21074935; PubMed=11206551; Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STY1230 OR T1729
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                                                                                                                                                                    34.2%; Score 26; DB 1; Length 48; 40.0%; Pred. No. 3.6e+02; ive 5; Mismatches 4; Indels
                          EMBL; U30821; AAA81282.1; -.
PIR; T06939; T06939; T06939
Hypothetical protein; Cyanelle.
SEQUENCE 48 AA; 5705 MW; 078F47EF024C26B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
50S ribosomal protein L32.
RPMF OR B1089 OR Z1728 OR ECS1467 OR STM1191 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 AA
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                                                                                                                                                                                                                                                                                     2 VYDALNVIMAMNIIS 16
                                                                                                                                                                                                                                                                                                                                        32 VFNNLSALIDKHIIS 46
                                                                                                                                                                                              Local Similarity 40.0 tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli,
Escherichia coli 0157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Salmonella typhi, and
Shigella flexneri.
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P02435;
                                                                                                                                                                       Query Match
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SPECIES-E.COli; STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Mayabh T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayawa K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES=S. typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
SPECIES=S. typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=S.Typh; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Cronin A., Larsen T.S., Moule S., O'Gaora P., Parry C.,
Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=E.coli; STRAIN=MRE-600;
Vinokurov L.M., Alakhov Y.B., Golov E.A., Ovchinnikov Y.A.;
"The primary structure of ribosomal protein L32 from E. coli MRE-600
ribosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=S.typhimurium; STRAIN=LT2;
MEDLINE=9831265; PubMed=9642179;
Zhang Y., Cronan J.E. Jr.;
"Transcriptional analysis of essential genes of the Escherichia colifatty acid blosynthesis gene cluster by functional replacement with the analogous Salmonella typhimurium gene cluster.";
J. Bacteriol. 180:3295-3303(1998).
                   Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
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Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=76119562; PubMed=765258;
Wittmann-Liebold B., Greuer B., Pannenbecker R.;
"The primary structure of protein L32 from the 50S subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoppe-Seyler's Z. Physiol. Chem. 356:1977-1979(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bioorg. Khim. 2:1013-1017(1976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli ribosomes.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                               SPECIES=E.coli; STRAIN=K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
(Dicyclohexylcarbodiimide-binding protein) ATPE OR SMU.1534.
                                                                  NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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    84444B
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                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                           "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4412-4441 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                       SPECIES-S. flexner; STRAIN=301 / Serotype 2a; MEDLINE=22272406; PubMed=12384590; Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang Q., Yuan Z., Zhang Y., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                         SPECIESE 201; STRAIN-KI2 / ATCC 25404;
MEDLINE=99196679; PubMed=10094780;
Arnold R.J., Reilly J.P.;
"Observation of Escherichia coli ribosomal proteins and their
"Observation of Escherichia coli ribosomal proteins and their
Anal. Biochem. 269:105-112 (1999).
-i- MASS SPECTROMETRY: MW=6315.1; METHOD=WALDI.
-i- SIMILARITY: BELONGS TO THE L32P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 11 Last annotation update)
(Cal. 41 (Lost annotation)
(Cohain (EC 3.6.3.14) (Lipid-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.2%; Score 26; DB 1; Length 56; 28.6%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AA; 6315 MW; B74A9510E78E4E94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAWAP; MF 00340; -; 1.
InterPro; IPR005718; 322 bact_org.
TIGREAMs; TIGR01031; rpmF bact; 1.
Ribosomal protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AEG00209, AAC74173.1; EMBL, D90744, BAA35897.1; EMBL, AEG05319, AAG58835.1; EMBL, AP044668, AAC38646.1; EMBL, AEG0455; BAB34890.1; EMBL, AEG04568, AAC38646.1; EMBL, AEG17689, CAD08315.1; EMBL, AEG1239, AAC69353.1; EMBL, AEG15336, AAC4712.1;
                     Bacteriol. 185:2330-2337(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; C90812; C90812.
PIR; G85671; G85671.
PIR; JV0048; R5EC32.
ECCOEBASE; 1011.7; 6TH EDITION.
ECCGENE; EG10890; rpmF.
StyGene; SG10698; rpmF.
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M29698; AAA24575.1; -.
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RSHDALTAVTSLSV 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                      SPECTROMETRY
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28-FEB-2003 (Rel
ATP synthase C o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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-!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A. B AND C.
-!- MISCELLANEOUS: DICYCLOREXYLCARBODIMIDE (DCDD) INHIBITS ATPASE.
-!- SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRANIB-ALIS9, ArCC 700610 / Serotype C;
STRANIB-ALIS9, ArCC 700610 / Serotype C;
MEDLINE-22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar P., Lai H., White J., Roe B.A., Perretti J.J.;
"Genome sequence of Streptococcus mutans UAIS9, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DICYCLOHEXYLCARBODIIMIDE (BY SIMILARITY) 56717BDA6A12FEDE CRC64;
                                                                                  Smith A.J., Quivey R.G., Faustoferri R.C.; Cloning and nucleotide sequence analysis of the Streptococcus mutans membrane-bound, proton-translocating ATPase operon."; Gene 183:87-96 (1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
-!- FUNCTION: THIS IS ONE OF THE THREE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE ATPASE COMPLEX.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pfam; PF00137; ATP-87nt C; 1.
PRINTS; PR00124; ATPASEC.
PROSITE; PS00605; ATPASE C; 1.
Hydrogen ion transport; CF(0); Transmembrane; Lipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26, DB 1; Length 67;
Pred. No. 5.2e+02;
2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, U31170; AAD13377.1; -.
EMBL, AE014985; AAM59184.1; -.
PIR, JG5735, JC5735, JC5735.
InterPor; IPR002379; ATPASE CSUb.
InterPro; IPR00454; Eub_ATFASE_CSUb.
                                           STRAIN=GS-5;
MEDLINE=97149283; Pubmed=8996091;
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SEQUENCE FROM N.A.
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SETTTTT BERREIT
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MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Maxino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                 Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R., Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.", Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin O., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun D., Xue Y., Zhao A., Zao A., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                 SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=29258224; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SECURESE Coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed=1120655;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Manther N., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melch R.A., Blattner F.R.;
                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borodovsky M., Rudd K.E., Koonin E.V.; "Intrinsic and extrinsic approaches for detecting genes in a
YIFL OR B3808.1 OR C4729 OR Z5325 OR ECS4737.1 OR SF3886
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SPECLESE.coli, STRAIN=K12;
Glaser P., Sigmeirc O., Danchin A.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
                                                                                      Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=E.coli;
MEDLINE=95075659; PubMed=7984428;
            Escherichia coli,
Escherichia coli O6,
Escherichia coli 0157:H7, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:529-533(2001).
                                                                                                                                                                                                                                Science 257:771-778(1992)
                                                              Shigella flexneri.
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                      Nucleic Acids Res. 22:4756-4767(1994).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDLINE=22495039; PubMed=12606174;
MEDLINE=22495039; PubMed=12606174;
MEDLINE=22495039; PubMed=12606174;
Morbia L.D., Pallen M.J., Harris D.E.,
Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,
von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
Barrell B.G., Parkhill J., Relman D.A.;
"Sequencing and analysis of the genome of the Whipple's disease
bacterium Tropheryma whipplei.";
Lancet 361:627-634(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Twist / Genotype 2A;
Raoult D., Audic S., Robert C., Ogata H., Suhre K., Drancourt M.,
Claverie J.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tropheryma whipplei (strain Twist) (Whipple's bacillus), and Tropheryma whipplei (strain Tw08/27) (Whipple's bacillus). Bacteria, Actinobacteria, Actinobacteria, Actinobacteria, Micrococcineae, Cellulomonadaceae; Tropheryma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL LIPOPROTEIN YIFL.
N-ACYL DIGLYCREIDE (POTENTIAL)
DGPSQNYY -> MVHPR (IN REF. 2).
4ASJCF48AS5SA7F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Tropheryma whipple; illustrates the diversity of gene loin small genome bacterial pathogens.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  EMBL, M87049; -; NOT ANNOTATED CDS.

EMBL, X66782; -; NOT ANNOTATED CDS.

EMBL, X66782; -; NOT ANNOTATED CDS.

EMBL, AE016769; AANB3162.1; -.

EMBL, AE016567; -; NOT ANNOTATED CDS.

EMBL, AE016567; -; NOT ANNOTATED CDS.

EMBL, AE016395; AAN4532.1; -.

EMBL, AE016395; AAN4532.1; -.

EMBL, AE016395; ANNOTATED CDS.

ENGL, ER667; E86667.

EOGENE, E112913; Yiff.

PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
UPP0233 membrane protein TWT010/TW010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26; DB 1; I
Pred. No. 5.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7177 MW;
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Best Local Similarity
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                                                                             (Potential).
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P59486;
bacterial
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CONFLICT
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XX STARIN-CO. Columbia;

XX STARIN-CO. Columbia;

XX Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

XX Salanoubat M., Lemcke K., Rieger M., Ansorge W., Obermaier B.,

XX Salanoubat M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

XX Belseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

XX Mincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

XX Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

XX Chaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

XX Wincker P., Drzonek H., Erfle H., Jordan N., Bangert S.,

XX Wezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

XX Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

XX Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

XX Navaro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,

XX Ocoke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

XX Ander Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta B.,

XX Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,

XX Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

XX Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
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OBLAIL 1, QBMC99;

OBLAIL 1, QBMC99;

OBLAIL 1, Created)

OBLAIL 2003 (Rel. 41, Last sequence update)

OBLAIL 2003 (Rel. 42, Last annotation update)

OBLAIL 4, Last annotation (ALPSK)

OBLAIL 4, Last annotation (ALPSK)

OBLAIL 4, Last annotation update)

OBLAIL 4, Last annotation (ALPSK)

OBLAIL 4, Last annotation update)

OBLAIL 4, Last annotation (ALPSK)

OBLAIL 4, Last annotat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: Belongs to the UPF0233 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 1; Length 69;
Pred. No. 5.4e+02;
2; Mismatches 2; Indels
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MEDLINE=21563059; PubMed=11706167;
Yang H., Mateubayashi Y., Nakamura K., Sakagami Y.;
Yang H., Mateubayashi Y., Nakamura K., Sakagami Y.;
Yang H., Mateubayashi Genes encoding precursors for phytosulfokine, a peptide growth factor.";
Plant Physiol. 127:842-851(2001).
                                                                                                                                                                                                                                                                                                                                                                                       3C83E5B3F154DD24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 AA
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                                                                                                                                                                                                                                                                                    EMBL; DALLLER PROBLEM 1 1. 1. HAMAP: MF 00631; -; 1. Transmembrane. Hypothetical protein; Transmembrane. 14
                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                 EMBL; AE016850; AAO44107.1; -. EMBL; BX251410; CAD66702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   34.2%;
                                                                                                                                                                                                                                                                                                                                                                                       69 AA; 7723 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55...
France 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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50 NILIAFGII 58
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Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P., Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S., Pai G., Militescher J., Sellers P., Gill J.B., Feldblyum T.V., Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Fraser C.M., Kaneko T., Nakamura Y., Sato S.L., White O., Venter J.C., Sasamoto S., Kimura T., Ideaawa K., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Mateumoto M., Matsuno A., Muraki A., Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Mateuche A., Yamada M., Yasuda M., Tabata S., Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Flagellar blosynthetic protein fliq (Flagellar blosynthetic protein mopp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AC002534; -; NOT ANNOTATED_CDS.
EMBL; AY088090; AAM55636.1; -.
Growth factor; Differentiation; Signal; Sulfation; Multigene family.
SIGNAL 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
--- SUBCELLULAR LOCATION: Secreted (By similarity).
--- PTM: SULfain is important for activity and for the binding to putative membrane receptor (By similarity).
--- PTM: PSK-beta is an enzymatic derivative of PSK-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erwinia carotovora.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.;
Feldmann K.;
Submirted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Promotes plant cell differentiation, organogenesis somatic embryogenesis as well as cell proliferation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
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55.6%; Pred. No. 6.4e+02;
tive 2; Mismatches 2; Indels
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
S -> T (IN REF. 3).
R -> H (IN REF. 3).
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-!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                              Nature 408:820-822(2000).
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MOD_RES
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DNA packaging
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MARAN 
                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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like channels in adrenal cells.";
J. Biol. Chem. 275:23965-23972 (20000).
-!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
PHOSPHATIDYLINOSITOL SECOND MESSENDER SYSTEM ACTIVATED BY RECEPTOR
TYROSINE KINASES OR G-FROTEIN COUPLED RECEPTORS. ACTIVATED BY
DIACYLGLYCEROL (DAG) IN A MEMBRANE-DELIMITED FASHION,
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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Mehlipp S., Trost C., Warnat J., Rautmann J., Himmerkus N.,
Schroth G., Kretz O., Nastainczyk W., Cavalie A., Hoth M.,
Flockerzi V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.2%; Score 26; DB 1; Length 89; 40.0%; Pred. No. 7.1e+02;
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20EC2F84A09E063B CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
Transient receptor potential channel 6 (Fragment).
TRPC6 OR TRP6.
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InterPro; IPR002191; Bac_export_3.
InterPro; IPR006305; FliQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01313; Bac_export_3; 1.
PRINTS; PR00922; TYPBZIMQPROT.
TIGRFAMS; TIGR01402; fliQ; 1.
Flagella; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X72969; CAA51477.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|: | :|:
11 YEAMKVALAL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    835277: 835277
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Matches 4; Conser
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                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 AA;
  NCBI_TaxID=554;
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                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION (BY SIMILARITY).
SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein (Probable).
SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJINE-86209997; PubMed-3010556;
Yamada M., Fujisawa H., Kato H., Hamada K., Minagawa T.;
"Cloning and sequencing of the genetic right end of bacteriophage T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada M., Fujisawa H., Kato H., Hamada K., Minagawa T.;
Virology 154:246-246(1986).
-!- FUNCTION: DURING THE GROWTH OF THIS PHAGE, DNA IS SYNTHESIZED
AS CONCATEMERS.
-!- FROM THE CONCATEMERS.
-!- SUBUNIT: GP18 AND GP19 ASSOCIATE WITH DNA AND PROHEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses, dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
T7-like viruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ271069; CACO1677.1; -.
InterPro; IPR002111; Cat_channel TrpL.
Ionic channel; Transmembrane; Ion transport; Calcium channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 89;
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Pred. No. 7.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1992 (Rel. 23, Last annotation update)
DNA maturase A (DNA packaging protein A) (GP18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VYDALNVLMAMNII 15
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71 VYNVTMVIVLLNML 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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88
89
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RESULT 29 VDMA_BPT7

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                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                     Kawarabayasi Y., Tuknechiologi, Kawarabayasi Y., Takahani Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahani M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijina K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamara Y., Nomura N., Sako Y., Kikuchi H.; Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl., DNA Res. 6.83-101(1999).

-- FUNCTION: PROMOTES THE EXCHANGE OF GDP FOR GTP IN EF-1-ALPHA/GDP, THUS ALLOWING THE REGENERATION OF EF-1-ALPHA/GTP THAT COULD THEN BE USED TO FORM THE TERNARY COMPLEX BF-1-ALPHA/GTP/AATRNA (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=99083443; PubMed=9866211;
Black W.C. IV, Roehrdanz R.L.;
"Mitochondrial gene order is not conserved in arthropods: prostriate and metastriate tick mitochondrial genomes.";
Mol. Biol. Evol. 15:1772-1785(1998).
-:- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parabitiformes; Ixodida; Ixodidae; Rhipicephalus.
NCBI_TaxID=34632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pfam; PF00736; EF1BD; 1.
TIGRPAMs; TIGR00489; aEF-1 beta; 1.
Elongation factor; Protein blosynthesis; Complete proteome.
SEQUENCE 90 AA; 9885 MW; B7BCBC94013536F4 CRC64;
                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: BELONGS TO THE EF-1-BETA/EF-1-DELTA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.2%; Score 26; DB 1; L
55.6%; Pred. No. 7.2e+02;
tive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhipicephalus sanguineus (Brown dog tick). Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP000064; BAA81496.1; ALT_INIT.
                MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; 027734; 1GH8.
HAMAP; WF 20043; -; 1.
INCEPPC; IPR004542; aEF-1 beta.
INCEPPC; IPR001326; EF1_BD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || :::|||
50 ALKLVIAMN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                SIMILARITY)
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NULM_RHISA
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Matches
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                                                                                         Gaps
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Dunn J.J., Studier F.W.;
Dunn J.J., Studier F.W.;
Dunn J.J., Studier F.W.;
Dunn J.J., Studier F.W.;
J. Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 genetic elements ";
J. Mol. Biol. 166:477-535(1983)
-!- FUNKTION: DURING THE GROWTH OF THIS PHAGE, DNA IS SYNTHESIZED AS CONCATEMERS. DRING DNA PACKAGING MATURE MONOWERS ARE CUT FROM THE CONCATEMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage T7.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
T7-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DB 1; Length 89;
Pred. No. 7.1e+02;
5; Mismatches 1; Indels
                                        Score 26; DB 1; Length 89;
Pred. No. 7.1e+02;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA packaging.
SEQUENCE 89 AA; 10145 MW; 344B03EC22B42145 CRC64;
    10033 MW; A131FE25FE1A8594 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Blongation factor 1-beta (EF-1-beta) (aEF-1beta).
                                                                                                                                                                                                                                                                                                                                          21-JUJ-1986 (Rel. 01, Created)
21-JUJ-1986 (Rel. 01, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
DNA maturase A (DNA packaging protein A) (GP18).
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NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.2%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; V01146; CAA24437.1; -. PIR; A04315; JVBPA7.
                                                 34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 40.0
Matches 4; Conservative
                         Query Match
Best Local Similarity 40...
A: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                        1 RVYDALNVLM 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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    89 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EF1B OR APE2480
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                                                                                                                                                                                                                                                                                                  VDMA_BPT7
P03693;
       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9Y904;
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RESULT 30

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Gaps

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Length 90;

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YCHH ECOLI
P31807;
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                                                                                                                                KCHH ECOLI
                                                                                                                      RESULT 33
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                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE=89345542; PubMed=2668946;
Nishi M., Chan S.J., Nagamatsu S., Bell G.I., Steiner D.F.;
"Conservation of the sequence of islet amyloid polypeptide in five
"Conservation of the sequence of islet amyloid polypeptide in five
mammals is consistent with its putative role as an islet hormone.";
Proc. Natl. Acad. Sci. U.S. A. 86:5738-742(1989).
-I- FUNCTION: SELECTIVELY INHIBITS INSULIN-STIMULATED GLUCOSE
UTILIZATION AND GLYCOGEN DEPOSITION IN MUSCLE, WHILE NOT AFFECTING
ADIPOCYTE GLUCOSE METABOLISM.
-I- SUBCELLULAR LOCATION: Secreted.
-I- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
AMIDATION (G-74 PROVIDE AMIDE GROUP).
67F3629014BF3F9C CRC64;
                                                                                                                                                                                                                                                                                                                                                Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000443; Amylin.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR001693; Calcitonin-B.
Pfan; PF00214; Calc CGRP IAPP; 1.
PRINTS; PR00817; CALCITONINB.
PRINTS; PR00818; ISLETAMYLOID.
SMART; SM00113; CALCITONIN; 1.
PROSITE; PS002258; CALCITONIN; 1.
Hormone; Cleavage on pair of basic residues; Amidation; Amyloid;
                                                                                                                                                         .;
0
                                                                                                                              Score 26; DB 1; Length 91;
Pred. No. 7.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISLET AMYLOID POLYPEPTIDE
                                                                   Pfam; PF00420; oxidored q2; 1.
ProDom; PD000359; Oxidred4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 91 AA; 10598 WW; D2E51EC5F1D056EE CRC64;
                                                                                                                                                                                                                                                                                      01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Islet amyloid polypeptide precursor (Amylin).
                                                                                                                                                                                                                                                                  92 AA.
                                                                                                                                                        4; Mismatches
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                 PRT;
                                 PIR; T11163; T11163.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
                       EMBL; AF081829; AAD05527.1; -.
                                                                                                                               34.2%;
50.0%;
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                                                                                                                  Query Match
Best Local Similarity 50.v.
A; Conservative
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82 LMMSMNLI 89
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SEQUENCE
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P12966;
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IAPP_CAVPO
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MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
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MEDLINE=22380234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Shou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
                                                                                             Gaps
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.K., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12;
MEDLINE=95129849; PubMed=7828865;
Galindo J.M., de la Vega F.M., Guarneros G.;
"Open reading frames flanking the peptidyl-tRNA hydrolase-encoding gene of Escherichia coll.";
Gene 151:153-156(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 217992, 83334;
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Buckingham R.H., Guarneros G.;
"Peptidyl-tRNA hydrolase is involved in lambda inhibition of host
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                             Score 26; DB 1; Length 92;
Pred. No. 7.4e+02;
.; Mismatches 4; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 26, Created)
(Rel. 26, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                             92 AA
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YCHH OR B1205 OR C1663 OR Z1976 OR ECS1710.
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                             34.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein synthesis.";
EMBO J. 10:3549-3555(1991).
Query Match
Best Local Similarity 58.5.
7; Conservative
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Escherichia coli 06, and
Escherichia coli 0157:H7.
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01-JUL-1993 (
28-FEB-2003 (
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NULM BALPH
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  genome sequence
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Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
                                                                                                  STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.
Apodaca J., Anantharanan T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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Pred. No. 7.4e+02;
3; Mismatches 2; Indels
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structure revealed by the complete
                     of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Hypothetical protein; Complete proteome
SEOUENCE 92 AA; 10486 MW; 8F75344F00
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                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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MEDLINE=99120557; PubMed=9923682;
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C85700; C85700
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Best Local Similarity
Matches 4; Conserv
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       Extensive mosaic
                                                                                              SEQUENCE FROM N.A.
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09ZJZ9;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.P.,
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
Balaenopteridae; Balaenoptera.
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HEME (COVALENT).
IRON (HEME AXIAL LIGAND) (1)
SIMILARITY).
IRON (HEME AXIAL LIGAND) (1)
SIMILARITY).
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01-MAR-1992 (Rel. 21, Last sequence update)
16-001 (Rel. 40, Last annotation update)
MADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
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INTERPRO, IPR003088, CY_CI.
INTERPRO, IPR003188, CY_CIC.
INTERPRO, IPR003185, CYCCIC.
INTERPRO, IPR000345, CYCCAROME c; 1.
PRIMTS, PR006051, CYTCCAROME c; 1.
PROMO, P0004020, CYT C Dact; 1.
PROSTIE, PS001901, CYTCCHROME C; 1.
Electron transport, Heme; Signal; Periplasmic; Consider.
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Pred, No. 7.7e+02;
2; Mismatches 1;
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MEDLINE=92139449; PubMed=1779436;
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Best Local Similarity 62.5
Matches 5; Conservative
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YC12 CHLRE
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                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CCAP 1204-17a;
MEDLINE=21080522; PubMed=11212895;
Gockel G., Hachtel W.;
"Complete gene map of the plastid genome of the nonphotosynthetic euglenoid flagellate Astasia longa.";
Protist 151:347-351(2000).
-!- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
Mol. Evol. 33:556-568(1991).
- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CCAP 1204-17a;
MEDLINE=95062725; PubMed=7972503;
Gockl G., Baier S., Hachtel W.;
Holstid ribosomal protein genes from the nonphotosynthetic
flagellate Astacia longa.";
Plant Physiol. 105:1443-1444(1994).
                                                                                                                                                                                                                                                              34.2%; Score 26; DB 1; Length 98; 44.4%; Pred. No. 7.9e+02; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
NCBL_TaxID=3037;
                                                                                                                                                                                               Pfam; PF00420; oxidored_q2; 1.
ProDon; PD000359; Oxidored4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10763 MW; 0070D3D6C3AE805F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
101-FEB-1994 (Rel. 28, Last sequence update)
10-CCT-2010 (Rel. 40, Last annotation update)
Chloroplast 50S ribosomal protein L23.
                                                                                                                                                                                                                                                                                                                                                                                                               98 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Astasia longa (Euglenophycean alga).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S38604; S38604.
InterPro, IPR001014; Ribosomal L23.
Pfam; PF00276; Ribosomal L23; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD001141; Ribosomal L23; 1.
                                                                                                                                                                     InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ294725; CAC24593.1; -.
                                                                                                                                            EMBL; X61145; CAA43447.1; -. PIR; A58851; S24920.
                                                                                                                                                                                                                                                                          Local Similarity 44.4
                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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6 MNILMAFSM 14
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RK23_ASTLO
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                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Khrebtukova I., Spreitzer R.J.; "Nucleotide sequences of the chloroplast trnS-GCU and ycf12 genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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phi-29-like viruses.
NCBI_TaxID=10753;
                                                                                                                                                            3.
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                                                                                                       33.6%; Score 25.5; DB 1; Length 98; 47.1%; Pred. No. 9.7e+02; tive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25; DB 1; Length 33;
Pred. No. 3.7e+02;
6; Mismatches 2; Indels
PROSITE; PS00050; RIBOSOMAL L23; 1.
Ribosomal protein; Chloroplast; rRNA-binding.
SEQUENCE 98 AA; 11944 MW; 7572EB84DA96D347 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 AA; 3332 MW; 022F633E416F349E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
12-UL-1998 (Rel. 36, Last annotation update)
Hypothetical 3.3 kDa protein ycf12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Tail protein (Late protein GP9) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (In) Plant Gene Register PGR95-117.
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RF; T08018; T08018.
Chloroplast; Hypothetical protein.
SEQUENCE 33 AA; 3332 MW; 022P6
                                                                                                                                                                                                                 2 VYDA---LNVLMAMNII 15
                                                                                                                                                                                                                                                                   31 VFDVDKKLNKLQIKNII 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.98;
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                                                                              Query Match
Best Local Similarity 47.1.
Best Local Similarity 67.1.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Conservative
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1 MNIELALTLVS 11
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Matches 3, Conserv
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SEQUENCE FROM N.A.
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Best Local Similarity
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"The primary structure of the antenna polypeptides of
"The primary structure of the antenna polypeptides of
"The primary structure of the antenna by
"The primary structure of the and Ectothiorhodospira halophila.";

"Ectothiorhodospira halochloris and E. halophila.";
"The antenna polypeptides in E. halochloris and E. halophila.";
"Encryon antenna polypeptides in E. halochloris.";
"TRANSFER THE EXCITATION ENERGY TO THE REACTION CENTERS.
"I FUNCTION: ANTENNA COMPLEX IS FORMED BY DIFFERENT ALPHA AND BETA CHAINS, BINDING BACTERIOCHICROPHYLL MOLECULES, AND BETA CHAINS, INDING BACTERIOCHICROPHYLL MOLECULES, AND ARRANGED MOST PROBABLY IN TETRAMERIC STRUCTURES DISPOSED AROUND THE MOST PROBABLY IN TETRAMERIC STRUCTURES DISPOSED AROUND THE ADDITIONAL COMPENSING.
"I SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane."

InterPro; IPROBOGO66; Antenna a/b.

Refan; PRO0566; LHC; 1.

REACTION PROBOGO66; Antenna a/b.

Refan; PRO0566; LHC; 1.

REACTION ANTENNA COMP ALPHA; 1.

REACTION ANTENNA COMP ALPHA; 1.

REACTION ANTENNA COMP ALPHA; 1.

"T DOMAIN BACTERIOCHICAPHYI! Inner membrane."

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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Light-harvesting protein B800/83011020, alpha-1 chain (EHS-alpha-1)
(Antenna pigment protein, alpha-1 chain) (Fragment).
Ectothiorhodospira halochloris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
PERIPLASMIC (POTENTIAL).
MAGNESIUM (BACTERIOCHLOROPHYLL AXIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92249336; PubMed-1577009;
Wagner-Huber R., Brunisholz R.A., Bissig I., Frank G., Suter F.,
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
Ectothiorhodospiraceae; Halorhodospira.
NCBI_TaxID=1052;
                                                                                                                                                                                                                                                                            32.9%; Score 25; DB 1; Length 48; 33.3%; Pred. No. 5.5e+02; tive 4; Mismatches 6; Indels
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                                                                                                                                                                                                                                                48 AA; 5517 MW; 515CF4F4841414FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIGAND) (POTENTIAL).
   Yoo S.K., Braithwaite D.K., Ito J.;
"Head fiber protein gene of bacteriophage Nf.";
J. Gen. Appl. Microbiol. 36:365-368(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 AA.
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6191 MW;
                                                                                                                                                                                      EMBL; X52807; CAA36996.1; -. PIR; S11639; S11639.
                                                                                                                                                                                                                                                                                                                                              1 RVYDALNVLMAMNII 15
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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NON TER 48
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SEQUENCE
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LHA1_ECTHL
ID _LHA1_ECTH
AC P80102;
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Length 52;

DB 1;

Score 25;

32.9%;

Query Match

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SERQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8668087;

MEDLINE-96337999; PubMed-8668087;

Built Co.J., White O., Olsen G.J., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Kerlavage A.R., Meinstor B.A., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.P., Fuhrmann J.L., Nguyen D.,

Scott J.L., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Сарв
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09U8D2; 09U522;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurotoxin BmP01 precursor (Potassium ion channel blocker P01).
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthidae; Mesobuthus
                Gape
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                      5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66CBFC395548BA5D CRC64;
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Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein MJ0546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 AA
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Pred. No. 6e+(
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AA; 6460 MW;
                                                                                                                  1 RVYDALNVLMAMNI 14
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Matches 3; Conservative
                           5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LNVLMAMNII 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B64368; B64368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR; MJ0546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSSEPPPR
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TRANSMEM
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                     TISSUE=Venom gland;
MEDLINE=99313193; PubMed=10386622;
Wu J.J., Dai L., Lan Z.D., Chi C.-W.;
"Genomic organization of three neurotoxins active on small conductance "Genomic organization of three neurotoxins active on small conductance Ca2+-activated potassium channels from the scorpion Buthus martensi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glerum D.M., Koerner T.J., Tzagoloff A.; "Cloning and characterization of COX14, whose product is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                               martensii.";
Kexue Tongbao 44:2295-2299(1999).
-i- FUNCTION: Blocks small conductance Calcium-activated potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                        Zhu S.-Y., Zeng X.-C., Li W.-X., Jiang D.-H.; "Molecular characterization of a K+ channel blocker from Buthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                -i- TISSUE SPECIFICITY: Expressed by the venom gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 1; Length 57;
Pred. No. 6.7e+02;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4265970F1250B53A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toxin; Neurotoxin; Ionic channel inhibitor;
Potassium channel inhibitor; Signal.
2 SIGNAL. 1 28 POTENTIAL.
CHAIN. 29 5.7 NEUROTOXIN BNPO1.
DISULFID 31 4.7 BY SIMILARITY.
DISULFID 34 5.2 BY SIMILARITY.
CONFLICT 17 17 V -> I (IN REF. 2).
CONFLICT 21 21 7 -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-Corchrome c oxidase assembly protein COX14.
COX14 OR YML129C OR YM4987.06C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=D273-10B;
MEDLINE=95318142; PubMed=7797555;
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF095781; AAF03045.1; -. EMBL; AF114024; AAF24057.1; -. HSSP; P56215; 1ACW.
                                                                                                                    FEBS Lett. 452:360-364(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6318 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RVYDALNVLMAMNII 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RLYAIILIALVFNVV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 AA;
 NCBI_TaxID=34649;
                                                                                                                                                                                                                                            channels.
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P39103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                         Karsch."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                              Nature 38:19-94(1997).
-1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF YEAST CYTOCHROME OXIDASE.
-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                              Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G., "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 1; Lengtn 'v',
Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016021; C:integral to membrane; IDA.
GO; GO:0005740; C:mitochondrial membrane; IDA.
GO; GO:0009060; P:aerobic respiration; IMP.
GO; GO:0008515; P:cytochrome c oxidase biogenesis; IMP.
Mitochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 38 POTENTIAL.
70 AA; 7959 MW; B26DEAE366707617 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yncH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
assembly of yeast cytochrome oxidase.";
J. Biol. Chem. 270:15585-15590(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Escherichia
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U15040; AAA50449.1; -. EMBL; Z50178; CAA90554.1; -. PIR; A57515; A57515. SGD; S0004598; COX14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RVYDALNVIMAMNII 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 RÝTDTLHRLTVLTLV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                      Nature 387:90-93(1997)
                                                                                            PubMed=9169872;
Bouman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
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P76118;
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82 A.A.

STANDARD;

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RANPI
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PROPEP
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RANA_RANPI
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  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.9%; Score 25; DB 1; Length 80;
44.4%; Pred. No. 9.6e+02;
iive. 3; Mismatches 2; Indels
                                                                                                    Score 25; DB 1; Length 70;
Pred. No. 8.3e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PÉGAI, PP00216; Bac_DNA_bInding; 1.
PR005ITE; PS00045; HISTONE_LIKE; FALSE_NEG.
DNA-binding; DNA_condensation; Complete proteome.
SEQUENCE 80 AA; 9795 WW; 3B465A23F9C3DC2C CRC64;
                                        EMBL; AE000242; AAC74537.1; -.
PIR; B64898; B64898.
BcoGene; EG13778; yncH.
Hypothetical protein; Complete proteome.
SEQUENCE 70 AA; 8270 MW; 9DFEB75318F25C85 CRC64;
                                                                                                                                                                                                                                         (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                      80 AA
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AE008632; AAL03295.1; -. PIR, E97794; E97794. InterPro; IPR000119; Bac_DNAbind.
                                                                                                          32.9%;
                                                                                                                                                                                                                                                                         DNA-binding protein HU-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                             | ||:|:
54 VGDAININTNKNI 66
                                                                                                  2 VYDALNVLMAMNI 14
                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::| || |
KIHDKLNCL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RVYDALNVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                             Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          STRAIN=Malish
                                                                                                                                                                                                                                         28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                        RICCN
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DBHL RICCN
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                                                                                                                                                                                                                                                                              Krane I.M., Naylor S.L., Helin-Davis D., Chin W.W., Spindel E.R.; "Molecular cloning of cDNAs encoding the human bombesin-like peptide neuromedin B. Chromosomal localization and comparison to cDNAs encoding its amphibian homolog ranatensin."; J. Biol. Chem. 263:13317-13323 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDATION (G-59 PROVIDE AMIDE GROUP). 09194FFD0E7436DE CRC64;
                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02044; bounce..., -
PROSITE; PS06257; BOMBESIN, 1.
Amphibian defense peptide; Bombesin family; Amidation;
Cleavage on pair of basic residues; Signal.
27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 1; I
Pred. No. 9.9e+02;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 17, 2004, 10:57:04 Job time : 6.06931 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RANATENSIN.
                                                                             Ranatensin precursor.
Rana pipiens (Northern leopard frog)
                                                                                                                                                                                                                                                         FISSUE=Skin;
MEDLINE=88330837; PubMed=2458345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; B28945; B28945.
InterPro; IPR000874; Bombesin.
Pfam; PF02044; Bombesin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M21552; AAA49533.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.9%;
38.5%;
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DFLTILLFSFIS 25
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nes 5; Conservative
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58
58
58
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                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 48-58.
                                                                                                                                                                      NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILY.
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Pebruary 17, 2004, 10:50:13 ; Search time 9.66337 Seconds
(without alignments)
159.230 Million cell updates/sec Run on:

US-09-900-147-5 76 1 RVYDALNVLMAMNIIS 16 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 · Gapext 0.5

283308 segs, 96168682 residues Searched:

37673 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	homeotic protein E	hypothetical prote	alpha-internexin	hypothetical prote	hypothetical prote		hypothetical prote		hypothetical prote	hypothetical prote		heat shock protein	hypothetical prote	t-complex polypept	hypothetical prote		hypothetical prote	_		ᇽ	hypothetical prote	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	hypothetical prote	hypothetical prote	phosphoenolpyruvat	hypothetical prote
SUMMARIES	QI	JC1386	D89831	PN0624	F84283	T42312	A99954	T27124	B86477	D83924	AI2346	H89910	PA0105	E89904	E49410	A81346	D83797	A84215	B82699	T30649	148172	800119	T17143	T17174	T17177	T17162	F90284	T40639	T03658	H85826
	Length DB	60 2		57 2	-			•	•	35 2		•		•					72 2			96 2					99 2	97 2	•••	68 2
عان	Query Match 1	46.1	44.7	43.4	43.4	43.4	42.1	42.1	42.1	40.8	40.8	40.8	39.5	σ	σ	σ	39.5	σ	39.5	σ	σ	39.8	σ	39.5	39.5	39.5	39.5	38.8	38.5	38.2
	Score	35	34	33	33	33	32	32	32	31	31	31	30	30	30				30						30	30	30	29.5	29	29
	Result No.	1	7	Э	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

truncated transpos	transcription regu	hypothetical prote	hypothetical prote	protein-export pro	hypothetical prote	hypothetical prote	NADH2 dehydrogenas	elongin C - fruit	truncated transpos	hypothetical prote	TodR protein - Pse	NADH2 dehydrogenas	hypothetical prote	hypothetical prote	conserved hypothet
F89891	C69425	T21426	F97704	E86742	E84290	D97817	T11449	JC5794	F89915	T38899	S53994	S15650	C90001	G69115	AB2812
7	Н	N	7	7	7	7	N	7	7	~	7	7	7	~	7
70	77	78	79	82	82	82	96	98	98	100	100	30	45	9	63
38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	36.8	36.8	36.8	36.8
53	29	29	29	29	29	29	29	29	29	29	29	. 28	28	28	28
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ALIGNMENTS

RESULT 1

	JC1386
	homeotic protein EgHbx1 - tapeworm (Echinococcus granulosus) (fragment)
	C, Species: Echinococcus granulosus
	C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Oct-1997
	C, Accession: JC1386
	R;Oliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlic
	Gene 121, 337-342, 1992
	A; Title: Homeoboxes in flatworms.
_	A; Reference number: JC1386; MUID: 93077050; PMID: 1359988
	A;Accession: JC1386
_	A; Molecule type: DNA
	A;Residues: 1-60 <oli></oli>
	A; Cross-references: EMBL: X66817
	C; Superfamily: unassigned homeobox proteins; homeobox homology
	C; Keywords: DNA binding; homeobox; nucleus; transcription
	F;2-58/Domain: homeobox homology <hox></hox>

Gaps ; 0 Length 60; Indels Score 35; DB 2; Pred. No. 21; 6; Mismatches Query Match
Best Local Similarity 38.5%;
Matches 5; Conservative 6

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2 VYDALNVLMAMNI 14 28 VYERLNLALSLNL 40 ઠે 셤

RESULT 2 D89831

hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: D898931
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146 A,Accession: D89831

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-74 <KUR>

A;Cross-references: GB:BA000018; PID:g13700510; PIDN:BAB41807.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics: A;Gene: SA0575

Gaps ö Ouery Match
Best Local Similarity 50.0%; Pred. No. 40;
Matches 6; Conservative 4; Mismatches 2; Indels

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1 RVYDALNVLMAMNIIS 16
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                                                                                   43.4%;
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RIYRAFEMSMEKDIIS
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Best Local Similarity 43.8
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                      Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                          1 RVYDALNVLMAM 12
                                                                                                                                                                                                                        : | | | | | : : | | : : | 40 QVYDAVSVLFTI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 RVYDDLNTI 55
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A, Gene: CESP: Y53C10A.11
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A;Residues: 1-66 <KUR>
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F94283
R;Ng W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;Isi, W.V.; Kennedy, S.P.; Mahairas, T.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld
Jung, K.H.; Alam, M.; Preites, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: F94283
A;Actatus preliminary
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C;Species: phage SPP1
C;Species: phage SPP1
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Date: 03-121312
C;Accession: T2.1 1997
Gene 204, 201-212, 1997
A;Pitle: The complete nucleotide sequence and functional organization of Bacillus subtil
A;Reference number: Z22137; MUD:98094274; PMID:9434185.
A;Accession: T42312
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                              alpha-internexin - pig (fragments)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999
C;Accession: Mo624
A;Title: Phosphorylation of a 62kD porcine alpha-internexin, a newly identified intermed A;Reference number: PN0624; MUID:94029981; PMID:8216281
A;Accession: PN0624
A;Molecule type: protein
A;Accession: PN0624
A;Molecule type: protein
C;Comment: This intermediate filament protein polymerizes to form filament itself, in vi C;Superfamily: cytoskeletal keratin
C;Superfamily: cytoskeletal keratin
C;Keywords: brain; intermediate filament
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C; Genetics:
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43.4%; Score 33; DB 2; Length 66;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 8; Conservative 4; Mismatches 4; Indels
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Matches 7; Conservative
                      |::| |::|| 35 DSMNALVDLNII 46
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A; Residues: 1-66 <STO>
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A;Gene: VNG1283H
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Extraction (1) Obta. T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc R; Kuxoda, M.; Ohta. Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89788; MUID:21311952; PMID:11418146
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A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyporhetical protein Y53C10A.11 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27124
                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: A99954
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A;Experimental source: clone Y53C10A
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                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein SA2292 [imported] - Staphylococcus aureus
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81;
                                                                                                 Length 82;
                                                                                                                                                     Indels
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5. 83;
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A;Molecule type: DNA
A;Residues: 1-67 <WIL>
                                                                                              Score 33; DB 2;
Pred. No. 68;
4; Mismatches 2
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A;Reference number: Z20314
A;Accession: T27124
A;Molecule type: DNA
A;Residues: 1-82 <ALO>
A;Cross-references: EMBL:X97918; PIDN:CAA66519.1
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Pred. No. 8
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Query Match
Best Local Similarity 66.7.,
6; Conservative
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Matches 5; Conservative
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                A; Accession: AI2346
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                                                                                                                                                                                                    A; Gene: a814328
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protein F1504.31 [imported] - Arabidopsis thaliana G'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Date: O'Z-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C'Accession: B86477
R'Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein BH2196 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Accession: D83924
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein as14328 [imported] - Nostoc sp. (strain PCC 7120)
Cispecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AI2346
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, SDNA Res. 8, 205-213, 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A,Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05915.1; GSPDB:GN00
A;Experimental source: strain C-125
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Pred. No. 61;
6; Mismatches 3; Indels
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Pred. No. 88;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.1%;
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Best Local Similarity 35.7%;
Matches 5; Conservative
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35 RIYDNMNISSQLVVI 49
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Matches 5; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-35 <STO>
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A;Residues: 1-71 <STO>
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C.Accession: H99910
C.Accession: H99910
R.Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R.; Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
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submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electropheresis of Fusarium sporotrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein SA1186 [imported] - Staphylococcus aureus (strain N315)
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A,Status: preliminary
A,Molecule type: DNA
A,Rosidues: 1-68 «KUR»
A,Cross-references: GB:BA000019, PIDN:BAB76027.1; PID:g17133464, GSPDB:GN00179
A,Experimental source: strain PCC 7120
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:BA000018; PID:g13701149; PIDN:BAB42444.1; GSPDB:GN00149. A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H89910
A;Status: preliminary
A;Molecule type: DNA

    fungus (Fusarium sporotrichioides) (fragment)

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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heat shock protein dnaJ type - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
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                                                                                                                                                                                                                                                                        Length 68;
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40.8%; Score 31; DB 2; I
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: SA1186
C;Superfamily: uncharacterized conserved protein
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A;Residues: 1-15 <CHO>
C;Keywords: heat shock; stress-induced protein
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39.5%;
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Best Local Similarity 25.9%;
Matches 7; Conservative
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Best Local Similarity
7; Conserv?
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Best Local Similarity
Matches 5; Conserv
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A, Molecule type: DNA
A, Residues: 1-59 <STO>
                                                                                                  A, Gene: Cj0742; Cj0747
A,Residues: 1-35 <PAR>
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N,Alternate names: chaperonin homolog (peak 2)

C;Species: Oryctcolagus cuniculus (domestic rabbit)

C;Species: Oryctcolagus cuniculus (domestic rabbit)

C;Date: 21-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998

C;Accession: E49410

R;Rommelaere, H.; Van Troys, M.; Gao, Y.; Melki, R.; Cowan, N.J.; Vandekerckhove, J.; Am Proc. Natl. Acad. Sci. U.S.A. 90, 1195-11979, 1993

A;Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven rela A;Reference number: A49410; MUID:94089752; PMID:7903455

A;Accession: E49410

A;Rolecule type: protein

A;Residues: 1-34 <ROM>
A;Residues: 1-34 <ROM>
A;Residues: 1-34 <ROM>
A;Role: sequence extracted from NCBI backbone

A;Note: sequence extracted from NCBI backbone (NCBIP:141043)

C;Superfamily: molecular chaperone t-complex-type
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C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: Janar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: A81346
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin Nature 4031, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypercension: A81346
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Status: preliminary
                                                                               C'Species: Staphylococcus aureus
C'Species: Staphylococcus aureus
C'Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C'Accession: E89904
R'Accession: E89904
R'Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
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A;Experimental source: strain N315
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A;Accession: B89904
A;Status: prelimiary
A;Molecule type: DNA
A;Residues: 1-29 < KUR>
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                                                    hypothetical protein [imported] - Staphylococcus aureus (strain N315)
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Pred. No. 91;
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Pred. No. 76;
2; Mismatches
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Best Local Similarity 35.7%;
Matches 5; Conservative
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Best Local Similarity 55.6%;
Matches 5; Conservative
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LYDTLNTLL 15
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A;Molecule type: DNA
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Ciprocessions process: Halobacterium ap. NRC-1.

Ciprocession: A84215

Cipate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

Cipate: 03-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Listic Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Cross-references: GB:AL139076; GB:AL11168; NID:96968128; PIDN:CAB73017.1; PID:9696819
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
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A;Experimental source: strain C-125
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Fitle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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A;Cross-references: GB:AE004437; NID:g10580165; PIDN:AAG19085.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein BH1180 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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Pred. No. 1.7e+02;
2; Mismatches 4;
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31.2%; Pred. No. 1.7e+02;
tive 6; Mismatches 5;
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                                                                                                                                                                     Score 30; DB;
Pred. No. 93;
5; Mismatches
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A,Title: Nucleotide sequence and comparative analysis of the frd operon encoding the fum definited ampC cephalosporinase gene.
A,Reference number: S00107; MUID:88004470; PMID:3308458
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glial fibrillary acidic protein - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 148172
F;Duguid, J.R.; Rohwer, R.G.; Seed, B.S. 5738-5742, 1988
A;Title: Isolation of coNas of scrapie-modulated RNAs by subtractive hybridization of A;Reference number: 148171; MUID:88289792; PMID:2456582
A;Accession: 148172
A;Accession: 148172
A;Accession: 148173
A;Accession: 148173
A;Accession: 148173
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A;Accession: 148175
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A;Molecule type: DNA
A;Residues: 1-98 «WAN»
A;Cross-references: EMBL:U92951; NID:g2290417; PID:g2290419; PIDN:AAD04678.1
A;Experimental gource: isolate DJ1
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A;Molecule type: DNA
A;Residues: 1-98 «WA2>
A;Cross-references: EMBL:U92957; NID:g2290441; PID:g2290443; PIDN:AAD08825.1
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C;Species: Proteus vulgaris
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 14-Apr-2003
C;Accession: 800119
Ex;Cole, S.T.
Bur. J. Biochem. 167, 481-488, 1987
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A;Residues: 1-96 <COL>
A;Cross-references: EMBL:X06151; NID:g45907; PIDN:CAA29511.1; PID:g45910
C;Superfamily: [NiFe]-hydrogenase maturation chaperone
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Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 2;
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Best Local Similarity
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NyAlternate names: MC047L
NyAlternate names: MC047L
Sipeciaes: Molluscum contagiosum virus 1
C;Speciaes: Molluscum contagiosum virus 05-Nov-1999 #text_change 11-May-2000
C;Accession: T30649
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re A;Reference number: Z20876; MUID: 96325459; PMID: 8670425
A;Accession: T30649
A;Accession: T30649
A;Accession: T30649
A;Accession: T30649
A;Cross-references: EMBL:UG0315; PIDN:AAC55175.1
C;Genetics:
A;Note: MC047L
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Pred. No. 2.1e+02;
0; Mismatches 3; Indels
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13 ALTVLMLLMVVS 24
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A; Gene: XF1305 Query Match

Matches

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hypothetical protein SSO1296 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Dates: 24-May-2001 #sequence_revision 24-May-2001 #sequence_revision 24-May-2001 #s. Acceptage 24-May-2001 
                                                                                                                                                                                                                                              NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L [similarity] - Pygathrix bieti mi C;Species: mitochondrion Pygathrix bieti C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 03-Jun-2002 C;Accession: T17162 C;Accession: T17162 The May W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.O.; Hu, H.G.; Xi Int. J. Primatol. 18, 305-320, 1997 A;Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences. A,Reference number: Z18709
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A;Residues: 1-99 <KUR>
A;Cross-references: GB:AE006641; NID:g13814497; PIDN:AAK41533.1; GSPDB:GN00155
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A;Reference number: Z21928
A;Recession: T40639
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.5%; Score 30; DB 2; Length 98; 55.6%; Pred. No. 2.9e+02; ative 3; Mismatches 1; Indels
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Pred, No. 2.9e+02;
6; Mismatches 1;
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36.4%;
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Best Local Similarity 36.43,
Best Local 4; Conservative
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6 LNVLMAMNI 14
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Best Local Similarity
Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-98 <WAN>
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A;Status: preliminary
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - Pygathrix roxellana mitochondris (Species 194 Mar-2000 #text_change 03-Jun-2002 (Species 04 Mar-2000 #text_change 03-Jun-2002 (Species 04 Mar-2000 #text_change 03-Jun-2002 (Species 04 Mar-17174; T17180 (Species 17178) (Species 171780 (
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A;Molecule type: DNA
A;Residues: 1-98 <WA3>
A;Residues: 1-98 <WA3>
A;Cross-references: BMBL:U92958; NID:g2290445; PID:g2290447; PIDN:AAD08828.1
A;Experimental source: isolate DJ5
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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39.5%; Score 30; DB 2; Length 98;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                           Query Match 39.5%; Score 30; DB 2; Length 98; Best Local Similarity 55.6%; Pred. No. 2.9e+02; Matches 5; Conservative 3; Mismatches 1; Indels
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43 MNTLMALNM 51
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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Accession: F89891
C;Accession: F89891
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Marutanl-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription regulator asnC - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Spacession: C69425
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.; Fleistchmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Tile: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo A;Reference number: A69250; MUID:98049343; PMID:9389475
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C;Superfamily: Archaeoglobus fulgidus transcription regulator asnC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-70 <KUR>
A,Cooss-references: GB:BA000018; PID:g13700994; PIDN:BAB42290.1; GSPDB:GN00149
A,Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
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                                                                                                                                                                                             truncated transposase [imported] - Staphylococcus aureus (strain N315)
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Best Local Similarity 66.7
Matches 6; Conservative
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22 VLMALNI 28
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C;Species: Zea mays (maize)
C;Species: Zea.1999 #sequence_revision 24-Mar-1999 #text_change 22-Jun-1999
C;Accession: T03658
R;Yanagisawa, S.; Izui, K.; Yamaguchi, Y.; Shigesada, K.; Katsuki, H.
FEBS Lett. 229, 107-110, 1988
A;Title: Purther analysis of cDNA clones for maize phosphoenolpyruvate carboxylase involong A; Reference number: S00348; MUID:88152202; PMID:2894322
A;Reference number: S00348; MUID:88152202; PMID:2894322
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary;
A;Molecule type: mRNA
A;Retus: preliminary;
A;Molecule type: mRNA
A;Retus: preliminary
A;Cross-references: EMBL:X07171; NID:922414; PIDN:CAA30159.1; PID:g929919
C;Function: catalyzes the irreversible beta-carboxylation of phosphoenolpyruvate carboxylase
C;Superfamily: phosphoenolpyruvate carboxylase
C;Superfamily: phosphoenolpyruvate carboxylase
C;Keywords: carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; phosphoprotein
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A;Coss-references: EMBL:AL049474; PIDN:CAB39365.1; GSPDB:GN00067; SPDB:SPBC685.08
A;Experimental source: strain 972h-; cosmid c685
C;Genetics:
A;Gene: SPDB:SPBC685.08
A;Map position: 2
A;Hartron: 2
A;Introns: 1/3
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38.2%; Score 29; DB 2; Length 56;
Best Local Similarity 53.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                       2; Indels
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Pred. No. 3.5e+02;
4; Mismatches 2;
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 23 VYDAVKLLKSALNL 36
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RESULT 29

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hypothetical protein Vng1357c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Jate: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84290
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. P; Mahairas, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Auchors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: E84290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein RC0940 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Accession: D97817
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Arnason, U.; Gullberg, A.; Janke, A.
Mol. Biol. Bvol. 14, 762-768, 1997
A;Title: Phylogenetic analysis of mitochondrial DNA suggest a sister group relationship
A;Reference number: Z17272; MUID:97357423; PMID:9214749
A;Accession: T11449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: GB:AE006914; PIDN:AAL03478.1; PID:g15620050; GSPDB:GN00173
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: AE004437; NID: 910580869; PIDN: AAG19689.1; GSPDB: GN00138
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Pred. No. 3.8e+02;
6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB 2; 1
Pred. No. 3.6e+02;
0; Mismatches 6;
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A;Molecule type: DNA
A;Residues: 1-98 <ARN>
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53.8%;
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34 SLNIVGTLNLVS 45
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-85 <KUR>
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C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: E86742
A;Fitle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Reference number: B86742
A;Resubs: Preliminary
A;Residues: 1-82 <STO>
A;Gross-references: GB:AE005176; PID:g12723877; PIDN:AAK05039.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: secG
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C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Accession: F97704
R;Ggata, H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, D.; F. Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: F97704
A;Accession: F97704
A;Residues: preliminary
A;Residues: 1-79 «KUR»
A;Residues: 1-79 «KUR»
A;Accession: F9704
A;Gross-references: GB:AE006914; PIDN:AAL02576.1; PID:g15619073; GSPDB:GN00173
C;Genetics:
A;Gene: RC0038
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A;Accession: T21426
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-78 < WIL.>
A;Cross-references: EMBL:Z81514; PIDN:CAB04190.1; GSPDB:GN00023; CESP:F26F2.4
A;Experimental source: clone F26F2
C;Genetics:
A;Gene: CESP:F26F2.4
A;Map position: 5
A;Introns: 25/3
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Pred. No. 3.4e+02;
4; Mismatches 4; Indels
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Pred. No. 3.5e+02;
1; Mismatches 4;
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Local Similarity 58.3%;
hes 7; Conservative
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19 RQHDFMKLMMEMN 31
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Best Local Similarity
Matches 5; Conserv
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Matches
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C;Accession: S53994

R;Wang, Y.; Rawlings, M.; Gibson, D.T.; Labbe, D.; Bergeron, H.; Brousseau, R.; Lau, P.C
R;Wang, Y.; Rawlings, M.; Gibson, D.T.; Labbe, D.; Bergeron, H.; Brousseau, R.; Lau, P.C
A;Title: Identification of a membrane protein and a truncated LysR-type regulator associ
A;Reference number: S53993; MUID:95214617; PMID:7535376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:U18304; NID:9747633; PIDN:AAC43317.1; PID:9747635
A;Note: the authors translated the codon GAG for residue 71 as Asp and CGC for residue 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: Repeated sequence sets in mitochondrial DNA molecules of root knot nematodes (M
A,Reference number: S15649; MUID:91227158; PMID:2027769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - root-knot nematode (Meloidogyne C;Species: mitochondrion Meloidogyne javanica C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-100 <SEE>
A;Cross-references: EMBL:AL122032; PIDN:CAB58727.1; GSPDB:GN00066; SPDB:SPAC513.04
A;Experimental source: strain 972h-; cosmid c513
                                                                                                                                                                                                    C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C;Accession: T38899
R;Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
aubmitted to the EMBL Data Library, October 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Pseudomonas putida
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
                                                                                                                                                                               hypothetical protein SPAC513.04 - fission yeast (Schizosaccharomyces pombe)
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A,MoLecule type: DNA
A,Residues: 1-30 cOKI>
A,Cross-references: EMBL:X57625; NID:g13102; PID:e1192325; PID:g2654262
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Nucleic Acids Res. 19, 1619-1626, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 100;
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Pred. No. 4.5e+02;
5; Mismatches 3; Indels
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50.0%; Pred. No. 4.5e+02;
tive 4; Mismatches 1; Indels
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A;Molecule type: DNA
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Best Local Similarity 33.3%;
Matches 4; Conservative
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Best Local Similarity 50.v.
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59 VLMALNI 65
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A;Molecule type: DNA
A;Residues: 1-100 <WAN>
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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F89915
R;Kuroda, M; Ohta, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L; Oguc
M; A: Mizutani-Ui, Y; Kobayashi, N; Sawano, T; Inoue, R; Kaito, C; Sekimizu, K;
C; Shiba, T; Hattcri, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Itle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F99915
A;Accession: F99915
A;Accession: Preliminary
A;Molecule type: DNA
A;Residues: 1-98 «KUR»
A;Residues: 1-98 «KUR»
A;Residues: 1-98 «KUR»
A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Accession: JC5794
R; Aso, T.; Conrad, M.N.
Biochem. Biochem. Biophys. Res. Commun. 241, 334-340, 1997
A; Title: Molecular cloning of DNAs encoding the regulatory subunits of elongin from Sacc A; Reference number: JC5792; MUID:98086352; PMID:9425272
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K.;
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C;Comment: This protein binds to each other in the absence of elongin A to form a binary
or induction of elongin A activity.
                                                                                       A;Genetic code: SGC1
A;Note: NADM4L
C;Superfamily: NADM dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A; Cross-references: EMBL:Y11832; NID:g2252500; PIDN:CAA72524.1; PID:g2255509
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C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                   Score 29; DB 2; Length 98; Pred. No. 4.4e+02;
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Pred. No. 4.4e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elongin C - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: PlyBase:FBgn0023211
C;Superfamily: elongin C
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85.7%;
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Similarity 55.6%;
5; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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86 ALELLMAANFL 96
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6 LNIIMAFSI 14
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Best Local Similarity
Matches 5; Conserv
                                                            A; Genome: mitochondrion
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A; Residues: 1-98 <ASO>
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB2812
A;Accession: AB2812
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 -KUR>
A;Cross-references: GB.AB008688; PIDN:AAL42912.1; PID:g17740367; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
36.8%; Score 28; DB 2; Length 63;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels
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20 AINISIFLNII 30
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C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: 069915
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
X; S.; Church, G.M.; Danielle, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: G69115
A;Accession: G69115
A;Accession: G69115
A;Accession: G69115
A;Accession: G69116
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-60 eMTH>
A;Residues: 1-60 eMTH>
A;Cross-references: GB:AE000806; GB:AE000666; NID:g2621222; PIDN:AAB84692.1; PID:g262123
A;Genetics:
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Pred. No. 3.9e+02;
4; Mismatches 2; Indels
                                                                                                                                                                            36.8%; Score 28; DB 2; Length 30; ilarity 41.7%; Pred. No. 1.8e+02; Conservative 3; Mismatches 4; Indels
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Pred. No. 2.9e+02;
2; Mismatches 5; Indels
        C,Genetics:
A,Gene: ND4
A,Geneme: mitochondrion
Code: SGC4
C,Keywords: mitochondrion; NAD; oxidoreductase
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ilarity 45.5%;
Conservative
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Best Local Similarity 46.2%;
Matches 6; Conservative
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5 YKKVNSMYYMNL 16
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBGOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 YDALNVLMAMNIISKEKKEIKWIGLPTNSA 30
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 100
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match Length DB	30	37	74	20	15	19	19	16	19	19	74	74	85	85	82
de	Query	Match	100.0	100.0	82.9	66.4	52.6	47.4	44.7	44.1	42.1	39.5	37.2	36.5	36.5	36.5	36.5
		Score	152	152	126	101	80	72	68	67	64	9	56.5	55.5	55.5	55.5	55.5
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Sequence 11, Appli Sequence 7, Appli Sequence 1380, Ap Sequence 1380, Ap Sequence 9, Appli Sequence 6, Appli Sequence 29071, A Sequence 2071, A Sequence 8, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 1370, Ap Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 16, Appli	Sequence 19, Appl Sequence 190, Appl Sequence 1920, Ap Sequence 43984, A Sequence 1259, Ap
10 US-09-900-147-11 15 US-10-214-188-7 12 US-10-242-515-1380 15 US-10-242-515-1380 15 US-10-242-515-1380 16 US-10-242-81-6 17 US-10-242-88-9 18 US-10-165-614-3 19 US-09-864-761-45697 19 US-09-864-761-45697 19 US-09-864-761-35559 10 US-09-864-761-35559 11 US-09-80-773-16	12 US-10-407-920-17 12 US-10-407-920-19 9 US-09-867-550-1920 9 US-09-864-761-43984 12 US-10-351-641-1259
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RESULT 2 US-09-900-147-1 Sequence 1, Application US/09900147 ; Patent No. US20020103121A1

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                                                GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INTENTION: Peptide antagonists of DP transcription factors
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPRENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: EARLIER PELLING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: GB 9626589.7
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTING VET. 2.1
SEQ ID NO 1

TENNEL OF THE OFFICE O
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC computeR: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IB
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BERNARDS, RENE
HIJANANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSE:
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 152; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.8e-16;
Matches 30; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: US/08/894,139
ATTORNEY AGENT THORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
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SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
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ORGANISM: Artificial Sequence
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Sequence 10, Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: La Thangue, Nicholas B

TITLE OF INVENTION:

PETER REPERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT PILING DATE: 2001-07-09

PRIOR PELING DATE: EARLIER APPLICATION NUMBER: 09/308,935

PRIOR PILING DATE: EARLIER PILING DATE: 1999-05-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7

PRIOR PILING DATE: EARLIER PILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTING DATE: 2.1

TENGTON 10 10
                                                                                                                                                                                                                                                  US-09-00-147-4

US-09-00-147-4

Sequence 4, Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITIS OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7

PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTING DATE: 1096-12-20

LENGTH: 20
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                                                        Gaps
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FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-900-147-4
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                                                           0; Indels
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66.4%; Score 101; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 20; Conservative 0; Mismatches 0;
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Pred. No. 2.7e-05;
     Score 126; DB 15;
Pred. No. 1.8e-11;
Query Match 82.9%; Score 126; Di
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 25; Conservative 0; Mismatches
                                                                                                                                               50 YDALNVLMAMNIISKEKKEIKWIGL 74
                                                                                                                1 YDALNVLMAMNIISKEKKEIKWIGL 25
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100.0%;
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Sequence 5, Application US/09900147 Patent No. US20020103121A1
                                                                                                              GENERAL INFORMATION
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                                                          JS-09-900-147-5
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Patent No. US2002010121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REPERBENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT PILING DATE: 2001-07-09

PRIOR FILING DATE: BARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: BARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: BARLIER FILING DATE: 1999-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PALENTING VATE: 1996-12-20

SOFTWARE: PALENTING VATE: 2.1

SEQ ID NO 15

LENGTH: 19
                                                                                                                                                                    Sequence 3, Application US/09900147

Sequence 3, Application US/09900147

Patent No. US20020103121A1

GENERAL INPORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: EARLIER FLING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FLING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOSTWARE: PATENTIN VET. 2.1
Gaps
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US-09-900-147-3
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Pred. No. 0.00056;
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0; Indels
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Pred. No. 0.0022;
0; Mismatches 1;
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Mismatches
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ORGANISM: Artificial Sequence
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                                       16 EKKEIKWIGLPTNSA 30
                                                                          1 EKKEIKWIGLPTNSA 15
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
  15; Conservative
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LENGTH: 19
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Matches
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APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09
PRIOR PELICATION NUMBER: RARLIER APPLICATION NUMBER: 09/308,935
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 16
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TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPRENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT PILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1996-05-27
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN OF: 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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Pred. No. 0.009;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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US-09-900-147-17
; Sequence 17, Application US/09900147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/09900147
Patent No. US20020103121A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Thangue, Nicholas B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity 100.0%;
14; Conservative 0
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDALNVLMAMNIIS 16
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Best Local Similarity 93.39
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 14; Conserv
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Length 74;
                                                                                         Length 74;
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COMPUTER: IN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30
CURSUT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION: «Unknown>
PRIOR APPLICATION LATA:
APPLICATION NUMBER: US/08/894,139
FILING DATA:
APPLICATION NUMBER: 13-Aug-1997
ATTORNEY/AGRY INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELEBPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indela
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               BERNARDS, RENE
HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR B2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.5%; Score 55.5; DB 15; Best Local Similarity 44.0%; Pred. No. 0.77; Matches 11; Conservative 6; Mismatches 7;
                                                                                      37.2%; Score 56.5; DB 15;
44.0%; Pred. No. 0.55;
tive 6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10214188
Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YDALNVLMAMNIISKE-KKEIKWIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YDALNVLMAMNIISKEKK-EIKWIG 24
                                                                                                                                                                                                                  CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 5, Application US/09932581; Publication No. US20030050264A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                              37.2%
Query Match
Best Local Similarity 44.0%
Matches 11; Conservative
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US-10-214-188-5
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                                               US-10-214-188-6
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US-09-900-147-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                       APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION Peptide antagonists of DP transcription factors
FILE REPERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
PRIOR PILING DATE: EARLIER FILING DATE: 1996-05-27
PRIOR PILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.1
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ZIP: 22201-4714

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/214,188

FILING DATE: 08-Aug-2002

CLASSIFICATION NUMBER: US/08/894,139

FILING DATE: 13-Aug-1997

ATTORNEY AREDITATION NUMBER: US/08/894,139

FILING DATE: 13-Aug-1997

ATTORNEY MAREN INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: $20-22

TELECOMMINICATION INFORMATION:

TELECOMMINICATION NUMBER: $20-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60; DB 10; Length 19;
Pred. No. 0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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Publication No. US20030022260A1
GENERAL IRFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
BERNARDS, RENE
HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 74 amino acids
                                  GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.5%;
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YDALNVLMAMNIISK 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON
         US20020103121A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-214-188-6
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LENGTH: 19
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JS-09-900-147-11
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Publication No. US20030171326A1

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

APPLICANT: Fraser, Christopher A.

APPLICANT: Fraser, Stephanie

APPLICANT: Praser, Stephanie

APPLICANT: Praser, Stephanie

APPLICANT: MCHAMMARANICH: Hamid

TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR MODULATING

TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION

FILE REFERENCE: SIER-005

CURRENT APPLICATION NUMBER: US/10/338,294

CURRENT APPLICATION NUMBER: US/09/932,581

PRIOR PAPLICATION NUMBER: 60/227,865

PRIOR PELING DATE: 2000-09-01

PRIOR PELING DATE: 2000-09-01

PRIOR PELING DATE: 2000-09-01

PRIOR PELING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 25

SOGTWARRE: FASESEQ for Windows Version 4.0
APPLICANT: Andrews, William H.
APPLICANT: Foster, Christopher A.
APPLICANT: Fraser, Stephaniae
APPLICANT: Praser, Stephaniae
APPLICANT: Mohammadpour, Hamid
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER-005
CURRENT APPLICATION NUMBER: 06/237,865
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR PILING DATE: 2000-09-01
PRIOR PLING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/238,345
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PRESEQ for Windows Version 4.0
SSOFTWARE: PRESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.5%; Score 55.5; DB 11; 44.0%; Pred. No. 0.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YDALNVLMAMNIISKE-KKEIKWIG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 44.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: human
US-10-338-294-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-932-581-5
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RESULT 15 US-10-165-614-2

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Fatent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 2001-07-09

FRICK PRENT PLING DATE: 2001-07-09

FRICK APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935

FRICK APPLICATION NUMBER: EARLIER PILING DATE: 1999-05-27

FRICK APPLICATION NUMBER: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 11

SEQ ID NO 11

LENGTH: 14
Sequence 2, Application US/10165614
Publication No. US20020193289A1
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER-018
CURRENT APPLICATION NUMBER: US/10/165,614
CURRENT FILING DATE: 2002-06-25
PRIOR PELLON NUMBER: 60/296,992
PRIOR FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.2%; Score 55; DB 10; Length 14;
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HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Prec. ...
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; Publication No. US20030022260A1
; GENEAL INCRMATION:
; APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YDALNVLMAMNIISKE-KKEIKWIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.v
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US-10-165-614-2
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Sequence 1380, Application US/10242515
Publication No. US20040009488A1
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APPLICANT: Rosen et al.
TITLE OF INVENTION NUCLEIC Acids, Proteins, and Antibodies
FILE REPERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Parentin Ver. 2.0
SEQ ID NO 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
35.2%; Score 53.5; DB 15; Length 74;
Best Local Similarity 40.0%; Pred. No. 1.5;
Matches 10; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 29;
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                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT TROFMARTION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 620-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 34.2%; Score 52; Best Local Similarity 62.5%; Pred. No. Matches 10; Conservative 2; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YDALNVLMAMNIISKE-KKEIKWIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 YDITNVLEGIHLIKKKSKNHVQWMG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1380, Application US/09764877 Patent No. US20020147140A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: (703) 816-400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 MNIISKEKKEIKWIGL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                      COUNTRY: U.S.A. ZIP: 22201-4714
                                         CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
US-09-764-877-1380
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RESULT 19

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BERNARDS, RENE
HIJMANS, ELERANORE M.
HIJMANS, ELERANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 12;
Pred. No. 0.93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/10214188
Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                         34.2%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               | | |||||:| | |:
13 MKIFSKEKKKIGWPGM 28
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                          CRGANISM: Homo sapiens US-10-242-515-1380
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11; Conservative
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ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 24
US-10-029-386-29071
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; Sequence 6, Application VG2003005264A1
; Publication No. US2003005264A1
; GENERAL INFORMATION:
APPLICANT: Forter, William H.
APPLICANT: Foster, Christopher A.
APPLICANT: Poster, Christopher A.
APPLICANT: Fraser, Stephanie
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT)
FILE REFERENCE: SIER-005
CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR PLING DATE: 2000-09-01
; PRIOR PLING DATE: 2000-09-01
; PRIOR PRILNG DATE: 2000-09-01
; PRIOR PILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    33.9%; Score 51.5; DB 15;
42.3%; Pred. No. 3.1;
tive 6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/694,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 620-22
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-10-214-188-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YDALNVLMAMNIISKE-KKEIKWIGL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDITNVLEGIDLIEKKSKNSIQWKGV 75
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Publication No. US20030171326A1
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Foster, Christopher A.
                                                                                                                                                                                                                                               LENGTH: 75 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 42.3 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 22
US-10-338-294-6
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US-09-932-581-6
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Sequence 29071, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
APPLICANT: Fraser, Stephanie
APPLICANT: Mohammadpour, Hamid
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELLORSE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER-005
CURRENT APPLICATION NUMBER: US/09/932,581
PRIOR PLLING DATE: 2001-01-07
PRIOR PLLING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR PLLING DATE: 2000-09-01
SPRIOR PLLING DATE: 2000-09-01
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Sequence 3, Application US/10165614

Publication No. US20020193289A1

Sequence 3, Application No. US20020193289A1

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING

TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION

TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT)

FILE REPERENCE: SIER-018

CURRENT FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASELSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.2%; Score 50.5; DB 14; Best Local Similarity 42.3%; Pred. No. 4.5; Matches 11; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.2%; Score 50.5; DB 12;
42.3%; Pred. No. 4.5;
tive 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 YDITNVLEGIGLIEKKSKNSIQWKGV 74.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YDALNVLMAMNIISKE-KKEIKWIGL 25
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.90
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.92
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.88
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.70
OTHER INFORMATION: STATHWAN HIT: BE880658.1, EVALUE 2.00e-51
OTHER INFORMATION: SWISSPROT HIT: Q61501, EVALUE 5.00e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.6%; Score 46.5; DB 9; Length 96; 36.0%; Pred. No. 23; tive 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 45697
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 08-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YDALNVLMAMNIISK-EKKEIKWIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 YDIVNVLESLHLVSRVAKNQYGWHG 31
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REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 62
                                                                                                                                                                                                                                                                                                                                                                                                          MAP TO AC021804.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8:
     FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 36.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-864-761-45697
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APPLICANT: Penn, Sharron G.
APPLICANT: Hand, David K.
APLICANT: Grave Hundan GENGME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENGME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENGME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMBER: US 60/180,312
PRIOR PELLON NUMBER: US 60/180,312
PRIOR PELLON NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELLON NUMBER: US 60/207,466
PRIOR PELLON NUMBER: US 60/207,466
PRIOR PELLON NUMBER: US 60/207,466
PRIOR PELLON NUMBER: PC/301/0666
PRIOR APPLICATION NUMBER: PC/301/0666
PRIOR APPLICATION NUMBER: PC/101/0666
PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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OTHER INFORMATION: MAP TO CHR20.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN HONE MARROW, SIGNAL = 4.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.4

OTHER INFORMATION: SWISSPROT HIT: QO1094, EVALUE I.00e-36

US-10-029-386-29071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.6%; Score 49.5; DB 12; Length 76; 41.7%; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YDALNVLMAMNIISKE-KKEIKWI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 YDITNVLEGIQLIAKKSKNHIQWL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 41.7
nes 10; Conservative
                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-864-761-45697
                                                                                                              SEQ ID NO 29071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                            LENGTH:
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Matches
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FILING DATE: 1997-12-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-097-065-532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-263-811-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
ITILE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT FILING DATE: 2001-07-09
FRIOR FILING DATE: BARLIER FILING DATE: 1999-02-27
FRIOR FILING DATE: BARLIER FILING DATE: 1999-02-27
FRIOR FILING DATE: BARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-900-147-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                     DB 15; Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.6%; Score 42; DB 10; Length 9; 100.0%; Pred. No. 7e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                    Indels
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Publication No. US20030055236A1

GENERAL INFORMATION:

TITLE OF INVENTION: 110 Human Secreted Proteins
FILE REFERENCE: PZ021P1

CURRENT APPLICATION NUMBER: US/10/097,065

CURRENT FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: PCT/US98/27059

PRIOR APPLICATION NUMBER: 60/070,923

PRIOR PILING DATE: 1998-12-17

PRIOR PILING DATE: 1997-12-18

PRIOR PILING DATE: 1997-12-19
                                                                                                                                                                               / Match 29.9%; Score 45.5; I Local Similarity 38.5%; Pred. No. 23; Pred. 10; Conservative 5; Mismatches
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                    1 YDALNVLMAMNIISKE-KKEIKWIGL 25
                                                                                                                                                                                                                                                                                                                       44 YDITNVLEGIGLIEKKSKNSTQWRGV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/09900147; Patent No. US20020103121A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 9; Conservative
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US-09-900-147-2
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US-10-214-188-8
                                                                                                                                                                                     Query Match
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Matches
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PRICE PLING DATE: 1997-12-19

PRICE
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US-09-864-761-35555
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                                                                                        Length 61;
                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                          Sequence 9, Application US/10259520;
Publication No. US20030027989A1
GENERAL INFORMATION:
TITULE OF INVERTION: He al.
TITULE OF INVERTION: Mammary Transforming Protein
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: 9410 KEY WEST AVENUE
CITY. ROCKVILLE
                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

APPLICATION DATE: 30-Sep-2002
CLASSIFICATION: -(Unknown)
PRIOR APPLICATION AUTHER:
APPLICATION NUMBER: US/09/263,811
FILING DATE: MAR-08-1999
APPLICATION NUMBER: 08/743,975
FILING DATE: 01-NOV-1996
APPLICATION NUMBER: 60/06,187
FILING DATE: 01 NOVEMBER 1995
ATTORNEY/AGENT INFORMATION:
NAME: MICHELE M. WALES
REGISTRATION NUMBER: 43,975
REFERENCE/DOCKET NUMBER: 975
TELEPHONE: 301-309-8634
TELEPHONE: 301-309-8639
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 AMINO ACIDS
                                                                                                         Pred. No. 68;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER: 1BM PS/2 OPERATING SYSTEM: MS-DOS SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: LINBAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-259-520-9
                                                                                          Score 42;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 VVFSINLLSRPERE--WEGMP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 VLMAMNIISKEKKEIKWIGLP 26
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                                                                                                                                                                                            14 VVFSINLLSRPERE--WEGMP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
STRANDEDNESS: <Unknown>
                                                                                            Query Match 27.6%;
Best Local Similarity 33.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MARYLAND
COUNTRY: USA
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-263-811-9
                                                                                                                                                                                                                                                                  RESULT 30
US-10-259-520-9
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RESULT 31 US-10-083-357-694

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APPLICANT: Penn, Sharron G.
APPLICANT: Fann, Sharron G.
APPLICANT: Fann, Sharron G.
APPLICANT: Fann, Sharron G.
APPLICANT: Fann, Sharron G.
APPLICANT: Hanzel, David R.
FILE OF INVERTION: HUMAN GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE OF INVERTION: 2001-02-04
CURRENT PILLYO DAVIE: 2001-02-04
PRIOR APPLICATION WIMBER: US 60/180,312
PRIOR APPLICATION WIMBER: US 60/207,456
PRIOR PAPLICATION WIMBER: US 60/207,456
PRIOR APPLICATION WIMBER: US 60/206,359
PRIOR APPLICATION WIMBER: US 60/206,359
PRIOR PLILING DATE: 2000-09-07
PRIOR PLILING DATE: 2000-09-07
PRIOR PLILING DATE: 2000-09-07
PRIOR PLILING DATE: 2001-01-07
PRIOR PRIOR PLILING DATE: 2001-01-07
PRIOR PLILING DATE: 2001-01-07
PRIOR PLILING DATE: 2001-01-07
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; Sequence 694, Application US/10083357; Publication No. US20030054370A1; GENERAL INFORMATION:
; APPLICANT: Qiandong Zeng et al.; TITLE OF INFUNION: Systemic Discovery of New Genes; FILE REFERENCE: 032796-090; CURRENT APPLICATION NUMBER: US/10/083,357; CURRENT FILING DATE: 2002-02-27; NUMBER OF SEQ ID NOS: 1346; SEQ ID NO 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35555, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LMAMNIISKE----KKEIKWIGL 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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Publication V0S0040009474A1

Publication No. US20040009474A1

Publication No. US20040009474A1

APPLICANT: Leach, Martin D.

APPLICANT: Shimkets, Richard A.

TITLE NOE FURNETION: NO. US20040009474A1e1 Human Polynucleotides and Polypeptides Encorrent Reference: 21402-012

CURRENT APPLICATION NUMBER: US/09/864,408A

CURRENT APPLICATION NUMBER: 60/206,690

PRIOR APPLICATION NUMBER: 60/206,690

PRIOR FILING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 9068

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 63

LENGTH: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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; OTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid
US-09-864-408A-3370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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NN. EXPRESSED IN HELA, SIGNAL = 25

NN. EXPRESSED IN HELA, SIGNAL = 25

NN. EXPRESSED IN ADULT LIVER, SIGNAL = 29

NN. EXPRESSED IN PLACENTA, SIGNAL = 29

NN. EXPRESSED IN PLACENTA, SIGNAL = 34

NN. EXPRESSED IN HEALTO, SIGNAL = 33

NN. EXPRESSED IN LIVEN, SIGNAL = 33

NN. EXPRESSED IN LIVEN, SIGNAL = 26

NN. EXPRESSED IN LIVER, SIGNAL = 33

NN. EXPRESSED IN LIVER, SIGNAL = 26

NN. EXPRESSED IN FETAL LIVER, SIGNAL = 26

NN. EXPRESSED IN LIVER, SIGNAL = 30

NN. EXPRESSED IN LIVER, SIGNAL = 36

NN. EXPRESSED IN LIVER = 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 9; Length 57; Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                        PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2001-01-29

NUMBER: OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 34417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                APPLICATION NUMBER: PCT/US01/00670
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CITER INFORMATION: EXPRESSED IN
CITER INFORMATION: EXPRESSED IN
CITER INFORMATION: EST HUMAN HIT
COTHER INFORMATION: SWIESPROT HIT
US-09-864-761-34417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.0%;
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                2001-01-30
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5 KKKIKNMKLPSNSA 18
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Best Local Similarity 64.37
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48 VQKESKENQWLGV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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Best Local Similarity
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OTHER INFORMATION:
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OTHER INFORMATION:
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US-09-864-408A-3370
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Sequence 3417, Application US/09664761

SERERAL INFORMATION:
APPLICAMT: Rank, David R.
APPLICAMT: Rank, David R.
APPLICAMT: Rank, David R.
APPLICAMT: Rank David R.
APPLICAMT: Gran, Weashang
ITILE OF INVENTION: HUMAN GRNOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: GREE EXPRESSION ANALYSIS BY MICROARRAY
ITILE OF INVENTION: GREE EXPRESSION ANALYSIS BY MICROARRAY
ITILE OF INVENTION: HUMBER: US 60/180,312
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-06-05-6
PRIOR FILING DATE: 2000-06-06-6
PRIOR PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PRIOR DATE: 2000-09-06
PRIOR PRIOR DATE: 2001-01-30
PRIOR PRIING DATE: 2001-01-30
PRIOR PRILIKG DATE: 2001-01-30
PRIOR PRILIKG DATE: 2001-01-30
PRIOR PRILIKG DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN PEACENTA, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN HEATO, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HEATO, SIGNAL = 2.4
OTHER INFORMATION: SYPESSED IN HEATO, SIGNAL = 2.4
OTHER INFORMATION: SYPESSED IN HEATO, SIGNAL = 2.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35555
LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
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                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO AL1099
OTHER INFORMATION: EXPRESSED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 40.vv
                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 33
US-09-864-761-34417
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Score 40; DB 10; Length 100;
Pred. No. 2.3e+02;
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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                   MEDIUM ITE:
COMBUTER: IBM Compatible
COMBUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/820,408
FILING DATE: 29-Mar-2001
CLASSIFICATION NUMBER: 09/024,024
APPLICATION NUMBER: 09/024,024
FILING:DATE: 1998-02-16
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
RECISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GMS0019
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
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ZET: 1910-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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APPLICATION NUMBER: US/09/820,473
FILING DATE: 29-Mar-2001
CLASSFIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear SEQ ID NO: 4: US-09-820-408-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09820473
Patent No. US20020173457A1
GENERAL INFORMATION:
APPLICANT: LONETC, Michael A.
TITLE OF INVENTION: 11cD1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
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67 INIFOKEKSKYKLLSLETD 85
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                                                                                                      ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: «UNKNOWN»
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.3%;
Best Local Similarity 42.1%;
Matches 8; Conservative
                                 Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: PA
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                                                                       Sequence 14, Application US/10205072
Publication No. US20030028921A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DUVICK, Jonathan P.
APPLICANT: DUVICK, Jonathan P.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Simmons, Carl R.
TITLE OF INVERSION: Maize Basal Layer Antimicrobial Protein Polynucleotides and Methor CIRRENT APPLICATION NUMBER: US/10/205,072
CURRENT PILING DATE: 2002-07-24
FRIOR FILING DATE: 2001-07-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Duvick, Jonathan P.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Davarro Acevedo, Pedro A.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Maize Basal Layer Antimicrobial Protein Polynucleotides and Methor FILE REFERENCE: 1406
CURRENT APPLICATION NUMBER: US/10/205,072
CURRENT FILING DATE: 2002-07-24
PRIOR FILING DATE: 2001-07-26
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26.6%; Score 40.5; DB 15; Length 93;
Best Local Similarity 44.4%; Pred. No. 1.8e+02;
Matches 12; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 26.6%; Score 40.5; I Local Similarity 44.4%; Pred. No. 1.8e nes 12; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 30
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 VLLASCVIHAHIISGETEEVSNIGSPT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VLMA-----MNIISKEKKEIKWIGLPT 27
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TITLE OF INVENTION: licD1
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/10205072
Publication No. US20030028921A1
GENERAL INFORMATION:
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Patent No. US20020102701A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
; ORGANISM: Zea mays
US-10-205-072-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT CORGANISM: Zea mays US-10-205-072-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -10-205-072-16
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Best Local S:
Matches 12
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APPLICANT: Shi, Lifang
TITLE OF INVENTION: MYB Transcription Factors and Uses for Crop Improvement
FILE REFERENCE: 38-21(52703)A
FULE REPERENCE: 38-21(52703)A
CURRENT APPLICATION NUMBER: US/60/370,759
PRIOR APPLICATION NUMBER: US/60/370,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Julius, David J.

APPLICANT: Caterina, Michael J.

APPLICANT: Caterina, Michael J.

APPLICANT: Caterina, Michael J.

APPLICANT: Caterina, Michael J.

APPLICANT: Brake, Anthony J.

TITLE OF INVENTION: Nucleic acid sequences encoding

TITLE OF INVENTION: polypeptides and uses thereof

CURRENT APLICATION NUMBER: US/09/978,303

CURRENT FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-01-22

PRIOR APPLICATION NUMBER: 60/072,151

PRIOR FILING DATE: 1998-01-22

PRIOR APPLICATION NUMBER: 08/915,461

PRIOR FILING DATE: 1997-08-20

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 75;
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Best Local Similarity 18.8%; Pred. No. 2.4e+02;
Matches 6; Conservative 10; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.7%; Score 39; DB 11;
Best Local Similarity 18.8%; Pred. No. 2.4e+02;
Matches 6; Conservative 10; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|::::| | ::::| 35 YSVINIIVLLNMLIAMMSNSYQIISERADVEW 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :|::::| | |::::| | 35 YSVINIIVLLIMMLIAMMSNSYQIISERADVEW 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ISKEKKEIKW 22
CURRENT APPLICATION NUMBER: US/09/978,303
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/235,451
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER: OF SEQ ID NOS: 48
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09978303 Publication No. US20030049728A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 19, Application US/10407920; Publication No. US20040006797A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YDALNVLMAMNI -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: D. melanogaster
US-09-978-303-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YDALNVLMAMNI ---
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
; ORGANISM: Caliphora
US-09-978-303-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-407-920-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 28032
LENGTH: 64
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Publication No. US20030049728A1
GENERAL INFORMATION:
APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
TITLE OF INVENTION: polypeptides and uses thereof
TITLE OF INVENTION: polypeptides and uses thereof
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Pred. No. 2e+02;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO AL159176.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.54
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.54
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                      26.3%; Score 40; DB 10; Length 10
42.1%; Pred. No. 2.3e+02;
tive 4; Mismatches 7; Indels
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REGISTRATION NUMBER: 36,795
REPERENCE/DOCKET NUMBER: GM5019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
TELEFAX: 215-994-222
TELEFAX: 215-994-222
TELEFAX: CURNOWN-
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 28032, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
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67 INIFQKEKSKYKLLSLETD 85
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                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 42.1%
Conservative
8, Conservative
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Best Local Similarity 35.3
Matches 12; Conservative
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US-10-029-386-28032
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US-09-978-303-16
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APPLICANT: Barney, S.
APPLICANT: Burney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERIES
FILE REFERENCE: 7872-100
CURRENT FILING DATE: 2003-01-24
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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IN PLACENTA, SIGNAL = 0.79
IN LUNG, SIGNAL = 0.86
IN FETAL LIVER, SIGNAL = 0.76
IN ADULT LIVER, SIGNAL = 0.74
IN BRAIN, SIGNAL = 0.74
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Pred. No. 1.3e+02;
4; Mismatches 2; Indels
                 PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: MAP TO ACOOS OTHER INFORMATION: EXPRESSED IN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.0%;
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Best Local Similarity 50.0
Matches 6; Conservative
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NMISKQSRKKKW 18
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| Patent No. US20020048763A1
| GENERAL INFORMATION:
| APPLICANT: Panh, Sharron G.
| APPLICANT: Rank, David K.
| APPLICANT: Hanzel, David K.
| APPLICANT: Hanzel, David K.
| APPLICANT: Hanzel, David K.
| APPLICANT: Chen, Wensheng
| TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
| FILE REFERENCE: Acomica-X-1
| CURRENT APPLICATION NUMBER: US/09/864,761
| CURRENT FILING DATE: 2001-05-23
| PRIOR APPLICATION NUMBER: US 60/180,312
| PRIOR FILING DATE: 2000-02-04
| PRIOR FILING DATE: 2000-05-26
| PRIOR FILING DATE: 2000-06-06-03
| PRIOR FILING DATE: 2000-08-03
| PRIOR FILING DATE: 2000-08-03
| PRIOR FILING DATE: 2000-08-03
| PRIOR PILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbise
APPLICANT: Law, Debbise
APPLICANT: Law, Debbise
APPLICANT: Topper, James
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867, 550
CURRENT APPLICATION NUMBER: USSN 60/208, 427
PRIOR APPLICATION NUMBER: USSN 60/208, 427
PRIOR APPLICANTE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1920
LENGTH: 77
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                                                                                                                                                                                                                                                                                                      Query Match 25.7%; Score 39; DB 12; Length 84; Best Local Similarity 42.1%; Pred. No. 2.7e+02; Matches 8; Conservative 5; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 LIARRVVGREAKEIERYWI 74
                                                                                                                                                                             TYPE: PRT ORGANISM: Arabidopsis thaliana
PRIOR FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 84
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ORGANISM: Homo sapiens
US-09-867-550-1920
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; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1559
; LENGTH: 39
; TYBE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1259
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B ITALLEGAQIQQEKNEYELQKLIKWAGL 35
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FEATURE:
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                                                                                                                           February 17, 2004, 10:50:13; Search time 21.6832 Seconds (without alignments) 58.540 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-308-935-1
US-08-428-131-11
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US-08-94-139-10
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US-09-308-935-15
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US-09-308-935-15
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US-09-308-935-17
US-09-308-935-17
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US-08-848-131-12
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US-08-894-139-7
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1 YDALNVLMAMNIISKEKKEIKWIGLPTNSA 30
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                    Sequence:
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Sequence 16, Appl
Sequence 17, Appl
Sequence 1259, Ap
Sequence 255, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 31, Appl
Sequence 33, Appli
Sequence 3, Appli
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| Sequence 1, Application US/09308935 |
| Sequence 1, Application US/09308935 |
| Sequence 1, Application US/09308935 |
| Sequence 1, Application US/0930835 |
| Sequence 1, Application Sequence 1 |
| APPLICANT: La Thangue, Nicholas B |
| APPLICANT: Bandarat, Lasantha R |
| TITLE OF INVENTION: Peptide antagonists of DP transcription factors |
| TITLE OF INVENTION: Peptide antagonists of DP transcription factors |
| TITLE OF INVENTION: Peptide antagonists of DP transcription factors |
| TITLE OF INVENTION NUMBER: US/09/308,935 |
| CURRENT FILING DATE: 1999-06-27 |
| EARLIER FILING DATE: 1997-12-22 |
| EARLIER PILING DATE: 1996-12-20 |
| NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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US-09-235-451-16
US-09-238-451-17
US-09-328-35-1148
US-09-082-279B-1259
US-09-082-279B-1259
US-09-315-304B-1263
US-09-834-784-1253
US-09-834-784-1253
US-09-107-5238-311
US-09-107-5238-311
US-09-107-5238-311
US-09-107-5238-311
US-09-107-5238-311
US-08-241-853-25
US-09-80-917-25
US-09-80-917-25
US-08-850-917-25
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-078-596-11
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                                                                                                              FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-308-935-1
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ZIP: 2221-4714
COMPUTER: EMADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-UUN-1995
CLASSIFICATION NUMBER: US/08/428,131
FILING DATE: 23-UUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Atthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 25,327
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TWORMATION acids
TWORMATION CALABORIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 152; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                              Query Match
100.0%; Score 152; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-08-428-131-11
Sequence 11, Application US/08428131
Sequence 11, Application US/08428131
Sequence 11, Application US/08428131
Setent No. 5863757
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 YDALNVLMAMNIISKEKKEIKWIGLPTNSA 40
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                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09078596; Patent No. 6150116; Patent No. 6150110.
GRAPHICANT: La Thangue, Nicholas Barrie
                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-09-078-596-11
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                                                                                                                     CITY: Arlington
STATE: Virginia
COUNTY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-00-19-10

Sequence 10, Application US/08894139

Patent No. 64484710N:
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: HIJMANS, REBANCE
TITLE OF INVENTION: TRANSCRIPTION PACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDERSS: ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/894,139 FILING DATE: 13-AUG-1997 CLASSIPICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-16; Matches 30; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-UTN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Archur R. Crawford
REGISTRATION NUMBER: 25,327
REFRENCE/DOCKET NUMBER: 117-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 amino acids
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 15
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US-09-308-935-4
; Sequence 4, Application US/09308935
; Patent No. 6268334
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas B
; APPLICANT: Bandara, Lasantha R
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; CURRENT PEPLICATION NUMBER: US/09/308,935
; CURRENT FILING DATE: 1999-05-27
; EARLIER FILING DATE: 1999-10-27
; EARLIER FILING DATE: 1999-12-20
; EARLIER FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *RESULT 7
US-09-308-395-10
is Sequence 10, Application US/09308935
j Patent No. 626834
j GENERAL INFORMATION:
j APPLICANT: La Thangue, Nicholas B
j APPLICANT: La Thangue, Nicholas B
j TITLE OF INVENTION: Peptide antagonists of DP transcription factors
j FILE REPRENCE: 620-67
j CURRENT APPLICATION NUMBER: US/09/308,935
j CURRENT APPLICATION NUMBER: PCT/GB97/03506
j EARLIER PILING DATE: 1997-12-22
j EARLIER PILING DATE: 1997-12-20
j EARLIER PILING DATE: 1996-12-20
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                      Length 74;
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                                                                                                                                                                                                                                                                                                                                      Score 126; DB 4; I
Pred. No. 2.7e-12;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                50 YDALNVLMAMNIISKEKKEIKWIGL 74
NAME: WILSON, PLANER: 32,955
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMONINICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEPAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
"WATH: 74 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 NVLMAMNIISKEKKEIKWIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVLMAMNIISKEKKEIKWIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.0
Marches 25, Conservative
                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-894-139-10
                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 20; Conserv
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LENGTH: 20
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APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT RILING DATE: 1999-05-27
EARLIER PILING DATE: 1999-12-22
EARLIER PILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SARLIER PLING DATE: 1966-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 19
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT PILING DATE: 1999-05-27
EARLIER PILING DATE: 1997-12-22
EARLIER PILING DATE: 1997-12-22
EARLIER PILING DATE: 1966-12-20
NUMBER OF SEQ ID NOS: 18
                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-3
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                                                                                                                                                          Query Match 52.6%; Score 80; DB 3; Length 15; Best Local Similarity 100.0%; Pred. No. 5.3e-06; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-308-935-15; Sequence 15, Application US/09308935; Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09308935
Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                          16 EKKEIKWIGLPTNSA 30
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SEQ ID NO 3
LENGTH: 19
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1 YDALNVLMAMNIIS 14
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US-09-078-596-13
                                                                                                                                                                                                                                                              US-08-428-131-13
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Sequence 10. 626834

Patent No. 626834

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

CURRENT PAPLICATION NUMBER: US/09/308,935

CURRENT FILING DATE: 1999-05-27

EARLIER FILING DATE: 1997-12-22

EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 5

LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                     ; FEATURE:
* OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide
US-09-3308-935-15
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-5
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                                                                                                 Length 19;
                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.1%; Score 67; DB 3; Le
100.0%; Pred. No. 0.00057;
tive 0; Mismatches 0;
                                                                                               Score 68; DB 3;
Pred. No. 0.00049;
                                                                                                                                               0; Mismatches
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FILING DATE: 23-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-428-131-13
; Sequence 13, Application US/08428131
; Patent No. 5863757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                    44.7%;
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              5 YDALNALMAMNIISK 19
                                                                                                                                                                                      1 YDALNVLMAMNIISK 15
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                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 14; Conserva
                                                                                                                       Best Local Similarity
Matches 14; Conserva
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                          RESULT 10
US-09-308-935-5
                                                                                                      Query Match
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44.1%; Score 67; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 14; Conservative 0; Mismatches 0; Indels
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Sequence 13, Application US/09078596

Patent No. 6150116

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie

TITLE OF INVENTION: Transcription Factor DP-1

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye

STREET: 1100 No. 6150116th Glebe Road, 8th Floor

CITY: Arlington

STREET: Virginia

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MENTIMM TYDE: VI.C. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMATE PATENTIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
                                                                                                                                                                                                                                                                                                                                                                        44.1%; Score 67; DB 2; L 100.0%; Pred. No. 0.00061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIPFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-UN-1995
ATTORNEY/AGENT INFORMATION:
NAMB: ATTHER R. CRAWFORG
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 180-4000
TELEFAX: (703) 816-4000
TELEFAX: (703) 816-4100
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFRENCE/DOCKET NUMBER: 117-
TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID No: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 YDALNVLMAMNIIS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YDALNVLMAMNIIS 14
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-078-596-13
                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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STRANDEDNESS: si
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-428-131-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 16
US-09-078-596-12
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Fatent No. 626834
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lesantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REPRENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1995-05-27
EARLIER APPLICATION NUMBER: PCT/GB97/03506
EARLIER APPLICATION NUMBER: PCT/GB97/03506
EARLIER APPLICATION NUMBER: 1997-12-20
MUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 17
INNORTHEN 19
                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT APPLICATION NUMBER: PCT/GB97/03506
EARLIER APPLICATION NUMBER: GB 9626589.7
EARLIER PILING DATE: 1997-12-22
ARALIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 19
TYPE: PRT
CORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Mutant peptide US-09-308-935-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.5%; Score 60; DB 3; Length 19; 86.7%; Pred. No. 0.0083; tive 0; Mismatches 2; Indels
                                                                       RESULT 13
US-09-308-935-16
; Sequence 16, Application US/09308935
; Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
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4 YDALNVLMAMNIIS 17
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Best Local Similarity
Matches 13; Conserva
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US-08-428-131-12
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Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Parentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-UUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                              ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
Sequence 12, Application US/08428131
Patent No. 5863757
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09078596
Patent No. 615016
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
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APPLICATION NUMBER: US/08/428,131
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: ATACHUR R. Crawford
REGISTRATION NUMBER: 25,327
REFRENCE/DOCKET NUMBER: 117-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.9
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                          CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
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STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
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44.0%; Pred. No. 0.14;
tive 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56.5; DB 3; Length 73;
Pred. No. 0.14;
6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REGISTRATION INFORMATION:
TELECOMMULCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08894139;
Patent No. 6448376
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: BENANCHS, RENE
APPLICANT: HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 YDITNVLEGIQLIAKKSKNHIQWLGSHT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YDALNVLMAMNIISKE-KKEIKWIGLPT 27
                                             NAME: Archur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTER.STICS:
LENGTH: 73 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 42.9%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 44.0°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-894-139-6
                                                                                                                                                                                                                                                                                                                                                                                 US-09-078-596-12
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Taboun 12

(Sequence 11, Application US/09308935

(Sequence 11, Application US/09308935

(Sequence 11, Application US/09308935

(Sequence 11, Application US/09308935

(SERERAL INFORMATION:

(APPLICANT: Bandara, Labantha R

(APPLICANT: Bandara, Labantha R

(CURRENT PLING DATE: 1999-05-27

(CURRENT APPLICATION NUMBER: US/09/308,935

(CURRENT APPLICATION NUMBER: US/09/308,935

(CURRENT APPLICATION NUMBER: US/09/306

(SARLIER PLING DATE: 1997-12-22

(SARLIER PLING DATE: 1997-12-22

(SARLIER PLING DATE: 1996-12-20

(NUMBER OF SEQ ID NOS: 18

(SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
1
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Pred. No. 0.2;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PAtentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-ANG-1997
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 620-22
REPERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
                                                                          GENERAL INPORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: BENENARDS, RENE
APPLICANT: HIJMANS, ELEANORE M.
APPLICANT: TRANSCRIPTION FACTOR E2F-5
TITLE OF INVENTION: TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YDALNVLMAMNIISKE-KKEIKWIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 YDITNVLEGIQLIAKKSKNHIQWLG 73
                                                                                                                                                                                                       NUMBER OF SEQUENCES: .25
CORRESPONDENCE ADDRESS:
ADDRESSEB: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
US-08-894-139-5; Sequence 5, Application US/08894139; Patent No. 6448376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 44.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 amino acids
                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON
STATE: VIRGINIA
COUNTY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: peptide US-08-894-139-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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Gaps

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33.9%; Score 51.5; DB 4; Length 75; 42.3%; Pred. No. 0.83;
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Sequence 8, Application US/08894139
Patent No. 6448376
SEQUENCE B. Patent INCOMATION:
APPLICANT: LA THANGUE, NICHOLAS B. APPLICANT: LA THANGUE, NICHOLAS B. APPLICANT: LA THANGUE, RENE
APPLICANT: HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: US.A.
CONDITER: US.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BEN PC COMPATIBLE
COMPUTER: BEN PC COMPATIBLE
COMPUTER: US.A.
SOFTWARE: PACENIIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/894,139
FILING APPLICATION NUMBER: US/08/894,139
                                                                                                                                                                                     STATE: VIRGINIA
COMPRES ELOPEY disk

ZIP: 22201-4714

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIPICATION SS6
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/POCKET NUMBER: 32,955
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                         HIJMANS, ELEANORE M.
JENTION: TRANSCRIPTION FACTOR E2F-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.83
6; Mismatches
  APPLICAT: HIUMAN, TRANSCALL
TITLE OF INVENTION: TRANSCALL
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
ATTENTION NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YDALNVLMAMNIISKE-KKEIKWIGL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 YDITNVLEGIDLIEKKSKNSIQWKGV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEO ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.99
Best Local Similarity 42.33
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-894-139-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-894-139-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 74;
                                                                                                                                                              36.2%; Score 55; DB 3; Length 14; 100.0%; Pred. No. 0.035; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SITATE: ILON NORTH GLEBE KOAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZID: 2.201-4714
ZODPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SUFTARE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM COMPATION
APPLICATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: BERNARDS, RENE
APPLICANT: HIJMANS, ELEANORE M.
ITILE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.2%; Score 53.5;
Best Local Similarity 40.0%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 YDITNVLEGIHLIKKKSKNHVQWMG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YDALNVLMAMNIISKE-KKEIKWIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                               RESULT 20
US-08-894-139-7
; Sequence 7, Application US/08894139
; Betent No. 6448376
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 21
US-08-894-139-9
; Sequence 9, Application US/08894139
; Patent No. 6448376
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 816-4100
INPORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                           1 YDALNVLMAMN 11
                                                                                                                                                                                                                                                                                                           4 YDALNVLMAMN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: peptide US-08-894-139-7
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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LENGIH: 14
                                                                   FEATURE:
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                        셤
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Gaps

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Indels

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14 ACDVAMLM---SRIESEASWMGLPVDA 37
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Sequence 228, Application US/08311731A

Patent No. 6583266

GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS

APPLICANT: MAO, JUN.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES:
ADDRESSEE: WOLF, GREENTIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STREET: MASSACHUSETTS

COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
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28.6%; Score 43.5; DB 4; Length 100;
Best Local Similarity 37.0%; Pred. No. 20;
Matches 10; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                  Score 45.5; DB 4; Length 69;
Pred. No. 6.3;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                                                                                                                                                                                                            1 YDALNVLMAMNIISKE-KKEIKWIGL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                            44 YDITNVLEGIGLIEKKSKNSTQWRGV 69
                                REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GAREN INFORMATION:
NAME: GAREN INFORMATION:
REGISTRATION NUMBER: 31,616
REGISTRATION NUMBER: 0004TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEPHONE: 617/720-2441
INFORMATION FOR SEQ ID NO: 228: SEQUENCE CHARACTERISTICS: LENGTH: 100 amino acids
TYPE: amino acid
TOPOLOGY: linear
                REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                         Query Match 29.9%;
Best Local Similarity 38.5%;
Matches 10; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-894-139-8
                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
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RESULT 24
US-09-308-935-2
i Sequence 2, Application US/09308935
j Sequence 2, Application US/09308935
j Patent No. 656834
j GENERAL INFORMATION:
j APPLICANT: La Thangue, Nicholas B
j TITLE OF INVENTION: Peptide antagonists of DP transcription factors
j TITLE OF INVENTION: Peptide antagonists of DP transcription factors
j TITLE OF INVENTION: Peptide antagonists of DP transcription factors
j FILE REFERENCE: 620-67
j CURRENT PILING DATE: 1999-05-27
j EARLIER PILING DATE: 1997-12-22
j EARLIER FILING DATE: 1997-12-20
j NUMBER OF SEQ ID NOS: 18
j SEQ ID NO 2
j LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
27.6%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-743-975-9

Sequence 9, Application US/08743975

Patent No. 6057434

GENERAL INFORMATION:

APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz TITLE OF INVENTION: Mammary Transforming Protein NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: CRRELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN CITY: ROSELAND

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 1507 FS74.

OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,975
FILING DATE: 01 NOVEMBER 1996
CLASSIPFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,187
FILING DATE: 02 NOVEMBER 1995
ATTORNEY/AGENT INFORMATION:
NAME: MULLINN, J.G.
REGISTARTION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 33,073
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-94-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201-994-1744
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OPERATING SYSTEM:
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; TOPOLOGY: linear
US-09-024-04-4
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                                                                                                                                                                                                     DB 3; Length 61;
                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammary Transforming Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09263811
Patent No. 6482922
GENERAL INFORMATION:
ITILE OF INVENTION: Mammary Transforming Pro;
NUMBER OF SEQUENCES:
ORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, IN.C
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
                                                                                                                                                                                                   Query Match 27.6%; Score 42; DB Best Local Similarity 33.3%; Pred. No. 19; Matches 7; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZUP: 1016.054
ZUP: 1016.054
ZUP: 2016.056
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 188 PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,811
FILING DATE: 01-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/743,975
FILING DATE: 01-NOV-1996
PRIOR APPLICATION NUMBER: 60/006,187
FILING DATE: 02 NOVEMBER 1995
ATTORNEY/AGENT INFORMATION:
NAME: MICHELE M. WALES
REGISTATION NUMBER: 43,975
REFERENCE/DOCKET NUMBER: PF212D1
TELECOMMUNICATION UNMBER: PF212D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 VLMAMNIISKEKKEIKWIGLP 26
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                                                                                                                                                                                                                                                                                              6 VLMAMNIISKEKKEIKWIGLP 26
                                                                                                                                                                                                                                                                                                                        14 VVFSINLLSRPERE--WEGMP 32
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 61 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-263-811-9
                                                                                                           TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN
US-08-743-975-9
                                                            TYPE: AMINO ACID STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMINO ACID
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US-09-263-811-9
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APPLICANT: Julius, David J.
APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
TITLE OF INVENTION: POLYBETIDES AND USES THEREOF
TITLE OF INVENTION: 00/04/21P
CURRENT APPLICATION NUMBER: US/09/2151
PRIOR FILING DATE: 1999-01-22
PRIOR FILING DATE: 1999-01-22
PRIOR PLING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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WS-09-024-024-4

Sequence 4, Application US/09024024

Sequence 4, Application US/09024024

Patent No. 6228838

GENERAL INFORMATION:

APPLICANT: Lonetto, Michael A.

TITLE OF INVENTION: licbl

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert, Price & Rhoads

STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SUSTWARE: FatelSOF for Windows Version 2.0
SUSTRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.3%; Score 40; 42.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICALLE.
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 60/039,581
FILING DATE: 28-ERB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
FREERRENCE/DOCKET NUMBER: 36,795
TREFRENCE/DOCKET NUMBER: GMS001
TELECOMMUNICATION INFORMATION:
""TRPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09235451 GENERAL INFORMATION:
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67 INIFQKEKSKYKLLSLETD 85
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                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                STATE: PA
COUNTRY: USA
ZIP: 19103-279
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
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LENGTH: 75
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Gape
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US-09-082-279B-1259
US-09-082-279B-1259
Sequence 1259, Application US/09082279B
Sequence 1258, Application US/09082279B
Sequence 1258, Application US/09082279B
SERRAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennie
APPLICANT: Lambert, Dennie
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
TITLE REPERBENCE: 7872-043
FILLE REPERBENCE: 7872-043
CURRENT APPLICANTON NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FBSESQ for Windows Version 3.0
SEQ ID NO 1259
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
25.0%; Score 38; DB 3; Length 39;
Best Local Similarity 35.7%; Pred. No. 47;
Matches 10; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Guthrie, Kelly
APPLICANT: Menutka, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennie
TITLE OF INVENTION: PHARMACCKINETIC PROPERTIES
TITLE OF SEPRENCE: 1912-043
CURRENT FILLING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: PASSES OF SEV ID NOS: 1515
SOFTWARE: PASSES OF SEV ID NOS: 1515
SOFTWARE: PASSES OF SEV ID NOS: 1515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 ITALLEGAQIQQEKNEYELQKLİKWAĞL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LNVLMAMNIISKEKKE----IKWIGL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 ITALLEQAQIQQEKNEYELQKLİKWAĞL 35
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8-09-315-304B-1259
; Sequence 1259, Application US/09315304B
; Patent No. 6348568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-082-279B-1263

US-09-082-279B-1263

Sequence 1263, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Core polypeptide US-09-082-279B-1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Core polypeptide US-09-082-279B-1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
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Patent No. 656258

PERERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7148

LENGTH: 78
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GENERAL INFORMATION

APPLICANT: JULIUS, David J.

APPLICANT: Caterina, Michael J.

APPLICANT: Brake, Anthony J.

TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING

TITLE OF INVENTION: POLYPETIONS AND CAPSAICIN RECEPTOR-RELATED

TITLE OF INVENTION: POLYPETIONS AND USES THEREOF

TITLE OF INVENTION: POLYPETIONS AND USES THEREOF

TITLE OF INVENTION: POLYPETIONS AND USES THEREOF

TITLE OF INVENTION: POLYPETIONS AND USES THEREOF

CURRENT FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-01-22

PRIOR FILING DATE: 1997-08-20

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSEG for Windows Version 3.0

SEQ ID NO 17

LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 75;
                                                                                               25.7%; Score 39; DB 4; Length 75; 18.8%; Pred. No. 70;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.7%; Score 39; DB 4;
18.8%; Pred. No. 70;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 YSVINIIVLENMELIAMMSNSYQIISERADVEW 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YDALNVLMAMNI-----ISKEKKEIKW 22
                                                                                                                                                                                                                             1 YDALNVLMAMNI-----ISKEKKEIKW 22
                                                                                                                                                    10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7148
                                                                                                                                                                                                                                                                                                                                                                ; Sequence 17, Application US/09235451; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||::|:: |: 40 VAMSLITRPRKALDWL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 MAMNIISKEKKEIKWI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: D. melanogaster
US-09-235-451-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 18.8
Matches 6; Conservative
                                                                                                                                                    6; Conservative
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Matches 5; Conserv
                                                                                                         Query Match
Best Local Similarity
          ; TYPE: PRT
; ORGANISM: Caliphora
US-09-235-451-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 30
US-09-328-352-7148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Buthrie, Kelly
APPLICANT: Guthrie, Kelly
APPLICANT: Guthrie, Kelly
APPLICANT: Herutka, Gene
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR PILING DATE: 1998-05-20
PRIOR PILING DATE: 1998-05-20
SOFTWARE: FASTERO for Windows Version 3.0
SOFTWARE: FASTERO for Windows Version 3.0
                                    APPLICANT: Metuck, Modmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID POLYPEPTIDES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 1090-104-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SEQ ID NO 1259
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-107-532A-5431
; Sequence 5431, Application US/09107532A
; Parent No. 6583270N:
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 4;
Pred. No. 47;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LNVLMAMNIISKEKKE-----IKWIGL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---IKWIGL 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1263, Application US/09834784 Patent No. 6562787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Core polypeptide US-09-834-784-1263
                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Core polypeptide US-09-834-784-1259
                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.0%;
Best Local Similarity 35.7%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
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Guthrie, Kelly
Merutka, Gene
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                                                                APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REPREMENT: 787-2-052
CURRENT APPLICATION NUMBER: US/09/315,304B
PRIOR PILING DATE: 1999-05-20
PRIOR PILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
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Pred. No. 47;
3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 4;
Pred. No. 47;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LNVLMAMNIISKEKKE-----IKWIGL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 ITALLEQAQIQQEKNEYELOKLIKWAGL 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1263
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1263, Application US/09315304B
; Patent No. 6348568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-834-784-1259
Sequence 1259, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Core polypeptide US-09-315-304B-1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Core polypeptide US-09-315-304B-1263
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 25.0%;
1 Similarity 35.7%;
10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LNVLMAMNIISKEKKE---
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Best Local Similarity 35.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-315-304B-1263
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APPLICANT:
APPLICANT:
APPLICANT:
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EARLIER APPLICATION NUMBER: 60/048,974
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER APPLICATION NUMBER: 60/048,996
EARLIER FILING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER APPLICATION NUMBER: 60/048,973
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-06-06
EARLIER PILLING DATE: 1997-07-06-06
EARLIER PILLING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER PILLING DATE: 1998-07-15
EARLIER FILLING DATE: 1998-07-15
EARLIER FILLING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,882

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,899

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,990

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,901

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,901

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,915

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,915

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,915

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,915

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,915

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,916

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,916

R APPLICATION NUMBER: 60/049,313

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/049,313

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/049,314

R APPLICATION NUMBER: 60/048,917

R APPLICATION NUMBER: 60/048,917

R APPLICATION NUMBER: 60/048,917

R APPLICATION NUMBER: 60/048,917

R APPLICATION NUMBER: 60/048,917

R APPLICATION NUMBER: 60/048,917

R APPLICATION NUMBER: 60/048,917

R APPLICATION NUMBER: 60/048,917

R APPLICATION NUMBER: 60/048,917

R PILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,917

R PILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,917

R PILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,917
                                                R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,020
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,876
R APPLICATION NUMBER: 60/048,895
R APPLICATION NUMBER: 60/048,895
R APPLICATION NUMBER: 60/048,894
R APPLICATION NUMBER: 60/048,894
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,894
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-06-06
APPLICATION UNMBER: 60/048,971
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins;
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,881
EARLIER APPLICATION NUMBER: 60/048,880
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                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: «UNKNOWN»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ATINIBLIO, PAMER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )
NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...87
; SEQUENCE DESCRIPTION: SEQ ID NO: 5431:
US-09-107-532A-5431
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                                                                                                                                                                                                         STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 381, Application US/09205258
Patent No. 6525174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5431:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
                                                               NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 LMAMNIISKEKKEIK 21
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Best Local Similarity
Matches 7; Conserva
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: USA
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STATE: New Jerse
                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-850-917-25
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                                                                                                                                                                     NAME/KEY: SITE
1 LOCATION: (62)
2 CTHEN INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-381
                                                                                                                 LOCATION: (14)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application US/08241853
Fatent No. 5693488
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
TITLE OF INVENTION: AT TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STREET: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.4%; Score 35.5; DB 1; Length 94; 39.1%; Pred. No. 3.2e+02; Live 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                     Score 36; DB 4; Length 66;
Pred. No. 1.8e+02;
8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPRENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                      36 SINLSLLLTLIKKKKKKK 54
                                                                                                                                                                                                                                                                                                                                               3 ALNVLMAMNIISKEKKEIK 21
                                                                                                                                                                                                                                                                   Query Match 23.7%;
Best Local Similarity 31.6%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 23.4
Best Local Similarity 39.1
Matches 9; Conservative
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                                       TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                     FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07601
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 39
US-08-241-853-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
SEQ ID NO 381
LENGTH: 66
                                                                                                                                                       FEATURE:
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4 LNVLMAMNIISKEKKEIKWIGLP 26

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Gaps
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APPLICANT: La Thangue, Nicholas B

APPLICANT: La Thangue, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/308,935

CURRENT FILING DATE: 1999-05-27

EARLIER APPLICATION NUMBER: PCT/GB97/03506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ï
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Best Local Similarity 39.1%; Pred. No. 3.2e+02;
Sequence 25, Application US/08850917

Patent No. 5854045

GENERAL INPOMATION:

APPLICANT: Hanafusa, Hidesaburo

TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Alauber & Jackson

STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LNVLMAMNIISKEKKEIKWIGLP 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-308-935-9; Sequence 9, Application US/09308935; Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 94 amin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Query Match 23.0%; Score 35; DB 2;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Sterne, Kessler, Goldstein & Fox
1225 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: 19920923
FILING DATE: 19920923
ATTONNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
TELECOMOTHICATION INFORMATION:
TELECOMOTHICATION INFORMATION:
TELEPHONE: (202) 466-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08449741 Patent No. 6022735
                                                                                                                                                                             US-08-450-417-3
; Sequence 3, Application US/08450417
; Patent No. 5981273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Curiel, David T.
APPLICANT: Birnstiel, Max L.
                                                                                                                                                                                                                                                                                              Curiel, David T.
Birnstiel, Max L.
Cotten, Matthew
Wagner, Ernst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
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                                                                  1 MAODIISTIGDLVKWI 16
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 MAMNIISKEKKEIKWI
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STRANDEDNESS: single
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALDALLA
STREET: 1225
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
7IP: 20036
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Curiel
APPLICANT: Birnst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-449-741-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-450-417-3
                                                                                                                                                           RESULT 43
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                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OLHS 195-99
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Birnstiel, Max L.
APPLICANT: Cotten, Matthew
APPLICANT: Cotten, Matthew
APPLICANT: Zarloukal, Kurt
APPLICANT: Zarloukal, Kurt
APPLICANT: Plank, Christian
APPLICANT: Oberhauser, Berndt
APPLICANT: Schmidt, Walter G.M.
APPLICANT: Schmidt, Composition for Introducing Nucleic Acid
TITLE OF INVENTION: Composition for Introducing Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.0%; Score 35; DB 1; Length 26; 50.0%; Pred. No. 85; ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPAGE.

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kesaler, Goldstein & Fox
STREET: 1225 Connecticut Avenue
CITY: Washington
CITY: Washington
CITY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAGE.DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/948,357
FLING DATE: 19920923
CLASSIFICATION NUMBER: 32,893
REGISTRATION NUMBER: 33,893
REGISTRATION NUMBER: 33,893
REGISTRATION NUMBER: 33,893
REGISTRATION NUMBER: 33,893
REGISTRATION NUMBER: 
                                 9626589.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-948-357-3
; Sequence 3, Application US/07948357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Curiel, David T.
Birnstiel, Max L.
Cotten, Matthew
Wagner, Ernst
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: GB 9
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.0
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-07-948-357-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 YDALNVL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YDALNVL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Curiel
                                                                                                                                                        SEQ ID NO 9
LENGTH: 11
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APPLICANT: Zatloukal, Kurt
APPLICANT: Zatloukal, Kurt
APPLICANT: Plank, Christian
APPLICANT: Schmidt, Walter G.M.
APPLICANT: Schmidt, Walter G.M.
TITLE OF INVENTION: Composition for Introducing Nucleic Acid
TITLE OF INVENTION: Composition for Introducing Nucleic Acid
TITLE OF INVENTION: Complexes Into Higher Eucaryotic Cells
NUMBER OF SEQUENCES: 13
NUMBER OF SEQUENCES: 13
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FOC Comparible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/450,417
FILING DATE:
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Search completed: February 17, 2004, 10:59:41
Job time : 21.6832 secs
                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
APPLICANT: Wagner, Enst
APPLICANT: Zatloukal, Kurt
APPLICANT: Plank, Christian
APPLICANT: Oberhauser, Berndt
APPLICANT: Schmidt, Walter G.M.
TITLE OF INVENTION: Composition for Introducing Nucleic Acid
TITLE OF INVENTION: Complexes Into Higher Bucaryotic Cells
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS: 13
CORRESPONDENCE ADDRESS: 3
STATE: D.C.
COUNTRY: Washington
STATE: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy A***.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Legendre, Jean-Yves
APPLICANT: Supersaxo, Andreas
APPLICANT: Supersaxo, Andreas
APPLICANT: Supersaxo, Andreas
APPLICANT: Tracciak, Arnold
TITLE OF INVENTION: Peptide Conjugates for Transfecting
TITLE OF INVENTION: Cells
NUMBER OF SEQUENCES: 37
CORRESPONDENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FURM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,741
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FLESHMER, RAZ E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0652.0940007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
"TUBENTH: 26 amino acids
"TUBENTH: 26 amino acids
"TUBENTH: 26 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08782997A Patent No. 6030602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAQDIISTIGDLVKWI 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-449-741-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 45
US-08-782-997A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 1..2
; OTHER INFORMATION: /note= "Position 1 is fMet."
US-08-782-997A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.0%; Score 35; DB 3;
50.0%; Pred. No. 85;
tive 2; Mismatches
PELLICATION NUMBER: US/08/782,997A
FILING DATE: 14-JAN-1997
CLASSIFICATION: 435
PRICH 435
PRICH 435
PRICH 545
PRICH 545
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PRICH 545
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PRICH 545
PRICH 545
PRICH 545
PRICH 545
PRESENCE 545
PRESENCE 545
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Best Local Similarity 50.03
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
PERATURE
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(OTSBU) XWAJB BDA9 SIHT

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DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW30507 standard; Peptide; 30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-OCT-1998 (first entry)
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW30507;
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| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS1/gcgdata/geneseq-embl/AA31980.DAT:*
| SIDS1/gcgdata/geneseq-embl/AA3198.DAT:*
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| SIDS1/gcgdata/geneseq-embl/AA393.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 YDALNVLMAMNIISKEKKEIKWIGLPTNSA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 100
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Location/Qualifiers

Key

3..9 /note= "Claim 3" 5..15 /note= "Claim 3"

Peptide Peptide

WO9828334-A1.

97WO-GB03506. 96GB-0026589.

22-DEC-1997; 02-JUL-1998

(PROL-) PROLIFIX LTD

20-DEC-1996;

521	Description	1		DP-1 transcription			DP-1 transcription			
SUMMAKIES	ΩI	AAW30507	AAW30501	AAW30505	AAB67766	AAY32163	AAW30510	AAU72601	AAW30504	AAW30515
	03	19	19	19	22	20	19	23	19	19
di	Query Match Length DB ID	30	37	20	26	83	15	35	19	19
	Query Match	100.0	100.0	66.4	65.1	59.2	52.6	50.0	47.4	44.7
	Score	152	152	101	66	90	80	9/	72	68
	Result No.	н	7	æ	4	2	9	7	80	σ

DP-1 transcription E2F activity inhib	F activity		H	Arabidopsis cell c	Human DNA binding	Repressor protein	DP-1 transcription	Human musculoskele	Novel human muscul	Human DNA binding	Repressor protein	E2F activity inhib	Human liver peptid	Peptide #10461 enc	Human brain expres	ne	Peptide #10814 enc	Human peptide enco	n E2	Wheat E2F derived	Streptococcus poly	DP-1 transcription	Fragment of human	Š	acid	iver		Peptide #2343 enco	Protein #2256 enco	Human brain expres	one	m	#2	ide #2		
AAW30506 AAW57051	AAW57055	AAW30516	AAW30517	AAU72561	AAU78095	ABB82986	AAW30511	ABB03433	ABU12727	AAU78096	ABB82987	AAW57052	ABG58365	ABB42955	AAM63859	AAM76672	AAM36777	ABG45881	AAY32167	AAY44493	ABP29212	AAW30502	AAY36705	ABB17294	AAY37764	ABG49671	ABB29659	ABB34837	ABB20257	AAM55645	AAM68025	AAM15843	AAM28353	AAM03581	ALIGNMENTS	
19	13	13	19	23	23	24	19	22	24	23	24	19	22	22	22	22	22	23	20	21	23	13	20	22	20	22	22	22	22	22	22	22	22	22		
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Bandara LR, La Thangue NB;
                                                                                                     Query Match
Best Local Similarity 100.
                                                                                                                                                                                                         (PROL-) PROLIFIX LTD
        WPI; 1998-377596/32.
                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                   WO9828334-A1.
                                                                                                                                                                                              22-DEC-1997;
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                                                                                                                                                                                        02-JUL-1998
  Bandara LR,
                                                                                                                                                                          Synthetic
                                                                                                                                            AAW30501;
                                                                                                  Sequence
                                                                                                                                 RESULT 2
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96GB-0026589 97WO-GB03506

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Location/Qualifiers
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/note= "Claim 3"
                                                                                                                                                Claim 1; Page 44; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 30; Conservative
              WPI; 1998-377596/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9828334-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
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                                                                                                                                                                                                                                        Peptide H7 comprises amino acid residues 170-199 in the DEF box (C (I) (see AAW30501) of transcription factor DP1. Claimed peptides (I) (see AAW30501) of transcription factor DP1. Claimed peptides (C (II) (see AAW30504-07) containing one or both of 2 motifis (see CAM30502-03) of the DEF box are capable of antagonising the certained are variants of these peptides, especially containing subscriptions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and a corresponding (I)-(III) are used (III) and host cells. (I)-(III) are used (III) and host cells. (I)-(III) are used to therapeutically to induce apoptosis, specifically in tumour or therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells either in vivo or in vitro, e-g. for purging cordiovascular cells either in vivo or in vitro, e-g. for purging (I)-(III) are used to cardiovascular sents comprising (I)-(III) are used to angioplasty. (I)-(III) function by inactivating the DNA-binding catavity of DP-1/E2F heterodimers. They are also used as research capants, as positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunosassy agents. C encoding (I)-(III) to control DP levels in cells, particularly by control DP levels in cells, particularly by control DP levels in cells, particularly by control DP levels in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                         Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 152; DB 19; 100.0%; Pred. No. 2.9e-17;
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                                                                                                                                                                                                              Claim 4; Page 44; 55pp; English
                                 La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1998 (first entry)
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peptide H (I) comprises residues 163-199, i.e. the DEF box region, of transcription factor DPI. Claimed fragments (II) (see AAW30502-07) of (I) are capable of antagonising the heterodimerisation of a DP protein with an E2F protein. Also claimed are fusion proteins (III) comprising (I) or (II) and amembrane translocation sequence (see AAW30508), expression vectors encoding (I) (III) and host cells. (I)-(III) are used therapeutically to induce apoptosis, expression specifically in tumour or acadiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding activity of EP/E2P heterodimers. They are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                have undergone angioplasty. (1)-(III) function by inactivating the DNA-binding activity of DP/22P heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunoassay agents. Also described is the use of sequences antisense to nucleic caids encoding (1)-(III) to control DP levels in cells, particularly by gene therapy. When formulated with cytotoxic or cytostatic agents, (1)-(III) enhance cell killing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 152; DB 19; 100.0%; Pred. No. 3.7e-17;
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(CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
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                        Claim 4; Page 44; 55pp; English
                                                                                                                                                                                                                                                                                                                     25-SEP-2000; 2000WO-EP09325.
                                                                                                                                                                                                                                                                                                                                    99ES-0002474
                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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                                                                                                                                                        20 AA;
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                                                                                                                                                        Sequence
                                                                                                                                                                                                                                   AAB67766;
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useful for e.g. altering cell proliferation characteristic such as to alter plant cell, organ or tissue size (DP) protein. The protein acts as a plant E2F transcription factor. E2F and DP are two proteins that hetero-dimerise to form an active transcription factor that regulates G1 to S phase of the cell cycle, and later, the expression of genes required for S-phase progression. E2F and retinoblastoma protein also interact as a hetero-dimer in cells to suppress certain genes. This repression involves binding of the retinoblastoma protein to the E2F-DP dimer that is in turn bound to sites on DNA through the E2F DNA binding domain. DP proteins can be medulated to alter plant cell, organ or tissue shape, and alter plant cell, organ or tissue state cateristic such as to alter plant cell, organ or tissue size. New isolated, enriched, cell free and/or recombinant nucleic acid AAB67764-68 represent fragments of a wheat E2F-dimerisation Length 56; Indels Match 65.1%; Score 99; DB 22; L. Local Similarity 68.0%; Pred. No. 2.3e-08; es 17; Conservative 6; Mismatches 2; DP-1; soybean; cell cycle regulatory protein; transcription factor; herbicide. GGN. ANT. note= "encoded by NAN" 'note= "encoded by GNC" /note= "encoded by GNC" "encoded by ANG" 'note= "encoded by NAT" "encoded by NAG" "encoded by CNT" 25 42 Location/Qualifiers 1 YDALNVLMAMNIISKEKKEIKWIGL 'note= "encoded by 'note= "encoded by AAY32163 standard; Protein; 83 AA Claim 10; Page 50; 77pp; English. Soybean DP-1 protein fragment. (first entry) note= 'note= note= 56 AA; Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference 01-FEB-2000 Glycine max AAY32163; Sequence Query Match Best Loc Matches AAY32163 RESULT 유 à ö (I) (see AAW30501) of transcription factor DP1. Claimed pebtides (II) (see AAW30501) of transcription factor DP1. Claimed pebtides (II) (see AAW30504-07) containing one or both of 2 motifs (see AAW30502-03) of the DFP box are capable of antagonising the heterodimerisation of the Drotein with an EZP protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (II) comprising (I) or (II) and embrane translocation sequence (see AAW30508), expression vectors encoding (I)-(III) and host cells. (I)-(III) are used to therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardiovascular cells, either in vivo or in vitro, e.g. for purging cardivity of DP/EZP heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-I/EZ pimerisation and as immunosasay agents. Gaps Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis Also described is the use of sequences antisense to nucleic acids encoding (I)-(III) to control DP levels in cells, particularly by gene therapy. When formulated with cytotoxic or cytostatic agents, (I)-(III) enhance cell killing. E2F-dimerisation partner; DP protein; E2F transcription factor; G1 phase; S phase; cell cycle; retinoblastoma protein; alter cell proliferation. Peptide H3 comprises amino acid residues 174-193 in the DEF box ö Fragment from a wheat E2F-dimerisation partner (DP) protein. Length 20; Indels Score 101; DB 19; Pred. No. 3.1e-09; 100.0%; Pred. ... NVLMAMNIISKEKKEIKWIG 20 5 NVLMAMNIISKEKKEIKWIG 24 66.48; 99ES-0002127

'note= "encoded by NAT"

Misc-difference Misc-difference Misc-difference Misc-difference

'note= "encoded by NTC" /note= "encoded by CNA"

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                                                                                                                                                                               This sequence represents 42% of the middle region of soybean cell cycle regulatory protein DP-1, as deduced from an isolated cycle regulatory protein DP-1, as deduced from an isolated cond. Conno. (see AAZ34575-81) and invention relates to nucleic acid fragments (see AAZ34575-83) encoding plant CDC-16, DP-1, DP-2 and E2F cell cycle regulatory proteins (see AAY32159-67). It also relates to the construction of a chimeric gene encoding all or a contentation, where expression of the chimeric gene results in producton of altered levels of the cell cycle regulatory protein in the atransformed host cell. The nucleic acids and protein in cused to facilitate studies of cell cycle regulation in plants, cused to facilitate studies of cell cycle regulation in plants, cused transfer efficiency and provide more stable.
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                         transformations. The proteins may also provide targets to facilitate design and/or identification of cell cycle regulatory proteins that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
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                                                                                                                                                                                                                                                                                                                                                                 59.2%; Score 90; DB 20; Length 83; 64.3%; Pred. No. 1e-06; ive 4; Mismatches 6; Indels
                                                                                                Sakai H;
                                                                                                                                              Plant-derived cell cycle regulatory proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                   DP-1 transcription factor peptide H4
                                                                             (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                               odell JT,
                                                                                                                                                                 Claim 10; Page 41; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW30510 standard; Peptide; 15
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                                                                                                                                                                                                                                                                                                                                                    83 AA;
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    WO9953075-A2
                                         08-APR-1999;
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                       21-OCT-1999.
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The invention relates to a novel cell cycle protein (CCP) and the polynuclectides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the eleptoperide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell cycle protein; CCP; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield; motif.
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                                                                                                                                                                                                                                                                      Peptide H4 comprises amino acid residues 185-199 in the DEF box region (see AAM30501) of transcription factor DP1. Unlike claimed peptides (see AAM30504-07) that contain one or both of 2 motifs (see AAM30502-03) of the DP1 DEF box, peptide H4 is not capable of antagonising the heterodimerisation of a DP protein with an E2F protein. The claimed peptides, their variants and fusion proteins can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g. to prevent restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                            Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
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Pred. No. 5.5e-06;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU72601 standard; Peptide; 35 AA.
                                                                                                                                                                                                                                 Example C; Page 41; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.6%; Scc.
100.0%; Pre
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La Thangue NB;
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                                                       WPI; 1998-377596/32
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      Bandara LR,
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cc maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola.

CCP nucleic acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of creat disorders characterised by insufficient or excessive production of corporate that bind to or modulate the activity compounds that bind to or modulate the activity of CCP polymeucleotide is useful for modifying cell fate, plant development, of CCP plant morphology, biochemistry and/or physiology, the length of the G1, C. S. G2 and/or M phase of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, ced development, nodule function, dwarfism in plants, ced size, seed development, nodule function, dwarfism in plants, cand the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due continuental conditions, including abiotic stress such as pathogen attack, to modulate e.g. enhance crop yields, and attenuate plant architecture, plant quality traits, plant controduction and seed development, endoreduplication in storage cells, storage tissues and/or storage organs of plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to expressing CCP protein, to detect CCP mRNA, or a generic represents a motif which may be found in a CCP protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 50.0%; Score 76; DB 23; Length 35; 1 Similarity 64.0%; Pred. No. 6.7e-05; 16; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DP-1 transcription factor antagonist peptide H2.
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Peptide H2 comprises amino acid residues 166-184 in the DEP box (II) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07).containing one or both of 2 mortifs (see AAW30502-03) of the DEP box are capable of antagonising the heterodimerisation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprishing (I) cit (III) and host cells. (I) -(III) are used cherapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding creativity of DP/E2P heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-1/E2P dimerisation and as immunoassay agents. Also described is the use of sequences antisense to nucleic acids encoding (I)-(III) enhance cell killing. (I)-(III) enhance cell killing.
               Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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                                                                                 Claim 4; Page 44; 55pp; English
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Matches 15; Conservative
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(PROL-) PROLIFIX LTD.

WPI; 1998-377596/32

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Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells,
                                                                                                                                                                                                                                                                                                   DP-1 transcription factor antagonist peptide H5.
                                                             Example D; Page 26; 55pp; English.
                                                                                                                                                                                                                                                         AAW30506 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                          5..11
/note= "Claim 3"
                                                                                                                                                                                                                                                                                                                                                                                      7..16
/note= "Claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-GB03506
                                                                                                                                                                                                        1 YDALNVLMAMNIISK 15
                                                                                                                                                                                                                 96GB-0026589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 La Thangue NB;
     Bandara LR, La Thangue NB;
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROL-) PROLIFIX LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-377596/32.
                    WPI; 1998-377596/32.
                                                                                                                                                                            Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                               19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-1996;
                                                                                                                                                                                                                                                                                     26-OCT-1998
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          WO9828334-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bandara LR,
                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-1998.
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                        AAW30506;
                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                    AAW30506
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Peptide H5 comprises amino acid residues 168-183 in the DEF box (I) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07) containing one or both of 2 motifs (see AAW30502-03) of the DEF box are capable of antagonising the cheerodimerisation of a DP protein with an E2F protein. Also heterodimerisation of a PP protein with an E2F protein. Also claimed are variants of these peptides, especially containing substitutions of residues orresponding to residues 167, 169, 171 and host cells (III) comprising (I) or (II) and host cells. (II-(III) are used cherapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to read or prevent restnesses in patients who have undergone treat or prevent restnesses in patients who have undergone activity of DP/E2F heterodimers. They are also used as research reagents, as positive controls in assays for identifying activity of DP/E2F dimerisation and as immunosassy agents. Also described is the use of sequences antisense to nucleic acids encoding (I)-(III) thoriton DP levels in cells, particularly by the farmalated with cytotoxic or cytostatic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E2F activity; inhibitor; treatment; tumour; arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67; DB 19; L
Pred. No. 0.00075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E2F activity inhibiting compound Ib-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57051 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.1%; Scc...
100.0%; Pre
                                         Claim 4; Page 44; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -(III) enhance cell killing
e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-JP03442.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 YDALNVLMAMNIIS 16
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                             Peptide HZmtl is based on peptide HZ (see AAW30504) from the DEF box (see AAW30501) of transcription factor DP1. The HZmtl peptide, in which HZ residues corresponding to DP1 residues Val169 and Val175 are substituted by Ala residues, behaves in a similar fashion to the wild-type HZ peptide in its ability to inactivate EZF site DNA binding activity in D9 EC cell extracts. HZ is an antagonist of the heterodimerisation of DP1 with EZF. Thus, the Val-169 and Val-175 residues of HZ play little role in this activity. HZ and other claimed peptides (see AAW30504-07) from the DEF box region of DP1 can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g. for the prevention of restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                          inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                             Polypeptide fragments of the DP-1 transcription factor - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.7%; Score 68; DB 19; Length 19; 93.3%; Pred. No. 0.00063; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Gaps . 0

Yoshida T;

Yamasaki M,

Mizukami T, Shibata K, WPI; 1998-240020/21

(KYOW) KYOWA HAKKO KOGYO KK.

30-SEP-1996;

Length 16;

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is of the formula R1 - A - R2 where R1 is an optionally substituted alkanoy1, alloy1, hetero-arylcarbony1, alkoy2, aryloxycarbony1, hetero-arylcarbony1, or M. R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2P activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This represents a compound that can inhibit E2F activity. The compound alkanoyl, alloyl, hetero-arylcarbonyl, alkoycarbonyl, aryloxycarbonyl, hetero-arylcarbonyl, alkoyl, respectively, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B2F activity inhibitors - for treatment and prevention of tumours
activity inhibitors - for treatment and prevention of tumours
                                                                                                                                                                                                                                                                                   ö
                                                                  This represents a compound that can inhibit E2F activity. The is of the formula R1 - A - R2 where R1 is an optionally substialkanoyl, alkoxycarbonyl, aryloxycarbonyl, aryloxycarbonyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E2F activity; inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                                                                                Score 67; DB 19; Length 28;
Pred. No. 0.0015;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "N-terminal lauroyl"
                                                                                                                                                                                                                                                            100.08; Pred. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E2F activity inhibiting compound Ib-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mizukami T, Shibata K, Yamasaki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                           Example 3; Page 27; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Page 33; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAW57055 standard; peptide; 28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-JP03442.
                                                                                                                                                                                                                                                    44.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96JP-0259432
                                                                                                                                                                                                                                                                                                                                  15 YDALNVLMAMNIIS 28
                                                                                                                                                                                                                                                                                                                1 YDALNVLMAMNIIS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and arteriosclerosis
                                                                                                                                                                                                                   28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1998
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                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                           ;
0
                                                                                                                                                                                                                                                                                     DP-1; transcription factor; E2F protein; apoptosis; cumour; cell proliferation; cardiovascular cell; restenosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.1%; Score 64; DB 19; Length 19; 93.3%; Pred. No. 0.0028; ive 0; Mismatches 1; Indels
                                    Length 28;
                                                           Indels
                                                                                                                                                                                                                                                            DP-1 transcription factor antagonist peptide H2mt2
                                 DB 19; Le
0.0015;
hes 0;
                                   Score 67; DB 1; Pred. No. 0.0000; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        note= "R167A mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "D171A mutation"
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
2
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                                                                                                                                                                             AAW30516 standard; Peptide; 19 AA.
                                       100.0%; Fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-GB03506
                                    44.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          La Thangue NB;
                                                                                     1 YDALNVLMAMNIIS 14
                                                                                                             15 YDALNVLMAMNIIS 28
                                                                                                                                                                                                                                  (first entry)
                                 Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                              surgical stent; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROL-) PROLIFIX LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-377596/32.
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          28 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1997;
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                                                                                                                                                                                                                                 26-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bandara LR,
                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                        AAW30516;
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          Sequence
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5 YAALNVLMAMNIISK 19

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Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                 DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                  DP-1 transcription factor peptide H2mt3
                                                                                                                                                                  note= "L173R mutation"
                                                                                                                                                                                    /note= "L176R mutation"
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   Example D; Page 26; 55pp; English.
              AAW30517 standard; Peptide; 19 AA.
                                                                                                                                                                                                                                                                                              Bandara LR, La Thangue NB;
                                                                                                                                                                                                                                          97WO-GB03506
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                                                  26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                            (PROL-) PROLIFIX LTD.
                                                                                                                                                                                                                                                                                                               WPI; 1998-377596/32.
                                                                                                                                                                             Misc-difference 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 AA;
                                                                                                                                                         Miśc-difference
                                                                                                                                                                                                                                                           20-DEC-1996;
                                                                                                                                                                                                                                          22-DEC-1997;
                                                                                                                                   Homo sapiens
                                                                                                                                                                                                        W09828334-A1
                                                                                                                                                                                                                        02-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                         Synthetic
                                 AAW30517;
RESULT 14
        AAW3051
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Peptide HZmt3 is based on peptide H2 (see AAW30504) from the DEF box (see AAW30501) of transcription factor DP1. In HZmt3, amino acid residues of H2 that correspond to DP1 residues Ieu173 and Leu176 are substituted by Arg residues. H2 is an antagonist of the heterodimerisation of DP1 with E2F. H2mt3 has none of the antagonistic activity of H2. H2 and other claimed peptides (see AAW30504-07) from the DEF box region of DP1 can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g. for the prevention of restenosis.
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1 YDALNVLMAMNIISK 15 13; Conservative Best Local Similarity Matches 13; Conserva Query Match

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Gaps

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YDARNVRMAMNIISK 19

AAU72561 standard; Protein; 93 AA. AAU72561; AAU72561

26-FEB-2002 (first entry)

Arabidopsis cell cycle protein AtDPa 121-293.

Cell cycle protein; CCP; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield; immunogen; mutant;

mutein.

Arabidopsis thaliana Synthetic.

WO200185946-A2.

.5-NOV-2001

14-MAY-2001; 2001WO-IB01307.

12-MAY-2000; 2000US-204045P.

CROP-) CROPDESIGN NV

Magyar Z; De Veylder L, Acosta JAT, Inze D, Boudolf V,

WPI; 2002-062249/08.

New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators -

Example 10; Page 285; 316pp; English.

The invention relates to a novel cell cycle protein (CCP) and the copynuclectides encoding them. CCP is useful for identifying a compound witch modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for modulating the cell and polypeptide and sarbidopsis thalians, rice, wheat, cycle or growth of a plant such as Arabidopsis thalians, rice, wheat, contoled and polypeptide molecules are useful as modulating cell copynomic and candle or regulation of CCP protein forms which have decreased or treat disorders characterised by insufficient or excessive production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CC copynomic of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CC copynomic of CCP protein forms which have decreased or copynomic of CCP protein forms which in the activity of a protein forms which intitation, promulated is useful for modifying cell fate, plant development, the polymodic order of the cell cycle of a plant, initiation, promotion, seed size, seed development, tuber, fruit, leaf formation, shoot and rock sensions. And/or physiology, the length of the GC seed size, seed development, to development, to actress CCP, the polymodiccide and the anti-CCP antibody are useful in agriculture to modulate the cold, nutrient deprivation, heat, drought, salt stress such as cold, nutrient deprivation, heat, drought, salt stress or biotic cold, nutrient deprivation, heat, drought, salt stress, or biotic cold, nutrient deprivation, heat, drought, salt stress, or biotic cold, nutrient deprivation, heat, drought, salt stress, or biotic cold, nutrient deprivation, or enhance plant architecture, plant quality traits, plant creased cold attenuate plant architecture, plant quality and so the substrate of secand or serving or secand or secand or secand or secand o

93 AA; Sequence

Gapa ö 38.8%; Score 59; DB 23; Length 93; llarity 66.7%; Pred. No. 0.12; Conservative 4; Mismatches 1; Indels Local Similarity nes 10; Conserva Query Match Best Loca Matches

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85 AA;

Sequence

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Human; telomerase reverse transcriptase; TERT; Site C; Progeria; burn; repressor binding site; Hutchinson-Gilford syndrome; AIDS; cancer; acquired immunodeficiency syndrome; cardiovascular disease; osteoporosis; skin rejuvenation; immune senescence; bone marrow transplant; skin graft; neoplastic disease; TERT minimal promoter; DNA binding domain; E2F-1.
                                                                                                                                                                                    Location/Qualifiers
18..59
/label= DNA_binding_domain
                                                                                                                                                                                                                                                                                                                          Fraser S,
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 8; 66pp; English.
                                                   AAU78095 standard; Protein; 85 AA
                                                                                                   Human DNA binding domain E2F-1.
                                                                                                                                                                                                                                                                       24-AUG-2000; 2000US-227865P.
01-SEP-2000; 2000US-230174P.
05-OCT-2000; 2000US-238345P.
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||IARDKKEIRWKGLP 15
                                                                                                                                                                                                                                                       17-AUG-2001; 2001WO-US25861
                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                          Andrews WH, Foster CA,
                                                                                                                                                                                                                                                                                                          (SIER-) SIERRA SCI INC
                                                                                                                                                                                                                                                                                                                                         WPI; 2002-280952/32
                                                                                                                                                                                                                     WO200216657-A1
                                                                                   18-JUN-2002
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                       28-FEB-2002
                                                                   AAU78095;
                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                    site
                                  RESULT
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The present invention relates to a new meeting of modulating expression that includes a TERT promoter and a Site C repressor binding site. The method of the invention involves modulating TERT transcription repression by the Site C repressor binding site. The method of the invention is cuseful for modulating expression of TERT for producing a mammalian attributes. The method of the invention is useful for method is also useful in a variety of different applications, including immortalisation of cells, production of reagents for use in life science research, therapeutic applications, and therapeutic agent screening applications. Increasing TERT expression delays natural telomeric shortening and/or increases telomeric length and is useful for treating disease conditions such as Progeria or Hutchinson-Gilford syndrome, acquired immunodeficiency syndrome (AIDS), cardiovascular disease, osteoporosis, in skin rejuvenation and to inhibit immune senescence. The method can be employed to lengthen telomerse of osteoblast and osteoclast stem cells, encouraging bone replacement and proper remodeling and reinforcement, and can thus be used in bone marrow transplants for the treatment of cancer and skin grafts for burn victims and as such the method improves the survival and effectiveness of bone marrow and skin cell transplants. Decreasing TERT expression is useful for treating cellular proliferative disease conditions, including cellular proliferative disease conditions, including cequence represents the human DNA binding domain E2F-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to a new method of modulating expression
Modulating expression of telomerase reverse transcriptase (TERT) in a
                                                                            cell, for regulating proliferative capacity of a cell, involves modulating TERT transcription repression by Site C repressor binding
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RESULT 18 AAW30511

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                                                                                                                                                                                                                                                                                         Telomerase reverse transcriptase; TERT; Site C repressor; transcription; cytostatic; immunostimulant; anti-HIV; vulnerary; telomerase; human; repressor protein; E2F-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to modulating expression of telomerase reverse transcriptase (TERT) expression system that includes a TERT promoter and a Site C repressor binding site. The method involves modulating TERT transcription repression by the Site C repressor binding site. The methods and compositions of the present invention are useful for the immortalization of cells, production of reagents in life science iresearch, therapeutic agent screening applications, diagnosis and treatment of disorders associated with aberrant telomerase activity such as cancer, Progeria, immune senescence, HIV, and in skin rejuvenation. The present sequence represents the DNA binding domain of a repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating expression of telomerase reverse transcriptase TERT by blocking repression of TERT transcription, useful for the diagnosis and treatment of disorders associated with aberrant telomerase activity
                                   Gaps
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   Length
                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrews WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
    23;
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Score 55.5; DB
Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.5%; Score 55.5; DB 44.0%; Pred. No. 0.4;
                                 6; Mismatches
                                                                                                                                                                                                                                                              Repressor protein E2F-1 DNA binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mohammadpour H,
                                                              24
                                                                               || ||| ::|:| |:|| XDITNVLEGIQLIAKKSKNHIQWLG 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDITNVLEGIQLÍAKKSKNHÍQWLG 83
                                                              1 YDALNVLMAMNIISKE-KKEIKWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 7; 47pp; English.
                                                                                                                                                                       ABB82986 standard; Protein; 85 AA
   36.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-2002; 2002WO-US17959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2001; 2001US-29692P.
                                                                                                                                                                                                                                14-APR-2003 (first entry)
                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SIER-) SIERRA SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     such as cancer and HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-167401/16.
   Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 AA;
                                                                                                                                                                                                                                                                                                                                                                                      WO2002101010-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein E2F-1.
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foster CA,
                                                                                                                                                                                                  ABB82986;
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                                   Matches
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                                                                                                                                        RESULT 17
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Mohammadpour H;

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2000US-0232401.
2000US-0233063.
2000US-0233064.
2000US-0233065.
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2000US-0229344.
2000US-0229345.
2000US-0229345.
2000US-0229519.
2000US-0230437.
2000US-0231243.
2000US-0231243.
2000US-0231244.
2000US-0231244.
2000US-0231244.
2000US-0231244.
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2000US-0235484.
2000US-0235834.
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2000US-0231968.
2000US-0232397.
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2000US-0225214.
2000US-0225266.
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2000US-0225758.
2000US-0225759.
2000US-0226279.
2000US-0226681.
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2000US-0227009.
2000US-0228924.
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2000US-0224519.
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2000US-0198123
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2000US-0220963.
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2000US-0189874
                                                   17-JAN-2001; 2001WO-US01338
           WO200155367-A1
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08-SEP-2000;
08-SEP-2000;
                                                                                                                 16-MAR-2000; 2
17-MAR-2000; 2
18-APR-2000; 2
19-MAY-2000; 2
                                                                                                                                                                                                                                                                                                  14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                         11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antibarasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system.
                                                                                                                                                                                                                                                                                                                                                                        Peptide H6 comprises amino acid residues 167-180 in the DEF box region (see AAW30501) of transcription factor DP1. Unlike claimed peptides (see AAW30504-07) that contain one or both of 2 motifs (see AAW30502-03) of the DP1 DEF box, peptide H6 is not capable of antagonising the heterodimerisation of a DP protein with an E2F protein. The claimed peptides, their variants and fusion proteins can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g. to prevent restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                          Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human musculoskeletal system related polypeptide SEQ ID NO 1380.
                                                                                 DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.2%; Score 55; DB 19; Length 14; 100.0%; Pred. No. 0.056; ive 0; Mismatches 0; Indels
                                                                  DP-1 transcription factor peptide H6
                                                                                                                                                                                                                                                                                                                                                         Example C; Page 41; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB03433 standard; Protein; 29 AA
     AAW30511 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                96GB-0026589
                                                                                                                                                                                                          97WO-GB03506
                                                                                                                                                                                                                                                                         La Thangue NB;
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                                                26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.2
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YDALNVLMAMN 11
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                                                                                                                                                                                                                                                    (PROL-) PROLIFIX LTD
                                                                                                                                                                                                                                                                                             WPI; 1998-377596/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                        Bandara LR,
                                                                                                                                              Homo sapiens
                                                                                                                                                                  WO9828334-A1
                                                                                                                                                                                                          22-DEC-1997;
                                                                                                                                                                                                                              20-DEC-1996;
                                                                                                                                                                                       02-JUL-1998
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                                                                                                                                    Synthetic
                            AAW30511;
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20-0CT-2000; 2000US-0241786.
20-0CT-2000; 2000US-0241786.
20-0CT-2000; 2000US-0241809.
20-0CT-2000; 2000US-0241809.
20-0CT-2000; 2000US-0241809.
20-0CT-2000; 2000US-0241809.
20-0CT-2000; 2000US-0244617.
08-NOV-2000; 2000US-0246475.
08-NOV-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246528.
08-NOV-2000; 2000US-0246519.
27-SEP-2000; 2000US-0235836.
29-SEP-2000; 2000US-0235327.
29-SEP-2000; 2000US-023567.
29-SEP-2000; 2000US-02356867.
29-SEP-2000; 2000US-0235369.
29-SEP-2000; 2000US-0236370.
02-OCT-2000; 2000US-02370370.
02-OCT-2000; 2000US-0237039.
02-OCT-2000; 2000US-0239935.
13-OCT-2000; 2000US-0239937.
20-OCT-2000; 2000US-0239937.
20-OCT-2000; 2000US-0239937.
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2000US-0251030
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KW cardiovascular condition; burneausers, mineral content;

KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;

KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;

KW post-operative tissue repair; limb regeneration; neuronal growth;

ALDS-related complex; chondrocyte growth; bone regeneration;

KW keratincyte growth; hair loss; melanocyte growth; cell profileration;

KW keratincyte growth; hair loss; melanocyte growth; cell profileration;

KW weight; hair colour; eye colour; skin; percentage of adipose tissue;

KW depression; tendency for violence; pain; reproductive capability;

KW depression; tendency for violence; pain; reproductive capability;

KW arbohydrate content; vitamin content; protein content;

KW arrivitional comment;

KW arrivitional content; vitamin content; content;
                                                                                                                                                                                                                                                              The invention relates to novel genes (AALJ4669-AALJ7666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, of gastrointestinal tract, luyer, lung, or urogenital; (b) immune asservants and search and search and sisease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myccardial isochaemias; (d) wound the soling; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                         Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    healing; (e) neurological diseases e.g. cerebral anoxia and epile
and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                      Claim 11; SEQ ID NO 1380; 781pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.2%; Score 52; DB 22; Length 29; 62.5%; Pred. No. 0.41; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Musculoskeletal system antigen; cancer; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human musculoskeletal system antigen #347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU12727 standard; Protein; 29 AA.
Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 MNIISKEKKEIKWIGL 25
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4atches 10; Conservative
Barash SC,
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                                          WPI; 2001-451937/48.
N-PSDB; AAL35015.
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Rosen CA,
                                                                                                                                                                                diagnosis
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US2002147140-A1 Homo sapiens

(HUMA-) HUMAN GENOME SCI INC

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or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis con ulcus, sock-operative tissue repair, and ulcers; stimulates angiogenesis conditions, such as, Alzheimer's disease, Parkinson's disease, and limb regeneration; stimulates conditions, such as, Alzheimer's disease, Parkinson's disease, and Albs-related complex; stimulates chondrocyte growth, thus they can be conditions, such as, Alzheimer's disease, Parkinson's disease, transports or bone grafts; prevents skin aging due to subburn by transports or bone grafts; prevents skin aging due to subburn by constitution grafts and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone constructed and differentiation of for supporting cells and bone constructed incombination with other cytokines; maintains organs before transplantation or for supporting cells and bone constructed increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation, size, and shape colour, skin, percentage of adipose tissue, pigmentation, size, and shape colour, skin, percentage of adipose tissue, pigmentation, size, and shape colour, skin, percentage of adipose tissue, pigmentation, size, and shape carteadic integery); modulates mammalian elements of printies of carteadic rhythms, depression, tendency for violence, tolerance for pain, carteadic rhythms, depression, tendency for violence, tolerance for printed specification, but was obtained in electronic format directly format directly format the sequence date for this patent did not form part of the parent of the parent of the patent of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; telomerase reverse transcriptase; TERT; Site C; Progeria; burn; repressor binding site; Hutchinson-Gilford syndrome; AIDS; cancer; acquired immunodeficiency syndrome; cardiovascular disease; osteoporosis; skin rejuvenation; immune senescence, bone marrow transplant; skin graft; neoplastic disease; TERT minimal promoter; DNA binding domain; E2F-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.2%; Score 52; DB 24; Length 29; 62.5%; Pred. No. 0.41;
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/label= DNA_binding_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 MNIISKEKKEIKWIGL 25
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Best Local Similarity 62.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Domain
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AAU78096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer
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22-A0G-2000; 2000US-228954P.
01-SEP-2000; 2000US-228954P.
01-SEP-2000; 2000US-228934P.
01-SEP-2000; 2000US-229344P.
01-SEP-2000; 2000US-229344P.
01-SEP-2000; 2000US-229509P.
05-SEP-2000; 2000US-229509P.
21-SEP-2000; 2000US-23959P.
21-SEP-2000; 2000US-23495P.
22-SEP-2000; 2000US-23495P.
23-SEP-2000; 2000US-23495P.
23-SEP-2000; 2000US-23636P.
23-SEP-2000; 2000US-23636P.
23-SEP-2000; 2000US-23636P.
23-SEP-2000; 2000US-23636P.
23-SEP-2000; 2000US-23636P.
23-SEP-2000; 2000US-23636P.
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2000US-237037P.
2000US-237039P.
2000US-237039P.
2000US-237040P.
2000US-239935P.
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2000US-241809P.
2000US-244617P.
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2000US-225270P.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABX58003
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14-AUG-2000;
14-AUG-2000;
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Synthetic.
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                                                                                                                                                                                                                     of telomerase reverse transcriptus (TERN) from a TERT expression system controlleds a TERT promoter and a Site C repressor binding site. The method of the invention involves modulating TERT transcription repression by the Site C repressor binding site. The method of the invention is useful for modulating expression of TERT for producing a mammalian antibody. The method is also useful in a variety of different applications, including immortalisation of cells, production of reagents of the repension of the reagents applications. Increasing TERT expression therapeutic agent exceening applications. Increasing TERT expression delays natural telomeric shortening and/or increasing TERT expression is useful for treating disease conditions such as Progeria or Hutchinson-Gilford syndrome, acquired immunodeficiency syndrome (AIDS), cardiovascular disease, osteoporosis, in skin rejuvenation and to inhibit immune sensecence. The method can be employed to lengthen telomerse of osteoblast and osteoclast stem cells, encouraging bour replacement and proper remodeling and reinforcement, and can thus be used in bone marrow transplants for the treatment of cancer and skin grafts for burn anyther and every victime and as such the method improves the survival and effectiveness of
                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for treating cellular proliferative disease conditions, including neoplastic disease conditions e.g. cancer. The present amino acid sequence represents the human DNA binding domain E2F-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Telomerase reverse transcriptase; TERT; Site C repressor; transcription; cytostatic; immunostimulant; anti-HIV; vulnerary; telomerase; human;
                                                                                                                                                                                                             present invention relates to a new method of modulating expression
                                                                                                                 Modulating expression of telomerase reverse transcriptase (TERT) in scell, for regulating proliferative capacity of a cell, involves modulating TERT transcription repression by Site C repressor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.2%; Score 50.5; DB 23; Length 76; 42.3%; Pred. No. 2.3; tive 5; Mismatches 9; Indels :
                                                                Mohammadpour H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repressor protein E2F-4 DNA binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YDALNVLAMANNIISKE-KKEIKWIGL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser S,
                                                                                                                                                                                   Disclosure; Page 8; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB82987 standard; Protein; 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-2002; 2002WO-US17959.
01-SEP-2000; 2000US-230174P. 05-OCT-2000; 2000US-238345P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                Andrews WH, Foster CA,
                                      (SIER-) SIERRA SCI INC
                                                                                          WPI; 2002-280952/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 AA;
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and
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to modulating expression of telomerase reverse transcriptase (TERT) expression system that includes a TERT promoter as Site C repressor binding site. The method involves modulating TERT transcription repression by the Site C repressor binding site. The methods and compositions of the present invention are useful for the immortalization of cells, production of reagents in life science research, therapeutic agent screening applications, diagnosis and treatment of disorders associated with aberrant telomerase activity su as cancer, Progeria, immune senescence, HIV, and in skin rejuvenation. The present sequence represents the DNA binding domain of a repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 76;
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                                                                                                                     Andrews WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.2%; Score 50.5; DB 24;
42.3%; Pred. No. 2.3;
tive 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mizukami T, Shibata K, Yamasaki M, Yoshida T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "C-terminal amide"
                                                                                                                     Mohammadpour H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YDALNVLMAMNIISKE-KKEIKWIGL 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E2F activity inhibiting compound Ib-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 7; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z
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07-JUN-2001; 2001US-296992P.
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les 11; Conservative
                                                       (SIER-) SIERRA SCI INC.
                                                                                                                  Fraser S,
                                                                                                                                                                         WPI; 2003-167401/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 AA;
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                                                                         This represents a compound that can inhibit E2F activity. The compound is of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                                                                                    Gaps
activity inhibitors - for treatment and prevention of tumours arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver
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                                                                                                                                                                                                                                                Score 49; DB 19; Length 15;
Pred. No. 0.56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human liver peptide, SEQ ID No 37013.
                                                        Example 4; Page 28; 52pp; Japanese.
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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nes 10; Conservative
                                                                                                                                                                                                                                                                                                                     1 YDALNVLMAM 10
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                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488898/53
                                                                                                                                                                                                                               15 AA;
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21-SEP-2000; 2
27-SEP-2000; 2
04-OCT-2000;
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                                                                                                                                                                                                                               Sequence
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
               is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at [tp.wipo.int/pub/published_pct_sequences.
hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
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                                                                                                                                                                                                                                                                                                                                                                                                        probe.
                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                             Peptide #10461 encoded by human foetal liver single exon probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a single exon nucleic acid probe for
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                                                                                                                               Length
                                                                                                                                                             Indels
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                                                                                                                                    22 ;
                                                                                                                                                             7;
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Pred. No. 13;
8; Mismatches
                                                                                                                                    DB
                                                                                                                                 30.6%; Score 46.5; I
36.0%; Pred. No. 13;
tive 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR;
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                                                                                                                                                                                                          || :||| ::|| ::::| | : | | XDIVNVLESLHLVSRVAKNQYGWHG 31
                                                                                                                                                                                           1 YDALNVLMAMNIISK-EKKEIKWIG
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                                                                                                                                                                                                                                                                                               ABB42955 standard; Peptide; 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.6%;
36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312
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                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483447/52
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hes 9; Conserv
                                                                                                                                                   Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 AA;
                                                                                                          96 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                        04-FEB-2002
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                                                                                                                                                                                                                                                                                                                             ABB42955;
                                                                                                            Sequence
                                                                                                                                     Query Match
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Matches
                                                                                                                                                                                                                                                                       RESULT 25
                                                                                                                                                                                                                                                                                    ABB4295
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RESULT 26

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AAM63859

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #10814 encoded by probe for measuring placental gene expression.
                                 Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
Human bone marrow expressed probe encoded protein SEQ ID NO: 36978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO: 36978; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.6%; Score 46.5; DB 22; 36.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
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26-MAY-2000; 2000US-0207456.
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                                                                                                                                                                                                                                                                   03-AUG-2000; 2000US-0632366
21-SEP-2000; 2000US-0234687
27-SEP-2000; 2000US-0236359
                                                                                                                                                                                    30-JAN-2001; 2001WO-US00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488900/53
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 AA;
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                                                                                                                  WO200157276-A2
                                                                                   Homo sapiens
                                                                                                                                                                                                                    04-FEB-2000;
                                                                                                                                                                                                                                     26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probes which are derived from enables expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                    Human brain expressed single exon probe encoded protein SEQ ID NO: 35964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                     Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 35964; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.6%; Score 46.5; 36.0%; Pred. No. 13
                    | | : | | | :::::|: | : | | XDIVNVLESLHLVSRVAKNQYGWHG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YDALNVLMAMNIISK-EKKEIKWIG 24
 YDALNVLMAMNIISK-EKKEIKWIG 24
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                                                                                                                  AAM63859 standard; Protein; 96 AA
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27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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2000US-0608408.
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les 9; Conserv
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                                                                                                                                                                                                                                                                                        epilepsy; cancer
                                                                                                                                                                                                                                                                                                                                                      WO200157275-A2
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RESULT 27

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AAM76672 ID AAM7 XX AC AAM7 XX DT 06-N

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Gaps

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The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human peptide encoded by genome-derived single exon probe SEQ ID 35546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; gaucher's disease; Niemann-Pick disease; hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
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                                                                                                                                                                                                                                                                                                                                              Score 46.5; DB 22; Length 96;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
                                                                                                                                                                                                  Claim 27; SEQ ID No 37046; 654pp; English.
                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                       1 YDALNVLMAMNIISK-EKKEIKWIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                31
                                                                                                                                                                                                                                                                                                                                                                                                                          7 YDIVNVLESLHLVSRVAKNQYGWHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG45881 standard; Peptide; 96 AA
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                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                     30.6%;
36.0%;
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2000US-0608408.
2000US-0632366.
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          03.AUG-2000; 2000US-0632366.
21.SEP-2000; 2000US-0234687.
27.SEP-2000; 2000US-0236359.
04.OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyaline membrane disease
                                                                                                                                                                                                                                                                                                  human genetic disorders.
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                         Hanzel DK,
                                                                                                                                   WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                             96 AA
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                         Penn SG,
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a cample derived from human lung; measuring gene expression in a cample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising of the eukaryote; and (b) detecting at least one exon from genomic sequences of the eukaryote; and (b) detecting at least one exon from genomic sequences of the eukaryote; and probe is included in the above mentioned microarray; assigning exons to a single exon probe; in the above mentioned microarray; assigning exons to a single exon in the above mentioned microarray; assigning exons to a single exon in the above mentioned microarray; assigning exons in the probe is included comprising (a) identifying exons from genomic sequence by the method contrary and the axons in the tissues and/or cell types using hybridisation, or encoded by the expression of the exons in the tissues and/or cell types indicates the exons should be assigned to a single gene; a peptide comprising one of 1011 sequences, mentioned in the specification, or encoded by the manylais, and for identifying exons in a gene, particularly cusing human lung derived mikh and for the study of lung disease (OPD), interstitial lung disease (LID), familial idiopathic pulmonary alveolar protein probes are used for gene probes of microded by a single 
                                                                               Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            te: The sequence data for this patent did not form part
the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Similarity 36.0%; Pred. No. 13;
9; Conservative 8; Mismatches 7:
                                                                                                                                                       claim 27; SEQ ID No 35546; 634pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YDALNVLMAMNIISK-EKKEIKWIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDIVNVLESLHLVSRVAKNQYGWHG 31
  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from WIPO at
  Hanzel DK,
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Best Local Similarity
                                              WPI; 2002-114183/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 AA;
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    SG,
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      셤
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Gaps

1;

E2F; soybean; cell cycle regulatory protein; transcription factor; herbicide.

protein fragment.

Soybean E2F

EXXXXXXXXXX

01-FEB-2000 (first entry)

AAY32167;

AAY32167 standard; Protein; 80 AA

RESULT 30 AAY32167 /label= Unknown 25

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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP29212;
                                                                                                                                                                                                                                                                                                                                                           activity.
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 32
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                This sequence represents 10% of the middle region of soybean cell cycle regulatory protein E2F, as deduced from an isolated C coll cycle regulatory protein E2F, as deduced from an isolated C coll cycle (Fig. 1992). The invention relates to nucleic acid fragments (see AAZ34575-83) encoding plant CDC-16, DP-1, DP-2 and E2F cell cycle regulatory proteins (see AAY3155-67). It also creates to the construction of a chimeric gene encoding all or a portion of the cell cycle regulatory protein, in sense or antisense corientation, where expression of the chimeric gene results in producton of altered levels of the cell cycle regulatory protein in a transformed host cell. The nucleic acids and proteins may be used to facilitate studies of cell cycle regulation in plants, convide genetic tools to enhance cell growth in tissue culture, concrease gene transfer efficiency and provide more stable transformations. The proteins may also provide targets to facilitate design and/or identification of cell cycle regulatory corrections that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wheat, transcription factor, TME2F, plant retinoblastoma, plant E2F, Rb protein, cell cycle regulation; plant growth regulation, DNA replication; differentiation, E2F-derived peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                           29.9%; Score 45.5; DB 20; Length 80; 39.1%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                        Sakai H;
                                                                                                                                                                                          Plant-derived cell cycle regulatory proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                       odell JT,
                                                                                                                                                                                                                Claim 20; Page 44-45; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || :||| :: ::| | : |
YDIVNVLESIGVLSRKAKNQYTW 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YDALNVLMAMNIIS-KEKKEIKW 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY44493 standard; peptide; 28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Unknown
Misc-difference 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wheat E2F derived peptide-1.
                                                                                             98US-0081132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 39.1
les 9, Conservative
                                                                                                                                      Klein TM, Morakinyo LO,
                                                                                                                                                            WPI; 1999-633830/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum monococcum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 2
                                                                                                                                                                                                                                                                                                                                                                                                                       80 AA;
                                                                                                                                                                      N-PSDB; AAZ34583
                               WO9953075-A2
                                                                        08-APR-1999;
                                                                                             09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-2000
           Glycine max.
                                                    21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44493;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a peptide comprising DNA-binding domain of wheat ESF protein that was identified in a wheat cDNA library by yeast two-hybrid screening. The E2F is a transcription factor that interacts with plant retinoblastoma (Rb) and is involved in cell cycle regulation. The present sequence has the ability to bind to E2F binding site in plant DNA and is used to control plant growth, cellular DNA replication, cell cycle progression, differentiation and development by altering its DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulating plant growth and/or cellular DNA replication and/or cell cycle progression, differentiation and development using a plant E2F polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.6%; Score 43.5; DB 21; 43.5%; Pred. No. 9.2; rative 3; Mismatches 9;
                                                                                                                                                                                                                                                                                                           (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                      Ramirez Parra E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus polypeptide SEQ ID NO 7600.
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YDITNVLEGIXLIEKXXKNXIRW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YDALNVLMAMNIISK-EKKEIKW 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 26; 45pp; English.
/label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP29212 standard; Protein; 51
                                                                                                                                                                                                                                                                                                                                                                      Xie Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                      Gutierrez-Armenta C,
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-116290/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200234771-A2.
                                                       WO9958681-A2
                                                                                                                                                                 07-MAY-1999;
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18-DEC-1997;
18-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                         streptococcus/GBS (Streptococcus agalacties) or group A streptococcus/GBS (Streptococcus/GBS GBS GBS), given in the proteins have antibacterial and antibiliammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71256 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detecrmine whether a compound binds to (I). A composition comprising (I) on a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromosomy and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                            New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                   invention relates to a protein (ABP25413-ABP30895) from group B
                       Margarit Ros YI, Grandi G, Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
                                                                                                                                                                                                                                                                                                                                                                                                            28.3%; Score 43; DB 23; Length 51; 38.5%; Pred. No. 23; cive 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DP-1 transcription factor antagonist peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNVLMAMNIISKEK----KEIKWIGL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNLLVAFLCMLREKTQINQEVKWLCL 43
                                                                                                                                            Claim 1; Page 3899; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW30502 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-GB03506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bandara LR, La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 38.5'
Matches 10; Conservative
                       Masignani V,
 (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PROL-) PROLIFIX LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-377596/32.
                                                           WPI; 2002-352536/38
                                                                                                                                                                                                                                                                                                                                                                                       51 AA;
                                                                        N-PSDB; ABN69843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-DEC-1996;
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                                     rettelin H;
                        ۵,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW30502;
                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                        Telford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
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                                                                                                                                                                                                     This peptide comprises amino acid residues 175-183 in the DEF box region (see AAW30501) of transcription factor DP1. Claimed peptides (11) (see AAW30502-07) containing this and/or another motif (see AAW30503) of the DEF box, are antagonists of the heterodimerisation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially containing substitutions of residues of corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (1) or (II) and a membrane translocation sequence (see AAW30508), expression vectors encoding (1)-(III) and specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical sents comprising (1)-(III) are used therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical sents comprising (1)-(III) are used therapeutically to induce apoptosis, thave undergone angioplasty. (1)-(III) function by inactivating the binding activity of DP/E2F heterodimers. They are also indentifying antagonists, as positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunoassay agents. Also described is the use of sequences antisense to nucleic acids encoding (1)-(III) to control DP levels in cells, or cytostatic agents, (1)-(III) enhance cell killing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitative disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; disorder; endocrine disorder; infection; AlDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.6%; Score 42; DB 19; I
100.0%; Pred. No. 9.3e+05;
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                                                                                                                                                      Claim 3; Page 44; 55pp; English.
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97US-0068006.
97US-0068007.
97US-0068053.
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97US-0068054.
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2000US-0230438.
2000US-0231242.
2000US-0231243.
2000US-0231244.
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2000US-0231414.
2000US-0232080.
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2000US-0216880.
2000US-0217487.
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2000US-0218290.
2000US-0220963.
2000US-0220964.
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2000US-0224519.
2000US-0225213.
2000US-025214.
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2000US-0225267.
2000US-0225268.
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2000US-0225757.
2000US-0225758.
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2000US-0226681.
2000US-0226868.
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2000US-0229345.
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2000US-0234274
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2000US-0236369
    17-JAN-2001; 2001WO-US01334
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2000US-0229343
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14-AUG-2000;
14-AUG-2000;
                                                     24-FEB-2000;
02-MAR-2000;
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    AAX97916 to AAX98029 represent 110 isolated human secreted protein
genes. AAY36224 to AAY36727 represent the secreted proteins encoded by
the 110 human genes. The genes and their corresponding secreted
polypeptides are useful for preventing, treating or ameliorating medical
conditions, e.g. by protein or gene therapy. Also pathological conditions
can be diagnosed by determining the amount of the new polypeptides in a
sample or by determining the presence of mutations in the new genes.
Specific uses are described for each of the 110 genes, based on which
itssues they are most highly expressed in, and include developing
products for the diagnosis or treatment of cancer, tumours, developmental
abnormalities and foetal deficiencies, blood disorders, diseases of the
immune system, autoimmune diseases, inflammation, allergies, Alzheimer's
and cognitive disorders, scherosclerosis, diabetes, cardiovascular
clisorders, kidney disorders, digestive/endocrine disorders, infections
and AIDS. The polypeptides are also useful for identifying their binding
partners. The sequences given in AAX97907 to AAX97915 and AAX3623 are
used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirhemmatic; hepatotropic; cerebroprotective; antiinflammatory; antiillergic; antidiabetic; antiuloer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches 10; Indels
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                                                                                         Carter KC, Duan RD, Feng P, Ferrie AM, Florence C; Florence K, Greene JM, Janat F, Kyaw H, Moore PA; Ni J, Rosen CA, Ruben SM, Shi Y, Soppet DR, Wei Y; Yu G;
                                                                                                                                                                                         New isolated human genes encoding secreted polypeptides
                                                                                                                                                                                                                      Disclosure; Page 526; 537pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 NVLMAMNIISKEKKEIKWIGLPTN 28
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                        97US-0068365.
97US-0068367.
97US-0068368.
                                                                             (HUMA-) HUMAN GENOME SCI INC
 97US-0070923.
97US-0068169.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 29.2<sup>3</sup>
Matches 7; Conservative
                                                                                                                                                                    WPI; 1999-418749/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 AA;
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18-DEC-1997;
19-DEC-1997;
19-DEC-1997;
19-DEC-1997;
19-DEC-1997;
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Ruben SM;
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08-NOV-2000; 2000US-0246528.

08-NOV-2000; 2000US-0246609.

08-NOV-2000; 2000US-0246610.

08-NOV-2000; 2000US-0246611.

08-NOV-2000; 2000US-0246611.

08-NOV-2000; 2000US-0249611.

17-NOV-2000; 2000US-0249209.

17-NOV-2000; 2000US-0249209.
29-SEP-2000; 2000US-0236370.
02-OCT-2000; 2000US-0236012.
02-OCT-2000; 2000US-0237039.
02-OCT-2000; 2000US-0237039.
03-OCT-2000; 2000US-0237039.
13-OCT-2000; 2000US-0237039.
13-OCT-2000; 2000US-0237039.
20-OCT-2000; 2000US-0241785.
20-OCT-2000; 2000US-0241785.
20-OCT-2000; 2000US-0241785.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-024181.
08-NOV-2000; 2000US-0246475.
08-NOV-2000; 2000US-0246525.
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05-DEC-2000; 2000US-025119.
06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
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17-NOV-2000; 2000US-0249210.
17-NOV-2000; 2000US-0249211.
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17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249215.
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2000US-0249218.
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17-NOV-2000;
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WPI; 2001-541565/60. N-PSDB; ABA13620.

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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are used isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful. The nucleic acids, proteins, antibodies and (ant) agonists are useful. The nucleic acids, proteins, antibodies and (ant) agonists are useful. The nucleic acids, proteins, antibodies and (ant) agonists are useful. The nucleic and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (D) immune disorders e.g. Addison's disease, allergies, autoimmune characters e.g. Addison's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections diseases such as viral, bacterial, fungal printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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                                                                               Claim 11; SEQ ID NO 5951; 1701pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a Chlamydia trachomatis protein.
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97FR-0015041.
97FR-0016034.
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17-DEC-1997;
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AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genttal diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, as and veneral lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
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                                                                                                                                                                                                                                               27.6%; Score 42; DB 20; Length 91;
56.2%; Pred. No. 66;
tive 0; Mismatches 7; Indels
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2000US-0608408.
2000US-0632366.
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es 9; Conservative
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                                                                                                                                                                                                               91 AA;
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21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to
                                                                                                                                                    Gaps
human liver single exon encoded peptides of the invention.

Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #2310 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
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                                                                                                                                                                                                                                                                                                                                                                                                                                      microarray; single exon probe; gene expression; breast;
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                                                                                                                   Length 75;
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40.0%; Pred. No. 63;
tive 4; Mismatches
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                                                                                                                                                                                                                                                                                                      ABB29659 standard; Peptide; 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0608408
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2000US-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0236359
2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-496933/54.
                                                                                                                                 Local Similarity
                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157271-A2
                                                                                    75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                     ABB29659;
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                                                                                    Sequence
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY
                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                   RESULT 38
                                                                                                                                                                                                                                                                                                       8 x 3 3 3 3
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(first entry)

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protein #2256 encoded by probe for measuring heart cell gene expression.
                                                                                                                             gene expression; heart; microarray; vascular system; vascular disease; hypertension; cardiac arrhythmia;
                                      ABB20257 standard; Protein; 75
                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00666.
                                                                                                                                                                                                                                                                                                                   21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                        congenital heart disease.
                                                                                                                                                                                                                                                                                     26-MAY-2000; 30-JUN-2000; 203-AUG-2000; 2
                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                            04-OCT-2000;
                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                     23-JAN-2002
                                                                                                                                                                                                                             09-AUG-2001.
                                                                 ABB20257;
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                             ABB2025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human feetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 27472; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                 Peptide #2343 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 75;
                                                                     Length 75;
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41.5; DB 22;
Pred. No. 63;
4; Mismatches 3;
                                                                      DB 22;
                                                                                           3;
                                                                                 Pred. No. 63;
4; Mismatches
                                                                      27.3%; Score 41.5; 40.0%; Pred. No. 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                   ABB34837 standard; Peptide; 75 AA.
                                                                                                                   13 ISKEKKEIKWIG----LPT 27
                                                                                                                                    |:||| ::| | : : | ITKEKSSLRWAGKKFEEIPT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                  (first entry)
                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483447/52
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hes 8; Conserv
                                                                       Query Match
Best Local Similarity
                                                    75 AA;
                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                  04-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                             ABB34837;
                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                      Best Loc
Matches
                                                                                                                                                                                 RESULT 39
                                                                                                                                                                                             ABB34837
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2000US-0608408. 2000US-0632366.

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                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying. Seque expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, human heart and vascular system e.g. cardiovascular diseases of the human heart and vascular system e.g. cardiovascular disease. Hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 75;
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40.0%; Pred. No. 63;
tive 4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                   Claim 15; SEQ ID No 22027; 530pp; English.
                                                      Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM55645 standard; Protein; 75 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 ISKEKKEIKWIG----LPT 27
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31 ITKEKSSLRWAGKKFEEIPT 50
(MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.0
Matches 8; Conservative
                                                                Hanzel DK,
                                                                                                                         WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM55645;
                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Indels

13 ISKEKKEIKWIG----LPT 27 |:||| ::|| ::|| 31 ITKEKSSLRWAGKKFERIPT 50

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Conservative

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #2277 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                   genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 28331; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                 analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.3%; Score 41.5; DB ilarity 40.0%; Pred. No. 63; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                                                                                                                                                  Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISKEKKEIKWIG----LPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITKEKSSLRWAGKKFEEIPT 50
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                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
   30-JAN-2001; 2001WO-US00668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM15843 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312
                                                   2000US-0207456
2000US-0608408
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2000US-0608408
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                                                                                2000US-0632366
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2000GB-0024263
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2000US-0236359
                                                                                                   2000US-0234687
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                                                                                                                                                                                                  Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488901/53
                                                                                                                                                                                                                                  WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157278-A2.
                                                                                                21-SEP-2000; 27-SEP-2000; 204-OCT-2000; 2
                                                                                03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000;
                                  04-FEB-2000;
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                                                   26-MAY-2000;
                                                                  30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
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                                                                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                Human brain expressed single exon probe encoded protein SEQ ID NO: 27750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                 Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human bone marrow expressed probe encoded protein SEQ ID NO: 28331.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM68025 standard; Protein; 75 AA
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|TKEKSSLRWAGKKFEEIPT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00667.
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2000US-0608408.
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 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                   epilepsy; cancer
                                                                                                                                                                 WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157276-A2
                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                  26-MAY-2000;
30-JUN-2000;
                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000;
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05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                  09-AUG-2001
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Gaps

2 75;

3;

Length Indels

for

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The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived
                                                                            The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #2390 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID No 28622; 654pp; English.
                                                                                                                                                                                                                                                                                                        27.3%; Score 41.5; D
40.0%; Pred. No. 63;
tive 4; Mismatches
                                                      Claim 27; SEQ ID No 20669; 487pp; English.
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31 ITKEKSSLRWAGKKFEEIPT 50
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2000US-0234687.
2000US-0236359.
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 40.0.
Best Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488897/53
                                                                                                                                                                                                                                                                               75 AA;
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27-SEP-2000;
04-OCT-2000;
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                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                      Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel single exon nucleic acid probe used to measuring gene expression in a human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                            Peptide #2263 encoded by probe for measuring breast gene expression.
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27.3%; Score 41.5; Dest Local Similarity 40.0%; Pred. No. 63; Matches 8; Conservative 4; Mismatches
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                                                                                           Pred. No. 63;
4; Mismatches
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Pred. No. 63
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                                                                                                                                        13 ISKEKKEIKWIG----LPT 27
                                                                                                                                                            31 ITKEKSSLRWAGKKFEEIPT 50
                                                                                                                                                                                                                                             AAM03581 standard; Protein; 75
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04-OCT-2000; 2000GB-0024263.
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21-SEP-2000; 2000US-0234687.
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30-JUN-2000; 2000US-0608408.
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                                                                                  27.3%;
40.0%;
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                                                                       Query Match
Best Local Similarity 40.v.
Rest Local Similarity
Si Conservative
                        human genetic disorders.
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                                                          Sequence
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Gaps

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13 ISKEKKEIKWIG----LPT 27 |:||| ::| || :|| 31 ITKEKSSLRWAGKKFEEIPT 50

Search completed: February 17, 2004, 10:53:43 Job time : 58.0297 secs

(OTYSU) XMALIB BDAY SIHT

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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February 17, 2004, 10:50:12; Search time 13.3069 Seconds (without alignments) 83.497 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-900-147-7 31

1 ALNVLMA 7 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 segs, 158726573 residues Searched:

717921 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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| SIDSI/gcgda /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SITMMARTES

Description	DP-1 transcription	DP-1 transcription	E2F activity inhib	DP-1 transcription	DP-1 transcription	DP-1 transcription	E2F activity inhib	E2F activity inhib	DP-1 transcription
QI	AAW30503	AAW30511	AAW57052	AAW30506	AAW30516	AAW30504	AAW57051	AAW57055	AAW30507
80	19	13	13	13	13	13	13	19	13
* Query Match Length DB ID	7	14	15	16	19	19	28	28	30
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	31	31	31	31	31	31	31	31	31
Result No.		7	e	4	S	9	7	œ	σ

Polypeptide fragments of the DP-1 transcription factor - used for

Bandara LR, La Thangue NB;

WPI; 1998-377596/32.

(PROL-) PROLIFIX LTD.

100.0 37 19 AAW30501 100.0 83 20 AAV32163 87.1 19 12 AAW30515 87.1 19 23 AAW722618 87.1 19 41 21 AAW30515 83.9 90 21 AAW303284 80.6 59 22 AAW304066 80.6 87 22 AAW304066 80.6 87 23 AAW304066 80.6 87 23 AAW3030 77.4 25 20 AAW3308 77.4 25 20 AAW3308 77.4 25 20 AAW3308 77.4 27 22 AAW3017 77.4 27 22 AAW3083 77.4 27 22 AAW3033 77.4 65 22 AAW37363 77.4 65 22 AAW37363 77.4 75 22 AAW30502	DP-1 transcription Soybean DP-1 prote Plant dimerisation DP-1 transcription Scorpion leiuropep DBF domain consens Human secreted pro Human pene 20 enco Human secreted pro Human secreted pro Human secreted pro Human secreted pro Human secreted pro Human secreted pro Human ngene 20 enco Human ngene 20 enco Human iduronate 2- Human iduronate 2- Human iduronate 2- Human inver peptide Amino terminal secreted Peptide #2239 enco Peptide #2239 enco Peptide #2239 enco Peptide #2206 enco Human bone marrow Peptide #2206 enco Peptide #2188 enco Peptide #2188 enco Peptide #2188 enco Human poptide accoluncan Regitted marcoluncan Regitted marrow Peptide #2188 enco Peptide #2188 enco Peptide #2188 enco Peptide #2188 enco Peptide #2188 enco Puman poptide marrow Regitted ma	Novel numan respir Human prostate can Novel bone marrow Bacteriophage Type DP-1 transcription
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	W W U U W W W W W W W W W W W W W W W W	4.4.6.6.

ALIGNMENTS

RESULT 1

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DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                         DP-1 transcription factor antagonist peptide motif.
       AAW30503 standard; Peptide; 7 AA.
                                                                                                                                                                                    96GB-0026589.
                                                                                                                                                                    97WO-GB03506
                                         26-OCT-1998 (first entry)
                                                                                                                                                                    22-DEC-1997;
                                                                                                                                                                                    20-DEC-1996;
                                                                                                         Synthetic.
Homo sapiens
                                                                                                                                   WO9828334-A1
                                                                                                                                                    02-JUL-1998.
                        AAW30503;
AAW30503
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                                                                               This peptide comprises amino acid residues 172-178 in the DEF box cregion (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30502-07) containing this and/or another motif (see Cath AW30502) of the DEF box, are antagonists of the heterodimeriaation of a DP protein with an E2P protein. Also claimed are variants of these peptides, especially containing substitutions of residues of these peptides, especially containing substitutions of residues of these peptides, especially containing substitutions of residues of these peptides (see AAW30508), expression vectors encoding (I)-(III) and sequence (see AAW30508), expression vectors encoding (I)-(III) and sequence (see AAW30508), expression vectors encoding (I)-(III) and sequence (see AAW30508), expression vectors encoding (I)-(III) and sequence (see AAW30508), expression vectors encoding (I)-(III) and sectors encoding (I)-(III) are used therator of sequence angiopathy to induce apoptosis, of the DNA-binding activity of DP/EZF heterodimers. They are also the vector and as immunoassay conclered in the DNA-binding activity of DP/EZF heterodimers. They are also enteritying antagonists of DP-I/EZF dimerisation and as immunoassay conclered angels encoding (I)-(III) to control DP levels in calls, or extostatic agents, (I)-(III) enhance cell killing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
inducing apoptogis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 31; DB 19; Length 7; 100.0%; Pred. No. 9.38+05; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP-1 transcription factor peptide H6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW30511 standard; Peptide; 14 AA
                                                              Claim 3; Page 44; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96GB-0026589
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Best Local Similarity lov.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
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This represents a compound that can inhibit E2F activity. The compound is of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, herero-arylcarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                           ö
                  Peptide H6 comprises amino acid residues 167-180 in the DEF box region (see AAM30501) of transcription factor DP1. Unlike claimed peptides (see AAM30504-07) that contain one or both of 2 motifs (see AAW30502-03) of the DP1 DEF box, peptide H6 is not capable 6 antagonising the heterodimerisation of a DP protein with an E2F protein. The claimed peptides, their variants and fusion proteins can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g. to prevent restenosis.
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E2F activity inhibitors - for treatment and prevention of tumours and arteriosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       B2F activity; inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                100.0%; Score 31; DB 19; Length 14; 100.0%; Pred. No. 0.69; or Indels 1.ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoshida T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              E2F activity inhibiting compound Ib-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 28; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            AAW57052 standard; peptide; 15 AA.
Example C; Page 41; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-JP03442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96JP-0259432.
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                             Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mizukami T, Shibata K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-240020/21.
                                                                                                                                                                                                                                                                         6 ALNVLMA 12
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                                                                                                                                                              Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                       RESULT 3
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Score 31; DB 19; Length 16; Pred. No. 0.81;

100.0%;

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(I) - (III) enhance cell killing.
                                                                                    Query Match
Best Local Similarity 100...
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                                                                     16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                          AAW30516;
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                                                                                                                                                                                                                                                                                                        RESULT 5
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
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                    100.0%; Score 31; DB 19; Length 15; 100.0%; Pred. No. 0.75; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      DP-1 transcription factor antagonist peptide H5.
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                                                                                                                                                                                                                                                           AAW30506 standard; Peptide; 16 AA.
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                                                                Conservative
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Query Match
Best Local Similarity
7; Conservē
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                                                                                                                                                                                                                                                                                                   AAW30506;
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide H2mt2 is based on peptide H2 (see AAW30504) from the DEF box (see AAW30501) of transcription factor DP1. In H2mt2, amino acid residues of H2 that correspond to DP1 residues Arg167 and Asp171 are substituted by Ala residues. H2 is an antagonist of the heterodimerisation of DP1 with E2F. H2mt2 retains some, but not all, of this antagonistic activity. H2 and other claimed peptides (see AAW30504-07) from the DEF box region of DP1 can be used to induce apoptosis, specifically in tumour and cardiovascular cells, e.g. for the prevention of restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP-1; transcription factor; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
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100.0%; Pred. No. 0.99;
tive 0; Mismatches 0; Indels
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            DP-1 transcription factor antagonist peptide H2mt2.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "R167A mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                 AAW30516 standard; Peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-GB03506
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                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   surgical stent; therapy.
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                                                                                                                 ALNIVLMA 11
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Peptide H2 comprises amino acid residues 166-184 in the DEF box (I) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07) containing one or both of 2 motifis (see AAW30502-03) of the DEF box are capable of antagonising the AAW30502-03 of the DEF box are capable of antagonising the beterodimerisation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially containing anbetrutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and and 175 of DP-1, fusion proteins (III) comprising (I) or (III) and host cells. (I) (III) are used to therapeutically to induce apoptosis, specifically in tumour or therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging create or prevent restenosis in patients who have undergone treat or prevent restenosis in patients who have undergone andioplasty. (I) (III) function by inactivating the DNA-binding cactivity of DP-1/E2F dimerisation and as immunosassy agents. They are also used as research antagonists of DP-1/E2F dimerisation and as immunosassy agents. Caccing (I)-(III) to control DP levels in cells, particularly by control DP levels in cells, particularly by control DP levels in cells, particularly by control DP levels in cells, particularly by control DP levels in cells, particularly by control DP levels in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
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                                                                                                                                                                                                               DP-1 transcription factor antagonist peptide H2.
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                                                                                                         AAW30504 standard; Peptide; 19 AA.
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/note= "Claim 3"
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Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                             surgical stent; therapy.
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7 ALNVLMA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9828334-A1
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                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                AAW30504;
                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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This represents a compound that can inhibit E2F activity. The compound is of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and prevention of tumours and arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E2F activity inhibitors - for treatment and prevention of tumours and arteriosclerosis
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                                                                                                                                                                               E2F activity; inhibitor; treatment; tumour; arteriosclerosis.
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                                                                                                                                                                                                                                                                       /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                   /note= "C-terminal amide"
                                                                                                                                                          E2F activity inhibiting compound Ib-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 27; 52pp; Japanese.
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                 AAW57051 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                   96JP-0259432.
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                                                                                                                                     (first entry)
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                  ALNVLMA 13
1 ALNVLMA 7
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                Synthetic
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                                                                                                               AAW57051;
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                                                               RESULT 7
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AAWS7055 standard; peptide; 28 AA.

17 ALINVLMA 23

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28-AUG-1998 (first entry)

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Gaps

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AAW57055;

AAWS7055 XX XX AC AAWS XX DT 28-A

RESULT 8

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Peptide H7 comprises amino acid residues 170-199 in the DEF box (II) (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30504-07) containing one or both of 2 motifs (see AAW30502-03) of the DEF box are capable of antagonising the heterodimerisation of a DP protein with an E2F protein. Also claimed are variants of these peptides, especially containing substitutions of residues corresponding to residues 167, 169, 171 and 175 of DP-1, fusion proteins (III) comprising (I) or (II) and a membrane translocation sequence (see AAW30508), expression vectors encoding (I)-(III) and host cells. (II-) are used to therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone artivity of DP/E2F heterodimers. They are also used as research reagents as positive controls in assays for identifying activity of DP/E2F heterodimers. They are also used as research reagents as positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunossay agents. Also described is the use of sequences antisense to nucleic acids encoding (I)-(III) to control DP levels in cells, particularly by the present the part of premalated with cytotoxic or cytostatic agents.
                                                                                                                                                                                                                                                                                                                    Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 31; DB 19; Length 30; 100.0%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DP-1 transcription factor peptide H (DEF box).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW30501 standard; Peptide; 37 AA.
                 /note= "Claim 3"
                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 44; 55pp; English.

    (I) - (III) enhance cell killing.

                                                                                                                                 97WO-GB03506.
                                                                                                                                                                    96GB-0026589.
                                                                                                                                                                                                                                              La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.vv
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1998 (first entry)
                                                                                                                                                                                                         (PROL-) PROLIFIX LTD.
                                                                                                                                                                                                                                                                                 WPI; 1998-377596/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALINVLMA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30 AA;
                                                                                                                               22-DEC-1997;
                                                                                                                                                                    20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                      WO9828334-A1
                                                                                                                                                                                                                                            Bandara LR,
                                                                                           02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW30501;
 Peptide
SSXXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This represents a compound that can inhibit E2F activity. The compound is of the formula R1 - A - R2 where R1 is an optionally substituted alkanoyl, alloyl, hetero-arylcarbonyl, alkoxycarbonyl, aryloxycarbonyl, hetero-aryloxycarbonyl, or H, R2 is OH, or optionally substituted alkoxy or amino, and A is an E2F family dimer forming region or DNA binding region, of at least 12 consecutive amino acids. Compounds of this formula can be used to inhibit E2F activity, and are useful in the treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity inhibitors - for treatment and prevention of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                  E2F activity; inhibitor; treatment; tumour; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 31; DB 19; Length 28; 100.0%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yoshida T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DP-1 transcription factor antagonist peptide H7
                                                                                                                                                                                     /note= "N-terminal lauroyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevention of tumours and arteriosclerosis
                                                                                                                                                                                                                         /note= "C-terminal amide"
               B2F activity inhibiting compound Ib-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mizukami T, Shibata K, Yamasaki M,
                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7; Page 33; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW30507 standard; Peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Claim 3"
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                                                                                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                      97WO-JP03442.
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Best Local Similarity luv.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and arteriosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 ALNVLMA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 AA;
                                                                                                                                                                  Modified-site
                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1996;
                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                              WO9814474-A1
                                                                                                                                                                                                                                                                                                                                      26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1998
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                                                                                         Synthetic
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02-JUL-1998.

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This sequence represents 42% of the middle region of soybean cell cycle regulatory protein DP-1, as deduced from an isolated cycle regulatory protein DP-1, as deduced from an isolated coll cycle regulatory protein by the invention relates to mucleic acid cand cargonize (see AAZ34579). The invention relates to uncleic acid cand construction of a chimeric gene encoding all or a relates to the construction of a chimeric gene encoding all or a contentation, where expression of the chimeric gene results in principal conformations of altered levels of the chimeric gene results in production of altered levels of the cell cycle regulatory protein in production and the candidates are active and proteins may be considered for facilitate studies of cell cycle regulation in plants, provide genetic tools to enhance cell growth in tissue culture, provide genetic tools to enhance cell growth in tissue culture, increase gene transfer efficiency and provide more stable transfer efficiency and provide targets to transformations. The proteins may also provide targets to transfer design and/or identification of cell cycle regulatory proteins that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 31; DB 20; Length B3; 100.0%; Pred. No. 5.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant-derived cell cycle regulatory proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                 notes "encoded by NAT"
                                                                                                                                                                                                                                             "encoded by NAG"
                                                                                                                                                                                                                                                                                      'notes "encoded by NAT"
                                                               'note= "encoded by CNT"
                                                                                                                                                                                                                                                                                                                                  note= "encoded by GNG"
                  'note= "encoded by GGN"
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                                                                                                                                                                                                                                                                                                                                                                               note= "encoded by
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                                                                                                                                                      'note= "encoded
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Best Local Similarity 100..
'.a 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein TM, Morakinyo LO,
                                                                                                              'note=
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N-PSDB; AAZ34579.
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ALNVLMA 19
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                                                                                       Misc-difference 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 AA;
Misc-difference 34
                                            Misc-difference 35
                                                                                                                                      Misc-difference 54
                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide H (I) comprises residues 163-199, i.e. the DEF box region, of transcription factor DP1. Claimed fragments (II) (see AAW30502-07) of (I) are capable of antagonising the heterodimerisation of a DP protein with an B2F protein. Also claimed are fusion proteins (III) comprising (I) or (II) and a membrane translocation sequence (see AAW30508), expression vectors encoding (I) (III) and host cells. (I) (III) are used therapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restenosis in patients who have undergone angioplasty. (I)-(III) function by inactivating the DNA-binding activity of DP/E2F heterodimers. They are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                         Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (I)-(III) are used angioplasty. (I)-(III) runction of they are also have undergone angioplasty. (I)-(III) runction of they are also the DNA-binding activity of DP/E2F heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-1/E2F dimerisation and as immunoassay identifying antagonists of DP-1/E2F dimerisation and as immunoassay agents. Also described is the use of sequences antisense to agents. Also described is the use of sequences antisense to nucleic acids encoding (I)-(III) to control DP levels in cells, nucleic acids encoding (I)-(III) to formulated with cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 particularly by gene therapy. When formulated with or cytostatic agents, (I)-(III) enhance cell killing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DP-1, soybean, cell cycle regulatory protein;
transcription factor; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encoded by GNC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY32163 standard; Protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 44; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soybean DP-1 protein fragment.
                                                                                                                          97WO-GB03506
                                                                                                                                                                         96GB-0026589
                                                                                                                                                                                                                                                                Bandara LR, La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2000 (first entry)
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Best Local Similarity 100.
Local 7; Conservative
                                                                                                                                                                                                                    (PROL-) PROLIFIX LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 AA;
                                        W09828334-A1
                                                                                                                               22-DEC-1997;
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Ouery Match
Best Local Similarity 100.0
          Glycine max.
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DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour;
                                                                                                                                                                                                                                                                                                               DP-1 transcription factor peptide H2mt1.
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                                                                                                                                                                                                                                                               26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               surgical stent; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PROL-) PROLIFIX LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9828334-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bandara LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                               AAW30515;
                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                          AAW30515
                                                                                                                                                                                                               8
8:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel cell cycle protein (CCP) and the polymorlacutides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for detecting the presence cycle crycle or growth of a plant such as Arabidopsis thalians, rice, wheat, maize, tomato, alfalfa, oilseed tape, soybean, sunflower and canola. Cycle nucleic acid and polypeptide molecules are useful as modulating of CCP nucleic acid and polypeptide molecules are useful as modulating of cry protein or production of CCP protein forms which have decreased or agents in regulating cell cycle progression in plants. CCP is useful to compute the activity computed are useful as metality or modulate the activity of ECP protein forms which have decreased or the polymorleotide are useful as herbicides or plant growth regulators. The polymorleotide is useful for modifying cell fath engine development, the polymorleotide is useful for modifying cell fath of the GI, S GZ and/or M phase of the cell division, Mwarfism in plants. S GZ and/or M phase of the cell division, Mwarfism in plants, initiation and/or development, thouse, fruit, leaf formation, seed set, seed development, thouse, fruit, leaf formation, seed set, initiation and/or development, nodule function, dwarfism in plants, initiation and activity of a protein in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due cold, nutrient deprivation, heat, drought, salt stress or biotic stress such as pathogen attack, to modulate e.g. enhance cold attenuate plant architecture, plant quality traits, CP protein levels or activity of a protein in storage cells, carge tissues and/or storage organs of plants or its parts. CC sorage tissues and/or storage organs of tissues and/or storage organs are insumanogen to generate antibodies. CCP protein is a corpored risues, plant quality, 
                                                                                                            Cell cycle protein, CCP, cell cycle regulation, herbicide, plant growth regulator, plant development, abiotic stress, biotic stress; nutrient deprivation; pathogen attack; crop yield; motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators
                                                               Plant dimerisation protein (DP) E2F heterodimerisation domain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Magyar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Veylder L, Acosta JAT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 9; Page 93; 316pp; English
                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-2001; 2001WO-IB01307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAY-2000; 2000US-204045P
                 (first entry)
                                                                                                                                                                                                                                   Lycopersicon esculentum.
Gossypium hirsutum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CROP-) CROPDESIGN NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boudolf V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-062249/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA;
                                                                                                                                                                                                                                                                                                          WO200185946-A2
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'note= "V169A mutation" /note= "V175A mutation"

97WO-GB03506, 96GB-0026589

La Thangue NB;

Location/Qualifiers

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                                                                                                                                                                                                                                            Peptide H2mtl is based on peptide H2 (see AAW30504) from the DEF box (see AAW30501) of transcription factor DP1. The H2mtl peptide in which H2 residues corresponding to DP1 residues Val169 and Val175 are substituted by Ala residues, behaves in a similar fashion to the wild-type H2 peptide in its ability to inactivate E2F site DNA binding activity in D9 EC cell extracts. H2 is an antagonist of the heterodimerisation of DP1 with E2F. Thus, the Val-169 and Val-175 residues of H2 play little role in this activity. H2 and other claimed peptides (see AAW30504-07) from the DEF box region of DP1 can be used to induce apoptosis, specifically in tumour and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                       Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular cells, e.g. for the prevention of restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 19; Length 19;
Pred. No. 9.3;
0; Mismatches 1; Indels
                                                                                                                                                                                        Example D; Page 26; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
WPI; 1998-377596/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 ALNALMA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALNVLMA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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AAB60781

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Gaps

; 0

87.1%; Score 27; DB 23; Length 8; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels

12-MAY-2000, 2000US-204045P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell cycle protein; CCP; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield; motif.
                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to scorpion toxins. The invention may be used for the creation of transgenic plants which express K-channel modifiers, useful as a means for controlling insect peets by producing insect-colerant plants. In the prevention and/or treatment of insect pest damage and parastric worm infections in animals and humans, the invention may also find use in creating specific new pesticides and antihelmintic drugs that are also non-toxic to humans, pets and
                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding scorpion venom potassium-channel agonist proteins for production e.g. of insect-tolerant transgenic plants for controlling insect pest damage and parasitic worm infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                Scorpion; toxin; K-channel; potassium; insect; pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 2; Pred. No. 33; 2; Mismatches
                                                                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU72601 standard; Peptide; 35 AA.
AAB60781 Btandard; protein; 56 AA
                                                                          Scorpion leiuropeptide I protein
                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Fig 3; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEF domain consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.18;
71.48;
                                                                                                                                                                                                                                                                                   Wong JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-2001; 2001WO-IB01307.
                                                                                                                                                                                                       21-JUN-2000; 2000WO-US17049
                                                                                                                                                                                                                                   99US-0140227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 71.4
Matches 5; Conservative
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AMNIVMMA 19
                                                                                                                                                                                                                                                                                                             WPI; 2001-071394/08.
                                                                                                                             Hottentotta judaica.
                                                                                                                                                                                                                                                                                      Lee J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALNVLMA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200185946-A2.
                                                                                                                                                        WO200078958-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2002
                                                                                                                                                                                                                                    22-JUN-1999;
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                                                  28-MAR-2001
                                                                                                                                                                                                                                                                                      Herrmann R,
                                                                                                                                                                                 28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAÚ72601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Livestock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                          AAB60781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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The invention relates to a novel cell cycle procein (CCP) and the copymucleotides encoding them. CCP is useful for identifying a compound copymucleotide and anni-CCP antibody is useful for detecting the presence of cycle or growth of a plant each which binds to the polypeptide and an anni-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for medulating the cell coff coff of a plant such as Arabidopsis thalians, rice, wheat, cycle or growth of a plant such as Arabidopsis thalians, rice, wheat, coff coff and polypeptide molecules are useful as modulating to compare the regulation collised trape, soybean, sunflower and candla. CC agents in regulating cell-cycle progression in plants. CCP is useful to a percent forms which have decreased or compounds that bind to or modulate the activity compounds that bind to or modulate the activity. Compounds that bind to or modulate the activity compounds that bind to or modulate the activity. Compounds that bind to or modulate the activity of polymentiation or enhancement of cell division, by production, so and/or M phase of the cell cycle of a plant, initiation, promotion, so and/or M phase of the cell cycle of a plant, initiation, seed set, crimilation or enhancement to cell division, My replication, seed set, initiation and/or development, thodule function, dwarfism in plants. CC seed size, seed development, thodule function, dwarfism in plants or intiation and/or development, modula function, dwarfism in plants. CC protein levels or activity of a protein involved in the cell cycle due cond, intromental conditions, including abiotic stress such as coling and activity of a protein in decrease corp yields, and attenuate plant architecture, plant duality traits, plant creases much as pathogen attack, to modulate e.g. enhance crop yields, carcage issues and/or storage organs of plants or its parts. CCP is creen for naturally occurring CCP pathoracy. The proper is enhance corp yields, croscell is an immunogen to generate antibodies. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; cytostatic; anti-proliferative; vulnerary;
immunosuppressive; antibacterial; diagnosis; immune system; chemotaxis;
hyperproliferative disorder; infectious disease; tissue regeneration;
                                                                                                                                                                        New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein sequence encoded by gene 11 SEQ ID NO:58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23; Length 35;
                                                                                             Magyar 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                 Acosta JAT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DB 2; Pred. No. 33; 0; Mismatches
                                                                                                                                                                                                                                                                       Disclosure; Page 25; 316pp; English.
                                                                                                   De Veylder L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB08901 standard; Protein; 41 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2000 (first entry)
                                                           (CROP-) CROPDESIGN NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALNVXMA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                   Boudolf V,
                                                                                                                                            WPI; 2002-062249/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALNVLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB08901;
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                                                                                                      Inze D,
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Local Similarity
hes 5; Conserv
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44 ALNILM 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 AA;
                                                                                                                                                                                                                                N-PSDB; AAC98041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200164835-A2
                                                                       WO200055351-A1
                                                                                                                                              12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                  Homo sapiens
                                                                                               21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO05442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA005442
  셤
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                                                                                                                                                                                                                                                                                                                                    The polynucleotide sequences given in AAA39052 to AAA39088 encode the human secreted proteins given in AAB08891 to AAB08984. The human secreted proteins given in AAB08891 to AAB08984. The human secreted proteins given in AAB08891 to AAB08984. The human secreted cells they are expressed in. Examples of the activities are: cytostatic; anti-proliferative; immunosuppressive; antibacterial; and vulnerary. The secreted proteins and their related polynucleotide sequences are useful to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to the secreted proteins. The proteins and proteins of the immune system, hyperproliferative disorders, infectious disease commune system, hyperproliferative disorders, infectious disease.

The proteins The proteins or polynucleotide sequences may be used as food additives or preservatives, to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, and animerals, co-factors or other nutritional components. Agonists or mannerals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antagonists of the proteins may be used to prevent scar tissue growth during wound healing, and hyper-vascular diseases. AAA39043 to AAA39051 and AAB08890 are sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                  Human secreted proteins and coding sequences useful in diagnostic and therapeutic methods for disorders such as immune system or proliferative disorders, related to the proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; colon cancer; colon cancer antigen; diagnosis; detection;
identification; oylostatic; cardioactive; neuroprotective; vulnerary;
immunomodulatory; muscular; gynaecological; gastrointestinal;
nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                              5
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                                                                                                                                                                                             Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 21; Length 41;
Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer antigen protein sequence SEQ ID NO:824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
screening; food additive; preservative; wound healing;
                                                                                                                                                                                           Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                           D, Shi Y,
Soppet DR;
                                                                                                                                                                                                                                                                                                                  Claim 11; Page 358; 416pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB53284 standard; Protein; 90 AA.
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0
                                                                                                                                                                                           Duan RD,
                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.9%;
85.7%;
                                                                                                         99WO-US22012.
                                                                                                                                98US-0101546.
98US-0102895.
                                                                                                                                                                                          Rosen CA, Duan F
s G, Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
            hyper-vascular disease
                                                                                                                                                                                                                               WPI; 2000-283538/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
ses 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALNVLFA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALNVLMA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 AA;
                                                                                                                                                                                                                                          N-PSDB; AAA39062
                                                                                                                                                                                                        Komatsoulis G,
                                                          WO200017222-A1
                                    Homo sapiens
                                                                                                        22-SEP-1999;
                                                                                                                                23-SEP-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAR-2001
                                                                                 30-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB53284;
                                                                                                                                                                                           Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 17
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AAC97891 to AAC88763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB51214 to AAB54006. The human colon cancer antigens can have cytostatic, candioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antilnfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune strength and cardiovascular disorders, and cardiovascular disorders, and cardiovascular disorders, AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy, accine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodilatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 1376; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 19334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAO05442 standard; Protein; 59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000; 2000WO-US05883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-587534/55.
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15-SEP-2000; 2000US-0663870.
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14-MAR-1997;
14-MAR-1997;
30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9840483-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW75232;
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW75232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                              The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymortocides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               horse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; ht tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 19334; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

80.6%; Score 25; DB 22; Length 59;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human EST encoded protein SEQ ID NO: 1591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM24066 standard; Protein; 73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2001; 2001WO-US02687.
                                                                                                                                                                     Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2001 (first entry)
                                                              26-FEB-2001; 2001WO-US04927.
                                                                                           28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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53 ALEVLMA 59
                                                                                                                                                                                                     WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALNVLMA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 AA;
                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                        Tang YT, Liu C,
                                                                                                                                                                                                                       N-PSDB; AAI85373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200154477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2001.
                                07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM24066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 19
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic abock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                               Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                     Chen R, Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 22; Length 73;
Pred. No. 1.4e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein encoded by gene 20 clone HSDEG01.
                                           ou P, Qian XB, Wang Z,
Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                            Claim 20; Page 1088; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW75232 standard; Protein; 87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= unknown
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97US-0040762.
97US-0048100.
97US-0048189.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5, Conservative
                                                          Zhou
                                                       Tang YT, Liu C, Zh
Cao Y, Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 86
                                                                                                                                  WPI; 2001-476164/51.
N-PSDB; AAH98725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALINVLMA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | | | | : |
2 SLNVLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
(HYSE-) HYSEQ INC
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This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV34277) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 28 novel genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W7535) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 28 polyhoucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                  Isolated human poly:nucleotide(s) encoding secretory peptide(s) used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders
                                                                                          CL, Gentz RL, Greene JM, Kyaw H;
PA, Rosen CA, Ruben SM, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (see AAV34286 for described uses).
                                                                                                                                                                                                                                       Claim 1; Page 177; 201pp; English
97US-0048357.
97US-0050934.
97US-0048970.
                                                                (HUMA-) HUMAN GENOME SCI INC
                                      97US-0057765
                                                                                                                    Zeng Z;
                                                                                      Ferrie AM, Fischer
Li H, Li Y, Moore
                                                                                                                                           WPI; 1998-520811/44.
                                                                                                                    Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 AA;
                                                                                                                                                         N-PSDB; AAV34322
30-MAY-1997;
30-MAY-1997;
06-JUN-1997;
                                      05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                 Wei YF,
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Gaps .; 0 Query Match 80.6%; Score 25; DB 19; Length 87; Best Local Similarity 71.4%; Pred. No. 1.7e+02; Matches 5; Conservative 2; Mismatches 0; Indels ઠે

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SLNVLLA 8 1 ALNVLMA 7

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AAE26996 standard; Protein; 87 AA.

AAE26996;

(first entry) 13-DEC-2002

Human gene 20 encoded secreted protein HSDEG01, SEQ ID NO:89.

Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer; Grave's disease; diabetes mellitus; haematopoietic disorder; stroke; respiratory disorder; asthma; allergy; gastrointestinal disorder; inflammatory bowel disease; neurodegenerative disorder; hepatitis; Parkinson's disease; ardiovascular disorder; atherosclerosis; myocarditis; renal disorder; fungicide; virucide; hyperproliferative disorder; acute glomerulonephritis; tonsillitis; respiratory disorder; Addison's disease; reproductive system disorder; endocrine disorder; Addison's disease; reproductive system disorder; endometriosis; vasotropic; vulnerary; cytostatic; nootropic; cardiant; anti-HIV; tranquilliser; gout; antiparasitic.

domo sapiens

Location/Qualifiers Peptide

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Novel human secreted polypeptides and polynucleotides for diagnosing, preventing, treating immune, hyperproliferative, cardiovascular, neurological, reproductive disorders and identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li Y, Zeng Z, Kyaw H, Fischer CL,
Wei Y, Moore PA, Young PE, Greene
               22..87
/note= "Human mature secreted protein"
                                                                                                           /label= Unknown
/note= "Encoded by AAN"
'label= Signal peptide
                                                             /label= Unknown
/note= "Encoded
                                                                                                                                                                                                                                                               98US-0152060.
                                                                                                                                                                                                                              11-MAY-2001; 2001US-0852659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA,
Gentz RL,
                                                                                                                                                                                                                                                                                                                            LI Y.
ZENG Z.
KYAW H.
FISCHER C L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-598780/64.
                                                                                                                                                                                                                                                                                                                                                                                                             SOPPET D R.
GENTZ R L.
WEI Y.
                                                                                                                                                                                                                                                                                            RUBEN S M.
ROSEN C A.
                                                                                              Misc-difference 86
                                              Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD44673
                                                                                                                                                               JS2002077287-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                               LI H.
                                                                                                                                                                                                                                                               11-SEP-1998;
                                                                                                                                                                                              20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soppet DR,
Ferrie AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM,
                                                                                                                                                                                                                                                                                                                                                              (KYAW/)
(FISC/)
               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                              (GENT/)
                                                                                                                                                                                                                                                                                             RUBE/)
                                                                                                                                                                                                                                                                                                               ROSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                (Vados)
                                                                                                                                                                                                                                                                                                                                               (ZENG/
                                                                                                                                                                                                                                                                                                                                                                                               LIHH
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Claim 11; Page 193; 209pp; English.

AMD44636-AAD44676 represent cDNAs corresponding to 28 human secreted protein genes, and AAE26959-AAE26999 represent the proteins they encode. AAE27000-AAE37025 represent human secreted protein fragments or their variants. The secreted protein fragments or their variants. The secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therety. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed and include contential memaclobulinaemia, B cell immunodeficiencies, severe combined immunodeficiencies, autoimmune disorders e.g., systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune to combined immunodeficiencies, autoimmune disorders e.g., systemic lupus erythematosus, rheumatoid arthritis, dermatitis, inflammatory conditions including septic shock, sepsis, reperfusion injury, inflammatory bowel disease, memolytic anaemia; goodpasture's syndrome, disorders e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory bowel disease, hameacopoietic disorders, vespiratory disorders e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory bowel disease, hameacopoietic disorders, covarian, lung, cancers e.g., gastric, ovarian, lung, disorders e.g., asthma and Alzheimer's disease, AlDS-related dementia and prion disease, and allogenic transplant rejection, blood-corporated disorders e.g., hepatitis, gout, trauma, pancreatitis, sarcoidosis and allogenic transplant rejection, blood-corporated disorders, respiratory disorders e.g., hepatitis, neurological diseases, hubberaliultarism, infectious diseases and reproductive system (Crelated disorders, endocrine disorders e.g., hyperthyroidism, Addison's liver disorders, endocrine disorders e.g., hyperthyroidism, hyders, inference e.g., hyperthyroidism, hyders, inference e.g., hyperthyroidism, hyders, hypersesents endocrine disorders e.g., hyperthyroidism, hyders, hyperpolitiers, endocrine disorders e.g., hyperp

Sequence

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Query Match

Matches

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Secreted protein; immunodeficiency; multiple sclerosis;
KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoletic disorder;
KW rheumatory condition; septic shock; inflammatory beal disease;
KW sinflammatory condition; septic shock; inflammatory beal disease;
KW sationiestinal disorder; central nervous system disorder;
KW gastrointestinal disorder; central nervous system disorder;
KW histopiamer's disease; cardiovascular disorder; atherosclerosis;
KW hyperpoliferative disorder; hrombosis; atherosclerosis; renal disorder;
KW hyperpoliferative disorder; acute glomerulonephirtish Addison's disease;
KW hyperproliferative disorder; particular disease; pancentlorespiritish Addison's disease;
KW modometriosis; infectious disease; panceatic disorder;
KW modometriosis; infectious disease; panceatic disorder;
KW modometriosis; infectious disease; panceatic disorder;
KW modometriosis; infectious disease; panceatic disorder;
KW modometriosis; infectious disease;
KW body height; hair colour; human.
                                                                                                                                                    ADD44854-AAD44984 represent CDNAs corresponding to 28 human secreted CC protein genes, and AAEZ7137 represent the proteins they encode. CC protein genes, and AAEZ7137 represent the protein strangments. The genes AAEZ7138-AAEZ7164 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing, corresponding secreted proteins, e.g., by protein or gene therapy. Secreted protein sequences of the invention are useful for the corresponding medical conditions, e.g., by protein or gene therapy. Secreted protein sequences of the invention are useful for the corresponding arthritis), hyperproliferative disorders (e.g. neoplasms of rhe breast or liver), cerebrovascular disorders (e.g. neoplasms of system disorders (e.g. cardiac arrest), nervous cystem disorders (e.g. Alzheimer's disease), infections caused by fungi, system disorders (e.g. correlai ischemmia, corporation, to prevent skin ading due to sunburn, to maintain organs proliferation, to prevent skin ading due to sunburn, to maintain organs corresponditures and order tanaplantation, for supporting cell culture of primary tissues, confict corresponditives or preservative to increase or decrease storage capabilities, and other untitional components. They can also be used as food and interest ingid, protein, carbohydrate, vitamins, minerals, cofactors
                        New nucleic acid molecules encoding 28 human secreted proteins, useful for diagnosing, preventing, treating or ameliorating medical conditions and as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25; DB 23; Length 87;
Pred. No. 1.7e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein gene 20, protein #2.
                                                                                                                          Claim 11; Page 193-194; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU65007 standard; Protein; 87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-2001; 2001US-0852797.
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Similarity 71.4%;
S; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALINVLMA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002172994-A1
N-PSDB; AAD44891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; autoimmune disease; hyperproliferative disorder; rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis; cerebral isohaemia; cardiovascular disorder; nervous system disorder; cardiac arrest; Alzheimer's disease; ocular disorder; wound healing; infection; corneal infection; skin aging; food additive; preservative; tissue regeneration; immunosuppressive; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy;
                                                                                                                                             ö
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li Y, Zeng Z, Kyaw H, Fischer CL, Li H; wei Y, Moore PA, Young PE, Greene JM;
                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene 20 encoded secreted protein HSDEG01, SEQ ID NO:89.
                                                                                                Score 25; DB 23; Length 87;
Pred. No. 1.7e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22..87
/note= "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Encoded by KGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Encoded by AAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         AAE27134 standard; Protein; 87 AA.
                   secreted protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-2001; 2001US-0853161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-FEB-2001; 2001US-265583P
                                                                                                            80.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                 Local Similarity 71.4
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LI Y.
ZENG Z.
KYAW H.
FISCHER C L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LI H.
SOPPET D R.
GENTZ R L.
WEI Y.
MOORE P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-574454/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GREENE J M.
FERRIE A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RUBEN S M.
ROSEN C A.
                                                                                                                                                                                                    1 ALNVLMA 7
                                                                                                                                                                                                                               SLNVLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                                     87 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002076756-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-DEC-2002
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vulnerary

Peptide Protein

AAE27134;

RESULT 22

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AAE27134 ID AAE

Suben SM,

(YOUN/) (GREE/) (FERR/)

MOOR/)

GENT/) WEIY/)

(KYAW/) (FISC/) (LIHH/) (SOPP/)

RUBE/) (ROSE/) (LIYY/) (ZENG/)

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Gaps ö

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The invention relates to an isolated polypeptide comprising an amino acid sequence at least 95% identical to sequence of 28 human secreted corresponding to a profession, epitope, secreted form, variant, allelic variant, or species homologue, or the encoded sequence included in ATCC 97921 and 97922. Also included are the encoding mucleic acids recombinant vectors, host cells, antibodies, and genes. The proteins and nucleic acids are useful for diagnosing, preventing, rreading, preventing, recombinant vectors, host cells, antibodies, and genes. The proteins and nucleic acids are useful for diagnosing, preventing, respiratories, severe combined immunodeficiencies, severe combined immunodeficiencies, severe combined immunodeficiencies, autoimmune thyroiditis, autoimmune hamolytic anaemia, classociatis (e.g. systemic erythematosus, rheumatoid arthritis, multiple discopature's syndrome, Grave's diabetes mellitus, dermatitis), hemmatopoietic disorders, inflammatory conditions (e.g. septic shock, sepsis reperfusion injury, inflammatory bowel disease, Crohn's disease), respiratory disorders (e.g. asthma and allergy), gastrointestinal breast). central nervous system (CRS) disorders (e.g. gischeemic brain injury), neurodegenerative disorders, cancers (e.g. asthma and allergy), gastrointestinal conditions and prion disease), cardiovascular disease, and cardiopulmonary bypass complications), inflammation (e.g. hepstitis, gout, trauma, pancreatitis, and prion disease), cardiovascular disease, and cardiopulmonary bypass complications), inflammation (e.g. hepstitis, gout, trauma, pancreatitis, sarcoidosis, dermatitis, alloganic transplant rejection), blood-related disorders (eng. and cardiopascular disease, and disease, and disorders (e.g. adute of gloomerulonephritis), endocrine disorders (e.g. adute of disorders (e.g. adute of disorders (e.g. adute of disorders and disorders (e.g. adute of engranderic disorders (e.g. adute of engranderic disorders (e.g. adute of engranderic disorders (e.g. adute of engranderic disorders (e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human secreted polypeptides and polynucleotides for diagnosing, prognosing, preventing and treating immune, hyperproliferative, liver, kidney, reproductive disorders and for identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zeng Z, Kyaw H, Fischer CL, Li
Moore PA, Young PE, Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 193; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li Y, Ze
Wei Y,
97US-040710P.
97US-040762P.
97US-048189P.
97US-048189P.
97US-050934P.
97US-050934P.
97US-050934P.
                                                                                                                                                            2001US-265583P
                                                                                                                                                                                             98US-0152060
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Gentz RL,
                                                                                                                                                                                                                                                                                 ZENG Z.
KYAW H.
FISCHER C L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-310989/30.
N-PSDB; ABX97003.
                                                                                                                                                                                                                              RUBEN S M.
ROSEN C A.
LI Y.
                                                                                                                                                                                                                                                                                                                                    LI H.
SOPPET D R.
                                                                                                                                                                                                                                                                                                                                                                                                                                            GREENE J M.
FERRIE A M.
                                                                                                                                                                                                                                                                                                                                                                       GENTZ R L.
WEI Y.
                                                                                                                                                                                                                                                                                                                                                                                                         MOORE P A. YOUNG P E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kidney, reproduc
therapeutic use
                                    30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
                                                                                   30-MAY-1997;
06-JUN-1997;
05-SEP-1997;
19-DEC-1997;
                                                                                                                                                                         12-MAR-1998;
11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM,
Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soppet DR,
Ferrie AM;
                                                                                                                                                                                                                                              (ROSE/)
                                                                                                                                                                                                                                                                                                 (KYAW/)
(FISC/)
                                                                                                                                                                                                                                (RUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (GREE/)
(FERR/)
                                                                                                                                                                                                                                                                                   (ZENG/)
                                                                                                                                                                                                                                                                                                                                                        SOPP/)
                                                                                                                                                                                                                                                                                                                                    (LIHH/)
                                                                                                                                                                                                                                                                                                                                                                       (GENT/)
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are useful to enhance or inhibit complement mediated cell lysis, for stimulating wound and tissue repair, angiogenesis, and the repair of vascular or lymphatic diseases or disorders. They are also useful to prevent hair loss, to modulate mammalian characteristics such as body height, weight, hair colour, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitemins, minerals, cofactors or other nutritional components. The proteins are represents a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A method has been developed for the production of glycosylated iduronate-2-sulphatase enzyme (IDS). The method comprises culturing a host cell containing a nucleic acid encoding the enzymatically active IDS polypeptide where the host cell glycosylates the polypeptide to a greater degree than a native IDS polypeptide expressed by a natural human liver cell. The present sequence represents an IDS amino terminal peptide used in an example from the present invention. The recombinant IDS is used to treat IDS deficiency where heparin sulphate and dermatan sulphate accumulates in lysosomes resulting in Hunter syndrome which is manifested by e.g. severe mental retardation, skeletal deformities and stiff joints. The recombinant IDS possesses inter alia an improved half life inter alia and improved uptake
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Production of glycosylated iduronate-2-sulphatase enzyme (IDS) -comprises culturing a host cell containing a nucleic acid encoding the enzymatically active iduronate-2-sulphatase polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morris CP;
                                                                                                                                                                                                                    Score 25; DB 24; Length 87;
Pred. No. 1.7e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human iduronate-2-sulfatase amino terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clements PR, Hopwood JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Column 31-32; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAW69785 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-0991973.
91US-0790362.
94US-0345212.
95US-0484494.
                                                                                                                                                                                                                      89.08
                                                                                                                                                                                                                                       ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0484494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anson DS, Bielicki J, C
Occhiodoro T, Wilson PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-480382/41.
                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                              1 ALINVLMA 7
                                                                                                                                                                                                                                                                                                                SLNVLLA
                                                                                                                                                                                   87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5798239-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW69785;
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        AAW69785
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The present sequence is derived from human iduronate 2-sulphatase (IDS) protein, and is used to design a probe for the isolation of CDNA encoding IDS. The specification describes recombinant human IDS produced in eukaryotic cells that has enzymatic activity and is more highly glycosylated than native IDS from the human liver, placenta or kidney, The protein is useful for treating IDS deficiency,
                                                                                                                                                                                                               Human; iduronate 2-sulphatase; IDS; IDS deficiency; Hunters syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human iduronate 2-sulfatase (IDS) peptide sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; iduronate 2-sulfatase; IDS; glycosylated; gene therapy; mucopolysaccharidosis inhibitor; IDS deficiency disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant iduronate 2-sulfatase useful for treating Hunters
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morris CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20; Length 25; 68;
                                                                                                                                                                                     Amino terminal sequence of iduronate 2-sulphatase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hopwood JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                         (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clements PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Column 11; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AABS1178 standard; Peptide; 25 AA.
                                                                                                      AAY23983 standard, Peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.4%;
                                                                                                                                                                                                                                                                                                                                                                    92US-0991973.
91US-0790362.
94US-0345212.
                                                                                                                                                                                                                                                                                                                                         94US-0345212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001 (first entry)
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Angon DS, Bielicki J, C. Occhiodoro T, Wilson PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.4
Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. Hunters syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-443569/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALNVLM 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 AA;
                      ||||||
ALNVLL 8
         ø
       ALNVLM
                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1991;
28-NOV-1994;
                                                                                                                                                                                                                                                                                                                                         28-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                       17-DEC-1992;
                                                                                                                                                                 21-SEP-1999
                                                                                                                                                                                                                                                                                   US5932211-A.
                                                                                                                                                                                                                                                                                                                03-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                       AAY23983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 27
                                                                                RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB51176
                                                                                                 AAY23983
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                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a human iduronate 2-sulphatase (IDS) peptide fragment. IDS deficiency can be treated by administering a recombinant human IDS that is more highly glycosylated than the naturally occurring enzyme, useful in the treatment of Hunter syndrome. The recombinant IDS may be administered in 0.5 microg/kg to 20 mg/kg doses. The administration route is oral, intravenous, intraperitoneal, intramesular, subcutaneous or intransaal. The recombinant IDS has better uptake properties and/or a longer half-life in vivo, and is thus more efficient than naturally glycosylated IDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
properties in comparison to the naturally glycosylated molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morris CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19; Length 25; 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                         19; Length 25
                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hopwood JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment of iduronate 2-sulphatase deficiency administering recombinant iduronate 2-sulphatase
                                                                                                                                                                                                                                                                                                                                     Human; iduronate 2-sulphatase; IDS; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 24; DB 1
Pred. No. 68;
1; Mismatches
                                                         Score 24; DB 1
Pred. No. 68;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clements PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Column 11; 53pp; English.
                                                                                                                                                                                                                        AAW47300 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 77.4%;
Best Local Similarity 83.3%;
Matches 5; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-0991973.
91US-0790362.
94US-0345212.
95US-0484493.
                                                              77.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0484493
                                                                                                                                                                                                                                                                                                            Human IDS peptide fragment
                                                                                                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anson DS, Bielicki J, (Occhiodoro T, Wilson PJ;
                                                  Query Match
Best Local Similarity 83.2
Lag 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIELICKI J.
CLEMENTS P R.
HOPWOOD J J.
MORRIS C P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-206530/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OCCHIODORO WILSON P J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANSON D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 AA;
                                                                                                                                       ||||||
ALNVLL 8
                                                                                                                      1 ALNVLM 6
                                    25 AA;
                                                                                                                                                                                                                                                                                                                                                        Hunter syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1991;
28-NOV-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                  01-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                  US5728381-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-1998.
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                                                                                                                                                                                                                                                     AAW47300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIEL/)
(CLEM/)
(HOPW/)
(MORR/)
(OCCH/)
                                    Sequence
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Gape

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human liver single exon encoded peptides of the invention.
Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #2239 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.4%; Score 24; DB 22; Length 27; 83.3%; Pred. No. 75; 0; Indels ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erom WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID No 28244; 658pp; English
                                                                                                                                                                                Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB29588 standard; Peptide; 27 AA.
                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                              Chen W,
                                                                            27-SEP-2000; 2000US-0236359
04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00662.
                                         2000US-0632366
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les 5; Conserv
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                                                            21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUN-2000;
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27-SEP-2000;
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                                       03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB29588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a recombinant human iduronate 2-sulfatase (IDS). The recombinant IDS is more highly glycosylated than the naturally occurring enzyme isolated from human tissue. The recombinant human IDS can be produced in Chinese Hamster Ovary (CHO) cells or in a human cell. The recombinant IDS comprises a fusion protein. It is a mucopolysaccharidosis inhibitor and can be used in gene therapy. The recombinant IDS is useful in treating and diagnosing subjects suffering from or suspected of having IDS deficiency disorders, e.g. Hunter syndrome (mucopolysaccharidosis type II). The present sequence represents a human IDS peptide which is used to produce an
                                                                                                                                                                                                                                                                                                                                                                                                                   New highly glycosylated recombinant human iduronate 2-sulfatase (IDS) useful for diagnosing or treating subjects suspected of having or suffering from IDS deficiency disorders, e.g. Hunter syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligonucleotide probe used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                        Clements PR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.4%; Score 24; DB 22; Length 25; 83.3%; Pred. No. 68; 0; Indels iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        Occhiodoro T, Bielicki J,
Hunter syndrome; mucopolysaccharidosis type II.
                                                                                                                                                                                                                                                                                (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human liver peptide, SEQ ID No 28244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Column 11; 53pp; English.
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                                                                                                                                                                                             92US-0991973.
94US-0345212.
91US-0790362.
                                                                                                                                                         99US-0249003
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                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-060076/07
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nes 5; Conserv
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                                                                                                                                                                                             17-DEC-1992;
28-NOV-1994;
12-NOV-1991;
                                       Homo sapiens
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Hopwood JJ,
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                                                                                                                  28-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Matches
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RESULT 28 ABG49596

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see
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                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human feetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                                                                                 Claim 27; SEQ ID NO 27403; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                77.4%; Score 24; DB 22; Length 27; 83.3%; Pred. No. 75; 0; Indels ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 15; SEQ ID No 21953; 530pp; English.
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Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB20183 standard; Protein; 27 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-062336.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488899/53
  Penn SG, Hanzel DK,
                                        WPI; 2001-483447/52
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                        27 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                            The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived nucleic acid probes to a collection of detectably labelled nucleic acids the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label cound to each probe of the microarray. The probes are useful for bound to each probe of the microarray. The probes are useful for encode proteins. They are useful for gene discovery, and for encode proteins. They are useful for gene discovery, and for encode proteins analysis is useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical diversity of probes for measuring gene expression, with far less bias diversity of probes for measuring gene expression, with far less bias diversity of probes for measuring gene expression, with far less bias contraction of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid manner and the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the Note: The sequence data for this patent did not format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                             New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #2274 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                Claim 27; SEQ ID NO 12556; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 22; Length 27; Pred. No. 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.4%; Scor.
83.3%; Pred. No. ...
                                                         Rank DR;
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2000US-0608408.
2000US-0612366.
2000US-0234687.
2000US-0234687.
                     (MOLE-) MOLECULAR DYNAMICS INC.
                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00669.
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                                                               Penn SG, Hanzel DK,
                                                                                                      WPI; 2001-496933/54.
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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Matches
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22; Length 27;

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Query Match
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ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human brain expressed single exon probe encoded protein SEQ ID NO: 27675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer.
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                                                                                                                                                                                                                                                                                                          77.4%; Score 24; DB 22; Length 27; 83.3%; Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
33-AUG-2000; 2000US-0533166.
21-SEP-2000; 2000US-0234687.
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                                                                                                                                                                                                                                                                                                                           Local Similarity 83.3
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LNLLMA 9
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                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                            Human bone marrow expressed probe encoded protein SEQ ID NO: 28260.
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Pred. No. 75;
1; Mismatches
Score 24; DB 2
Pred. No. 75;
1; Mismatches
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  77.4%;
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llarity 83.3%;
Conservative 1
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
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04-OCT-2000; 2000GB-0024263.
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                                       Conservative
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5; Conserva
                    Best Local Similarity Matches 5; Conserv
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Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #2188 encoded by probe for measuring breast gene expression.
                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 22; Length 27;
Pred. No. 75;
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                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID No 28550; 654pp; English.
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2000US-0608408.
2000US-0632366.
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27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                               03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                30-JAN-2001; 2001WO-US00663
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2000US-0608408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human genetic disorders.
                                                                                                                                                                                                                                                     Hanzel DK,
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Best Local Similarity
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30-JUN-2000;
03-AUG-2000;
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30-JUN-2000;
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                09-AUG-2001
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                   Peptide #2206 encoded by probe for measuring cervical gene expression.
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                                                                    Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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Pred. No. 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-053366.
21-SEP-2000; 2000US-0233687.
27-SEP-2000; 2000US-0233559.
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Best Local Similarity 83...
Lag S; Conservative
        (first entry)
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4 LNLLMA 9
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                                                                                             cervical cancer
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                                                                                                                                               The present invention relates to novel single exon nucleic acid probes such probe. The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human peptide encoded by genome-derived single exon probe SEQ ID 27154.
                                                                 Novel single exon nucleic acid probe used to measuring gene expression
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Pred. No. 75;
1; Mismatches 0; Indels
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                                                                                                                    Claim 27; SEQ ID No 12246; 322pp; English.
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 Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG37489 standard; Peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                              77.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-180312P.
2000US-207456P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG, Hanzel DK,
 Hanzel DK,
                                 WPI; 2001-476286/51
                                                                                   in a human breast
                                                                                                                                                                                                                                                                                                                                                                                           27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LINVLMA 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000;
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 Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 37
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from thuman lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12187 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes the novel set of probes the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring sene expression in a collection of detectably labeled nucleic acid derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acid derived from human lung a collection of detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene, comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene of 12011 sequences, mentioned in the specification, or encoded by the expression of the exons in a definite exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases (COMP), interstitial lung disease (ILDP), interstitial lung disease 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.
                                                             Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen protein SEQ ID NO:7824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                       measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB;
Pred. No. 75;
1; Mismatches
                                                                                                                                Claim 27; SEQ ID No 27154; 634pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG77060 standard; Protein; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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Best Local Similarity
Local 5; Conserve
                     WPI; 2002-114183/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 AA;
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WO200192523-A2
Homo sapiens.
                                                 06-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 40
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                                                                                                                                                                                                                                                                                               AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where cancer antigens are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic acid, and can be used in gene cancer tantigens have cytostatic acid, and production. N and P may be used in the prevention, therapy and vaccine production. N and P may be used in the prevention, clasmosis and treatment of diseases associated with the prevention of associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing to in a patient's genome that affect the activity of P by expressing to conscrive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, colorected cancer and AAH37196 to AAH37204 and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and and AAH37049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; deprepared iferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.
                                                                                                                                                                                                                               Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.4%; Score 24; DB 22; Length 32; 83.3%; Pred. No. 91; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ORFX protein sequence SEQ ID NO:21946.
                                                                                                                                                                         Rosen CA;
                                                                                                                                                                                                                                                                             Claim 11; Page 9172; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP10982 standard; Protein; 61 AA.
                                                                                                                                                                           Ruben SM, Barash SC, Birse CE,
                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                           99US-0157137.
99US-0163280.
                                                                                  28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                     2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||||
22 SLNVLM 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALNVLM 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 AA;
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                                  WO200122920-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-2002
                                                                                                            29-SEP-1999;
03-NOV-1999;
        Homo sapiens.
                                                         05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP10982;
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The present invention describes substantially purified human proteins

(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1

(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1

c) in the specification). ABN15762 to ABN27252 encode the human ORFX

c) proteins given in ABP0010 to ORFX proteins are useful for

c) creating or preventing a pathology associated with an ORFX-associated

disorder in humans, and in the manufacture of a medicament for treating a

c) creating or preventing a pathology associated with an ORFX-associated

c) syndrome associated with ORFX-associated disorder. ORFX polymucleotide

c) syndrome associated with ORFX-associated disorders, cirrhosis of 11/err,

c) squences can be used in gene therapy. ORFX sequences can be used in the

c) psoriasis, bening tummours, kebloid, degenerative disorders, intendiated

c) psoriasis, bening tummours, kebloid, degenerative disorders, infectious

c) costeoarthritis, neurodegenerative disorders, disorders, infectious

c) costeoarthritis, autoimmune thyroiditis, myasthenia solarosis, infectious

c) clorage disease, various immune deficiencies and disorders, infectious

c) costeoarthritis, autoimmune thyroiditis, myasthenia grafts, graft-versus-host

c) costeoarthritis, autoimmune inflammatory eye disease. ORFX proteins are also

c) costeoarthritis, autoimmune inflammatory eye disease.

c) costeoarthritis, autoimmune inflammatory eye disease.

c) costeoarthritis, autoimmune inflammatory eye disease.

c) costeoarthritis, autoimmune inflammatory eye disease.

c) costeoarthritis, autoimmune inflammatory eye disease.

c) costeoarthritis, autoimmune inflammatory eye disease.

c) costeoarthritis, autoimmune inflammatory eye disease.

c) costeoarthritis, autoimmune inflammatory eye disease.

c) costeoarthritis, autoimmune inflammatory eye disease.

c) costeoarthritis, autoimmune inflammatory eye disease.

c) costeoarthritis, autoimmune inflammatory eye disease.

c) costeoarthritis, autoimmune eye eye eye eye eye eye eye eye 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polypeptides and polymucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C glutamicum protein fragment SEQ ID NO: 4982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID 21946; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG91228 standard; Protein; 64 AA.
                                                                                          30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
29-MAY-2001; 2001WO-US10836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-2001 (first entry)
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Best Local Similarity 71.7
Best Local Similarity 5, Conservative
                                                                                                                                                                                                                                                                                                                                      Shimkets RA, Leach MD;
                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-106308/14.
N-PSDB; ABN26734.
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7 ALNILYA 13
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2000US-0236367
2000US-0236368
                17-JAN-2001; 2001WO-US01333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, Coryneform bacterium and identifying a homologue of a gene derived from oxide, nucleic acids, vitamins, saccharides and organic acids, in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                              Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, respiratory antigen, respiratory disorder; throat disorder,
lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;
anti allergic; anti asthmatic; anti inflammatory; olfactory;
                                                                                                                                                                                                                                    H, Ando S, Hayashi M, Ochiai K, Yokoi H;
Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; SEQ ID NO: 4982; 246pp + Sequence Listing; English.
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Pred. No. 2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human respiratory antigen #236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU17920 standard; Protein; 65 AA.
                                                                                                                                      16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                         18-DEC-2000; 2000EP-0127688.
              Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                    Nakagawa S, Mizoguchi
Tateishi N, Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
5; Conserv
                                                                                                                                                                                                                                                                                  WPI; 2001-376931/40.
N-PSDB; AAH66447.
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24 ALNVLL 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 AA;
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                                              EP1108790-A2.
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                                                                           20-JUN-2001
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SM;
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                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
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2000US-0250160.
2000US-025031.
2000US-0251030.
2000US-0251988.
        02-0CT-2000; 2000US-0226802.
02-0CT-2000; 2000US-0237037.
02-0CT-2000; 2000US-0237038.
02-0CT-2000; 2000US-0237039.
02-0CT-2000; 2000US-0239935.
13-0CT-2000; 2000US-0239937.
20-0CT-2000; 2000US-0239937.
20-0CT-2000; 2000US-0241221.
                                                                                                                                                                                                                                                                           2000US-0249265.
2000US-0249297.
2000US-0249299.
                                                                                                                                                                                                                                                                                                                                                                   05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                                                 2000US-0249245.
                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-476224/51.
                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS28104.
                                                                                                            08-NOV-2000; 20
08-NOV-2000; 20
08-NOV-2000; 20
08-NOV-2000; 20
08-NOV-2000; 20
                                                                                                                                                                                                                                                                                                                                                               11-DEC-2000;
                                                                                                                                                   08-NOV-2000;
                                                                                                                                                                                    08-NOV-2000;
                                                                                                                                               08-NOV-2000;
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The present invention relates to the isolation of novel human respiratory antigens, and cDNA (AAS2/869-AAS28159) and genomic respiratory antigens, and cDNA (AAS2/869-AAS28159) and genomic respiratory antigens, and cDNA (AAS2/869-AAS28159) and genomic cord sequences encoding for these polypeptides. Treating and/or prognosing invention are useful for preventing, treating and/or prognosing disorders leaf. Phenomenia, allergic disorders e.g. asthma, allergic disorders e.g. asthma, concers of pleuristy, cystic fibrosis, emphysema, nose disorders and cancers of pleuristy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy. ANUTYSES-ARUTYSES represent novel human respiratory antigens. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat fip. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
 Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection {\rm e.g.}, diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate cancer antigen protein sequence SEQ ID NO:1456.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SED ID No 538; 546pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB56878 standard; Protein; 71 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              77.4
Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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28 LNIIMA 33
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                                                                                                                                                                                                                                                                                                                                                                                                           65 AA;
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Claim 11; Page 1890; 2338pp; English.

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          AAPI5566 to AAPI6505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56361 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAP16514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel bone marrow-expressed nucleic acids and polypeptides for research, diagnosis and treatment of haematopoietic, autoimmune, inflammatory disorders and cancer and for use in stem cell survival,
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                                                                                                                                                                                                                                                                                                               Score 24; DB 21; Length 71;
Pred. No. 2.3e+02;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel bone marrow polypeptide #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU27363 standard; Protein; 75 AA.
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                                                                                                                                                                                                                                                                                                              77.4%;
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18-MAY-2000; 2000US-0577409.
30-NOV-2000; 2000US-0250583.
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Best Local Similarity 66.7
Matches 4; Conservative
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N-PSDB; AAS43306.
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                                                                                                                                                                                                                                                                                71 AA;
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                                                                                                                                                                                                                                                invention.
                                                                                                                                                                                                                                                                                Seguence
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The invention relates to novel isolated bone marrow-expressed

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polymucleotide (I) (or its complement) comprising a sequence selected from 150 sequences of defined base pair sequences given in the specification, its mature coding portion or active domain coding portion.

(I) provided as a collection on a nucleic acid array is useful for detecting full-matches or mismatches to any one of the collection on a nucleic acid array is useful comparation in land its encoded polypeptides (II) are useful for treating inflammatory conditions such as arthritis, comparation and proliferation in increasing haematopoiesis, stem cell generation and proliferation in metastasis (II) is involved in cancer cell generation and proliferation in metastasis (II) and modulators of (I) are useful for creating transgenic animals useful for studying modulators or useful for creating transgenic animals useful for studying modulators of collypeptides (II) induces the proliferation of neurol cells and response and anyotrophic as well as for studying modulators of the polypeptide as well as for studying modulators of the polypeptide as well as for studying modulators of the polypeptide as well as for studying modulators of the polypeptide as well as for studying modulators of the creatment of nerve and brain tissue and is useful for treatment of central and peripheral nervous system diseases and anyotrophic lateral sclerosis. (II) is involved in chemotractic or chemokinetic activity, regulation of haematopoiesis and stonders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, constending the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the profice of the pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (II) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, and autoimmune disorders e.g. multiple sclerosis. AAU27323-AAU27472 represent human bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 2.5e+02;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                marrow polypeptide sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative 3
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AAE09109
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WO200158481-A2

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Novel vaccine for alleviating or preventing autoimmune disorders induced Epstein-Barr virus (EBV) infection e.g. systemic lupus erythematosus, juvenile onset diabetes mellitus, comprises EBV virus or
                                                                                                 Example 10; Page 56; 114pp; English.
                                        (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                  Harley JB, James JA, Kaufman KM;
                   09-FEB-2001; 2001WO-US04191.
                             09-FEB-2000; 2000US-0500904
                                                             WPI; 2001-522437/57
                                                                                                                                                                                                                                                                                                                                7 AA;
                                                                                        component
                                                                                                                                                                                                                                                                                                                                  Sequence
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The present invention relates to a vaccine for alleviating or preventing cautoimmune disorders induced by infection with Epstein-Barr virus (BEW), comprising BEW or its component in a carrier. The vaccine is useful for preventing or alleviating autoimmune disorders induced by EBW, e.g. preventing or alleviating autoimmune disorders induced by EBW, e.g. careful curve systemic lugus erythematosus (EBL), sjogener s syndrome, juvenile onset diabetes mallitus, rheumatoid arthritis, Wegener's granulomatosis, configuration at the standard provided in the standard provided in sease, adrenalitis, primary billary cirrhosis, demagnowish, multiple configurations and haemolytic anaemia, lupoid haparitis, demyelinating perindiculs and haemolytic anaemia, lupoid haparitis, demyelinating in the particular, pressler's syndrome, wystehenic layers, autoimmune cystitis, pemphigoid, dermaritis haparitis, alopecia areata, autoimmune cystitis, pemphigoid, dermaritis haparelic formis, alopecia areata, autoimmune cystitis, pemphigoid, dermaritis haparelicular, pressler's syndrome (articular), sclerosis, subbetes) male or female autoimmune inferrility, anticular cystitis, pemphigoid, sclerosis, systemic necrotising spondylitis, ulabetes) male or female autoimmune inferrility, analylosing spondylitis, ulabetes) male or female autoimmune inferrility, analylosing spondylitis, ulabetes) male or female autoimmune inferrility, and relanglecraisal, adult oner diabetes any submitties (Type II diabetes) male or female autoimmune inferrility, and relanglecraisal, atopic dermaritis, atopic dermaritis, and sease, maxed connective risue diaease, polyarteritis nodes, systemic necrotising carporering trisue diaease, polyarteritis in nodes, systemic necrotising erythema multiforme, posterony syndrome, custing, and sease, and posterony proderma gangrenome, custing, and and polycis, and proderma gangrenome, ribricange arcoindossum, transfund and solvanding syndrome, fibromyalgia, Takayasu's arteritis, wassaki's diaease, caplaris syndrome (triaditis, memo
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Length 7;
Query Match 74.2%; Score 23; DB 22; Length 7; Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 5; Conservative 0; Mismatches 0; Indels
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2 LNVLM 6

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Gaps ö

This peptide comprises amino acid residues 175-183 in the DEF box region (see AAW30501) of transcription factor DP1. Claimed peptides (II) (see AAW30502-07) containing this and/or another motif (see AAW30502-07) containing this and/or another motif (see C AAW30503) of the DBE box, are antagonists of the heterodimerisation of a DP protein with an B2F protein. Also claimed are variants of these peptides, especially containing substitutions of residues of these peptides, especially containing substitutions of residues of corresponding to residues 167, 169, 171 and 175 of DP-1, fusion of proteins (II) comprising (I) or (II) and a membrane translocation of sequence (see AAW30508), expression vectors encoding (I)-(III) and sequence (see AAW30508), expression vectors encoding (I)-(III) and sequence apoptosis, control, e.g. for purging bone marrow. Surgical stents comprising cuttor, e.g. for purging bone marrow. Surgical stents comprising cuttor, or prevent restenosis in patients who cut he DNA-binding activity of DP/E2F heterodimers. They are also cused as research reagents, as positive controls in assays for capturitying antagonists of DP-1/E2F dimerisation on dissimunossay identifying antagonists of DP-1/E2F dimerisation on dissimunossay identifying antagonists of DP-1/E2F dimerisation of controls in cells, cuttoric agents. Also described is the use of sequences antisense to particularly by gene therapy. When formulated with cytotoxic or cytostatic agents, (I)-(III) enhance cell killing. Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing restenosis ô DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy. Query Match 74.2%; Score 23; DB 19; Length 9; Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 5; Conservative 0; Mismatches 0; Indels DP-1 transcription factor antagonist peptide motif. AAW30502 standard; Peptide; 9 AA. Claim 3; Page 44; 55pp; English 97WO-GB03506. La Thangue NB; (first entry) (PROL-) PROLIFIX LTD. WPI; 1998-377596/32. 9 AA; 3 NVLMA 22-DEC-1997; 20-DEC-1996; Homo sapiens. WO9828334-A1. 02-JUL-1998. Bandara LR, 26-OCT-1998 Sequence AAW30502; 4AW30502 ð

Search completed: February 17, 2004, 10:53:44 Job time : 14.3069 secs

1 NVLMA 5

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Q989f3 fagopyrum e Q99f94 sulfolobus Q977x18 sulfolobus Q97x18 sulfolobus Q97x18 sulfolobus Q95x12 meisseria m Q95417 ceratosolen Q98f15 vibrio chol Q81100 hordeum vul Q81100 hordeum vul Q9519 macaca fasc Q9519 macaca fasc Q9519 macaca fasc Q9549 macaca fasc Q9540 listeria in Q98x12 bacillus an Q88x12 bacillus an Q88x12 bacillus an Q88x12 bacillus an Q88x13 excinia vi Q9501 witebesia br Q8901 witebesia br Q89410 vitebesia br Q89410 vitebesia br Q89410 vitebesia pr Q8741 sulfaberia de Q8741 sulfaberia

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182.261 Million cell updates/sec
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 YDALNVLMAMNIISKEKKEIKWIGLPTNSA 30
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                                                                   February 17, 2004, 10:50:12
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                                               - protein search, using sw model
                                                                                                                                                                                                                                                                                    SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_tungi:*
5: sp_invertebrate:*
5: sp_mammal:*
6: sp_mhc:*
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6: sp_phage:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Maximum Match 100%
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seq length: 100
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                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 84;
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                                                                                                                                                                                                                                                                                                                          Robison K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U15187; AAA63127.1; -.
SEQUENCE 84 AA; 9348 MW; D980B686AABDJEDA CRC64;
                                                                                                                                                                                                                                                              Smith D.R.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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01, Last sequence update)
01, Last annotation update)
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ALIGNMENTS
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Conservative
                                                                      Q50148 PRELIMINARY,
Q50148;
01-NOV-1996 (TTEMBLEG1. 0.
01-NOV-1996 (TTEMBLEG1. 0.
                                                                          PRELIMINARY;
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                                                                                                                                                                  Mycobacterium leprae
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Q9RIG5 Q9S895 Q9S896

Q50148 mycobacteri

Q50148 023974 Q8LR77 Q98R59

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STEAIN-EALB/C; TISSUE-Breast tumor;
MEDLINE=95024046; PubMed=7937892;
Bera T.K., Guzman R.C., Miyamoto S., Panda D.K., Sasaki M., Hanyu K.,
Enami J., Nandi S.;
"Identification of a mammary transforming gene (NATI) associated with
mouse mammary cardinogenesis.";
Proc. Natl. Acad. Sci. U.S.A. 91:9789-9793(1994).
EMBL: L31958; AAC3765-1; -
MGD: MGI:104799; Pea15.
SEQUENCE 61 AA; 7137 MW; DDC1F91842892171 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                               "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
EMBL; AL445563; CAC13324.1; -.
COMPLETE, MYPU.1510; -.
Complete proteome.
SEQUENCE 78 AA; 9386 MW; 05018A7BF7DB7TE46 CRC64;
                                                                                                                                                                                         STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson Moszer I., Pybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                     MYPU 1510.
Mycoplasma pulmonis.
Bacteria; Pirmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2107;
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Pred. No. 94;
5; Mismatches 6; Indels
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Last annotation update)
 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
01-OCT-2001 (TremBlrel. 18, Last annotation update)
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PEAIS OR MATI.
Mus musculus (Mouse).
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                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Epermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Oryza sativa (japonica cultivar-group).

Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideee; Oryzeae; Oryza.
                                                                                                                                                                  STRAIN=cv. Columbia;
MEDLINE=98416763; PubMed=9744100;
Simpson C.G., Mcquade C., Lyon J., Brown J.W.S.;
"Characterisation of exon skipping mutants of the COP1 gene from
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STRAIN-EV. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC olone:P0408003.",
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP0033241; BAB93228.1; -.
SEQUENCE 75 AA; 8520 MW; 608CC28EA3177DE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 28.3%; Score 43; DB 10; Length 75; Local Similarity 28.6%; Pred. No. 91;
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8; Mismatches
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PROSITE; PS00679; WD REPEATS_1; 1.
PROSITE; PS50002; WD REPEATS_2; 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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DKLRATYAFDVLHREKATIRFLGSASRS
                                               Arabidopsis thaliana (Mouse-ear cress).
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Plant J. 15:125-131(1998).
EMBL; AJ000536; CAA04169.1; -.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 24.1%; 7; Conservative
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Matches 7; Conserv
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                                                                                                                   NCBI_TaxID=3702;
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RESULT 4 Q98R59

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Best Loc Matches

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MEDLINE-21311952; PubMed=11418146;
MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                         Ectromelia virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                    Chen N., Buller R.M.L., Wall E.M., Upton C.,
"Analysis of host response modifier ORFs of ectromelia virus, the
causative agent of mousepox.";
Virus Res. 66:155-173(2000).
EMBL, AF012825; AAC99564.1; --
SEQUENCE 87 AA, 9879 MW; ECAC2FA1023BAACE CRC64;
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MEDLINB=22040717; PubMed=12044378;
MEDLINB=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi Nagai Y., Takeuchi F., Kuroda H., Cui L., Yangamoto K., Hiramatau K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 12; Length 87;
Pred. No. 1.5e+02;
2; Mismatches 7; Indels
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1-JUNAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SAVI595 (Hypothetical protein MW1546)
SAVI595 OR SA1423 OR MW1546.
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96 AA; 11081 MW; E3C1845499AB3CA4 CRC64;
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Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879, 196620;
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MEDLINE=20192152; PubMed=10725549;
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Pfam; PF01985; UPF0044; 1.
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Best Local Similarity 52.6%;
Matches 10; Conservative ;
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                                                                                                                                           Orthopoxvirus.
NCBL_TaxID=12643;
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SEQUENCE 90
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                                                                                                                                                                                                                                                                                                                                    STRAIN=Ankara;
Antoine G., Scheiflinger F., Falkner F.G., Dorner F.;
"The complete genomic sequence of the Modified Vaccinia Ankara (MVA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                       Vaccinia virus (strain Ankara).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Pred. No. 1.3e+02;
2; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U94848; AAB96552.1; -. SEQUENCE 74 AA; 8501 MW; 7152A06380829716 CRC64;
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SEQUENCE 76 AA; 8966 MW; 67D288E4D56D431F CRC64;
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Last annotation update)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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First ORF in transposon ISC1491,
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STRAIN=GOED / GOI / ATCC BAA-199 / DSM 3647 / OCM 88;

STRAIN=GOED / GOI / ATCC BAA-199 / DSM 3647 / OCM 88;

STRAIN=22120827; PubMed=12125824;

DEPDERMEIST V., Johann A., Hartsch T., Merkl R., Schmitz R.A.,

Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,

Martinez-Arias R., Henne A., Wiezer A., Boemecke M., Steckel S.,

Brueggemenn H., Lienard T., Christmann A., Boemecke M., Steckel S.,

Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,

Fritz H.-J., Gottschalk G.;

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transfer between Bacteria and Archaea..;

J. MOI. Microbiol. Biotechnol. 4:453-461(2002).

EMBL; AE013382; AAM31179.1; -.
                                                                 Gaps .
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STRAIN=MB4 / JCM 11007;
MEDLINE=21992816; PubMed=11997336;
Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
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40.7%; Pred. No. 1.6e+02;
trive 4; Mismatches 8; Indels
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
VCBL_TaxID=119072;
   Length 96;
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Methanosarcinaceae, Methanosarcina
27.6%; Score 42; DB 16; Length 96
40.0%; Pred. No. 1.6e+02;
ive 6; Mismatches 9; Indels
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EMBL; AE013159; AAM25286.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 97 AA; 11081 MW; 62E2381204D99127 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Ferrous iron transport protein B.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein TTE2120.
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                                                                                                                                         2 DALNVLMAMNIISKEKKEIKWIGLP 26
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Best Local Similarity 40.7
Matches 11; Conservative
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SEQUENCE 74 AA;
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Matches 10; Conserv
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                 Query Match
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XI MEDIANE=2297686; PubMed=12368813;

Read T.D. J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
Read T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
A. Meyer T., Tsapin A., Scott J., Beanan M., Brinker L., Daugherty S.,
DeBoy R.T., Dodson R.J., Umayam L.A., White O., Wolf A.M.,
Madupu R., Peterson J., Umayam L.A., White O., Wolf A.M.,
A. Wanthevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
Medone sequence of the dissimilatory metal ion-reducing bacterium
Strand Decembol. 20.1118-1123(2002).

EMBL; AE015551; AANS4141.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales,
Alteromonadaceae, Shewanella.
NCBI_TaxID=70863;
                                                  1;
  Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.0%; Score 41; DB 16; Length 75; 23.8%; Pred. No. 1.8e+02;
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                  Indele
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SEQUENCE 75 AA; 8592 MW; D243608FA8177F2C CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Score 41.5; DB 17;
Pred. No. 1.5e+02;
5; Mismatches 12;
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MEDLINE=21176366; PubMed=11277691;
Lee H.J., Essani K., Smith G.L.;
                                                                                                                                                                                                                                                                                        PRT;
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01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
          27.3%;
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     Query Match
Best Local Similarity 37.99
Matches 11; Conservative
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Best Local Similarity
   buckwheat seed.";
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EMBL; AJ238284; CAB57394.1; -...

Interpro; IPR002178; PTS_EIIA_2.

Pfam; PF00359; PTS_EIIA_2:

Hypochetical proteIn.
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01-MAY-2000 (TrEMBLEAL: 13, Last sequence update)
01-JUN-2001 (TrEMBLEAL: 17, Last annotation update)
BTI-2=TRYPSIN inhibitor isoform.
Fagopyrum esculentum (Common buckwheat).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Polygonaceae; Fagopyrum.
NCBI_TAXID=3617;
"The genome sequence of Yaba-like disease virus, a yatapoxvirus.";
Virology 281:170-192(2001).
                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                              Lee H.J.;
Thesis (2000), Sir William Dunn School of Pathology, University EMBL; AJ293568; CAC21388.1; -. SEQUENCE 100 AA; 12130 MW; 5C5F098C03D6C337 CRC64;
                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                       Bach S., Buchrieser C., Prentice M., Guiyoule A., Maadek T.,
Carniel E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.6%; Score 40.5; DB 2; Length 65; 42.9%; Pred. No. 1.9e+02; ive 7; Mismatches 4; Indels
                                                                                                          27.0%; Score 41; DB 12; Length 100; 35.5%; Pred. No. 2.4e+02; ive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 AA; 7404 MW; 90E14C97C1216DF6 CRC64;
                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                         59 YSFFNPLRLINKINPFYKEEKKEGILNWLGM 89
                                                                                                                                                                                                                                              65 AA.
                                                                                                                                                          1 YDALNVLMAMNIIS----KEKKE--IKWIGL 25
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Hypothetical 7.4 kDa protein (Fragment).
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WDRSNVMFIAIGVIAKEKEHI 30
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Matches 9; Conservative
                                                                                                                     Local Similarity 35.5
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                                    SEQUENCE FROM N.A.
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Q9RIG5
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Belozersky M.A., Dunaevsky Y.E., Musolyamov A.X., Egorov T.A.; "Complete amino acid sequence of the protease inhibitor from buckwheat
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01-UNN-2001 (TERMELEE) 17, Last annotation update)
BWI-1-PROTEASE inhibitor/trypsin inhibitor.
Fagopyrum esculentum (Common buckwheat).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Caryophylidae, Caryophyllidae, Polygonaceae; Fagopyrum.
NCBI_TAXID=3617;
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                                                                                                                                                                                                           Length 69;
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                                                                                                                                                               69 AA; 7748 MW; B2189CFC60C7E178 CRC64;
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40.9%; Pred. No. 2.4e+02;
tive 4; Mismatches 9;
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Pred. No. 2.4e+02;
4; Mismatches 9
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Pfam; PF00280; potato inhibit; 1.
ProDom; PD002864; Potato inhibit; 1.
PROSITE; PS002865; POTATO INHIBITOR; 1.
SEQUENCE 69 AA; 7634 WW; ADC20CFC
                                                                 Pfam; PF00280; potato inhibīt; 1.
PRINTS; PR00292; POTATOINHETR.
PROBOD ; PD002604; POTATO inhibīt; 1.
PROSITE; PS00285; POTATO INHIBITOR;
SEQUENCE 69 AA; 7748 MW; B2189CP
Phytochemistry 43:327-331(1996).
HSSP, P19873, 1HYM.
InterPro, IPR000864; Potato inhibit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97015347; PubMed=8862028;
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HSSP; P19873; 1HYM.
                                                                                                                                                                                               Query Match
Best Local Similarity 40.9%;
Matches 9; Conservative
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She Q., Singh R.K., Confaioneri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Madina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gasterland T.,
Charlebois R.L., Regan M.A., Sensen C.W., Van der Oost J.;
The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                           Complete protecme.
SEQUENCE 76 AA; 8938 MW; 97C59FE4D56D5A22 CRC64;
STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
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Q9JZ72
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SERRAINEATCG 35092 ( DSM 1617 / P2;

MEDLINE=21332296; PubMed=11427726;

She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Claumen I.G., Curtis B.A.,

Awayez M.J., Chan-Weiher C.C.-Y., Claumen I.G., Curtis B.A.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Haikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schen M.B., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A., 98:7835-7840(2001).
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Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobases;
Sulfolobus.
Sulfolobus.
YOCH _ TaxID=2287;
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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Pred. No. 2.6e+02;
6; Mismatches 6; Indels
                                                                                                                                                                                                                                                   Query Match 26.3%; Score 40; DB 10; Length 69; Best Local Similarity 40.9%; Pred. No. 2.4e+02; Matches 9; Indels Matches 9; Indels
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                                             FEES Lett. 371:264-266(1995).
HSSP, P19873; 1MIT.
INTECPEO, IPROODG64; POTATO inhibit.
Pfam, PRO0280; POTATOINHBIT.
PRODDOM; PRO0260; POTATOINHBIT.
PRODOM; PRO02604; POTATO_INHIBIT.
PROSTITE; PSO0285; POTATO_INHIBITOR; 1.
SEQUENCE 69 AA; 7748 MW; A91887E760DCE178 CRC64;
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01-077-2001 (TrEMBLrel. 18, Last sequence update)
01-077-2001 (TrEMBLrel. 18, Last annotation update)
First ORF in transposon ISC1491.
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 18, Last annotation update)
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Best Local Similarity 40.0%;
Matches 8; Conservative
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SEQUENCE FROM N.A.
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097YB4
AC 097YB
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"Complete genome sequence of Neisseria meningitidis serogroup B strain
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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Score 40; DB 17; Length 76;
Pred. No. 2.6e+02;
6; Mismatches 6; Indels
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SEQUENCE 90 AA; 10394 MW; E8C7B77BD078225A CRC64;
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Last sequence update)
Last annotation update)
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein NMB1264.
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TIGR; NMB1264; -.
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                        Query Match 26.3%;
Best Local Similarity 40.0%;
Matches 8; Conservative
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      WavE (Fragment).
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                                                                Vibrio cholerae.
                                                                                                                                                          NCBI_TaxID=666;
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QBLLBO;
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                             Mustela putorius furo (Ferret).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Pissipedia, Mustelidae, Mustelinae,
                                                                                                                                                                                                                                              TISSUE=Retina;
Obbson P.T., Reese B.E.;
"Developmental patterns of protein expression in photoreceptors
implicate distinct environmental vs. cell intrinsic mechanisms.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR26527; AAL2734.1; -.
InterPro; IPR001622; K+channel_pore.
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Neopera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
Agaonidae; Agaoninae; Ceratosolen.
NCBI_TaxID=130003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Phylogenetic analyses of dioecious fig pollinators based on mitochondrial DNA sequences and morphology."; Submitted (CCT.1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF200391; AAK00090.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 26.3%; Score 40; DB 6; Length 93; I Similarity 43.5%; Pred. No. 3.2e+02; 10; Conservative 3; Mismatches 8; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Cytochrome oxidase subunit II (COII) gene (Fragment)
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|DAIKQYMHFRNVSKDMEKRVIKW 87
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cGMP-gated channel (Fragment)
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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Best Local Similarity
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                             NCBI_TaxID=9669;
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NON TER
SEQUENCE
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SEQUENCE
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QBRJL5
ID QBRJL
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DT 01-JU
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"Comparative and genetic analysis of the putative Vibrio cholerae LPS core oligosaccharide biosynthesis (wav) gene cluster.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF443847; AAL71348.1; -.
NON TER.
1 1 1
SEQUENCE 74 AA, 8845 MW; 2BDCD57E37F6FCE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Morex;
PubMed=1217030;
Whei F., Wing R.A., Wise R.P.;
"Genome dynamics and evolution of the Mla (powdery mildew) resistance
                                                                                                                                        STRAIN=V209;
Nesper J., Kraiss A., Schild S., Blass J., Klose K.E., Bockemuehl J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.7%; Score 39; DB 10; Length 72; 37.0%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD002604; Potato_inhibit; 1.
SEQUENCE 72 AA; 7676 MW; 2030854E398438AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         Score 39.5; DB 2;
Pred. No. 3e+02;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YDALNVLMAMNIISK----EKKEI-----KWIGL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 YDLKDWLYLNGLÍSKNTLIDKKRÍYRAYKKWTGĽ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                locus in barley.";
Plant Cell 14:1903-1917(2002).
EMBL; AF427791; AAM22827.1; -.
InterPro; IPR000864; Potato inhibit.
Pfam; PF00280; potato inhibit,
PRINTS; PR00292; POTATOINHBTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Best Local Similarity 38.2%;
Matches 13; Conservative 3
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TISSUB=Testis;
Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
Terao K., Sugano S.;
"Isolation of novel full-length cDNA clones from macaque testis cDNA
                       Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 6; Length 83;
Pred. No. 4e+02;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB070133; BAB63078.1; -.
Hypothetical protein.
SEQUENCE 83 AA; 9450 MW; 7EC2FFA2706CA3F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein lin0631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 AA.
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STRAIN=CLIP 11262 / Serovar 6a;
PubMed=11679669;
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Hypothetical 9.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.7%;
38.9%;
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Best Local Similarity 32.0
Matches 8; Conservative
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                                                                                                                                         Cercopithecinae, Macaca
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                            NCBI_TaxID=9541;
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Q9K1V1
ID Q9K1V1
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Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHockins J., Alborn W.E. Jr., Arnold J., Fuller W., Geringer C., Estrem S.T., Fritz L., Fuller W., Geringer C., Gilmour R., Glass J.S., Knoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McCaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
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                                                                                                                                                                                                                                                              MEDLINE-22220767; PubMed-12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Genome of the bacterium Streptococcus pneumoniae strain R6.";

J. Bacteriol. 183:5709-5717(2001).

EMBL; AE008411; AAK99104-11; -1.

Hypothetical protein; Complete proteome.

SEQUENCE 80 AA; 9100 MW; 72BA09DAS83E8980 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.7%; Score 39; DB 16; Length 73; 27.6%; Pred. No. 3.5e+02; ive 9; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMEL, AP004664, BAC15339.1, -.
Hypothetical protein, Complete proteome.
SEQUENCE 73 AA, 8225 MW, 5BFFE3515EB4A152 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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   Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Oceanobacillus.
NCBI_TaxID=182710;
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-HTE831 / DSM 14371 / JCM 11309;
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Matches 7; Conservative
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01-DEC-2001 (
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Q8CZ72
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Q95JP8
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Glaster P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
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Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkar G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Sinoes N., Tierrez A.,
"Comparative genomics of Listeria species.";
Science 294:849-855(2001).
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STRAIN=A2012;
MEDLINE=22061436; PubMed=12004073;
Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
Roltrapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
Keim P., Fraser C.M.;
Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
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Science 296:2028-2033(2002).
Science 296:2028-2033(2002).
Hypothetical protein; Plasmid.
SRQUENCE 39 AA; 4581 MW; 8D485CBCDCE3E177 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi J. Agaba Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramateu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.0%; Score 38; DB 16; Length 44; 44.4%; Pred. No. 3e+02; 1ive 3; Mismatches 7; Indels
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                                                                                                                                                                        Plasmid pXO1.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1392;
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Last annotation update)
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Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus
                     39 AA.
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EMBL; AP004829; BAB95824.1; -.
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1 MDIFRKNEKSILWVNM 16
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Matches 8; Conservative
                   QBKYL2
QBKYL2;
01-OCT-2002 (TEMBLrel. 22,
01-OCT-2002 (TEMBLrel. 22,
01-OCT-2002 (TEMBLrel. 22,
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Best Local Similarity 37,55
Best Local 6; Conservative
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                                                                                                         Hypothetical protein. BXA0150.
                                                                                                                                                    Bacillus anthracis.
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Q98P05;
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Q98P05
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                                                                                                                                                                                                                                              Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
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"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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                                                                                                             Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
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Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical Trp-Asp repeats containing protein (Fragment).
SPAC18B11.10
SChizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 45 AA; 5716 MW; 499DD769E7EE4BE3 CRC64;
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Q9K1V1;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein CP0930.
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Nucleic Acids Res. 28:1397-1406(2000).
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01-MAY-2000 (TrEMBLrel. 13, Last seg
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INKLKRELEELGVEANTA 22
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NCBI_TaxID=4896;
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les 7; Conserv
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Matches

RESULT 31

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Gaps

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Vaccinia virus (strain Tian Tan).
Vaccinia virus (strain Tian Tan).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                   STRAIN=Tian Tan;
Jin Q., Hou Y.D., Cheng N.H., Yao B.M., Cheng S.X., Yang X.K.,
Jin Q., Hou Y.D., Yu W.H., Yuan J.S., Ma X.J.;
Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;
"Complete genomic sequence of vaccinia virus (Tian Tan strain).";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF095689; AAR34080.1;
SEQUENCE 76 AA; 8616 MW; 7066B8FlA9D2F522 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bukaryota; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea; Agaonidae; Agaoninae; Wiebesia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATAIN=B120;
Weiblen G.D.;
Weiblen G.D.;
Weiblen G.D.;
Weiblen G.D.;
Weiblen G.D.;
Weiblen G.D.;
Weiblen G.D.;
Weiblen G.D.;
Weiblen G.D.;
Weiblen G.D.;
Weiblen G.D.;
Weiblen G.D.;

Intechondrial DNA sequences and morphology.";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

InterPro; IPR00442; ARK00126.1; -.

InterPro; IPR005429; Cyt.c.ox.2.

Pram; PR02190; COXZ TW; T..

PRINTS; PR01166; CYGOXIDASEII.

Oxidoreductase; Transmembrane; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.0%; Score 38; DB 12; Length 76; ilarity 47.4%; Pred. No. 5.2e+02; Conservative 3; Mismatches 7; Indels
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25.0%; Score 38; DB 8; Length 81;
Best Local Similarity 36.7%; Pred. No. 5.5e+02;
Matches 11; Conservative 5; Mismatches 10; Indels
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SEQÜENCE 81 AA; 9471 MW; 921D08E561CAB91A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Cytochrome oxidase subunit II (COII) gene (Fragment)
Miebesia brusi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8Y9B0;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein lmo0622.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TB11R.
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tes 9; Conserva
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                     Orthopoxvirus.
NCBI_TaxID=10253;
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Q8Y9B0
ID Q8Y9B
AC Q8Y9B
DT 01-MADT 01-MADT DT HYPOT
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Matches
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MEDLINE-21082930; PubMed=11214968;
MEDLINE-21082930; PubMed=11214968;
MEDLINE-21082930; PubMed=11214968;
MEDLINE-21082930; PubMed=11214968;
Mathemater T., Nakamura Y., Sato S., Asamira T.,
Mathida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,
Kishida Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
Mochizuki Y., Namada M., Tabata S.;
Mochizuki Y., Mamada M., Tabata S.;
Mochizuki J., Samada M., Tabata S.;
Esperi J., Apologori J., Bab54850.1; -
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 48 AA; 5187 MW; ABA2FC02CA77D6C4 CRC64;
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
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STEALNECV. Nipponbare;
Sasaki T., Matsuncto T., Yamamoto K.;
Gasaki T., Matsuncto T., Yamamoto K.;
Granati anipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0663E10.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP004317; BAB90729.1; -.
Gramene; Q8RXN3; -.
SEQUENCE 62 AA; 7432 MW; BA2F84ADB7B913EA CRC64;
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Pred. No. 4.2e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.0%; Score 38; DB 16; Length 48; 40.0%; Pred. No. 3.3e+02; tive 7; Mismatches 3; Indels
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
00663E10.12 protein.
                             01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein msr9763.
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1 MNLIS--KGQLREVGLPAHA 18
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58.3%;
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Best Local Similarity 40.0°
Matches 8; Conservative
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Matches 7; Conserv
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ID Q9JF42
AC Q9JF42;
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QBRYN3

DDT DDT REP REP BE REP

RESULT 34

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RESULT 35

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Foissac X., Svanella-Dumas L., Gentit P., Dulucq M.-J., Candresse T., "PDO RT-PCR : a polyvalent detection tool for an etiological and variability studies for tricho-, capillo- and foveaviruses of
                                                                                                                                                                                                                                                                                                                                        STRAIN=Casertal2;
Foissac X., Svanella-Dumas L., Gentit P., Dulucq M.-J., Candresse "PDO RT-PCR : a polyvalent detection tool for an etiological and variability studies for tricho-, capillo- and foveaviruses of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.0%; Score 38; DB 12; Length 96; 28.6%; Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 AA; 10982 MW; E264C91952F00474 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apricot latent virus.
Viruses; ssRNA positive-strand viruses, no DNA stage.
NCBI_TaxID=75387;
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                                                                                                                                                                                                Apricot latent virus.
Viruses; ssRNA positive-strand viruses, no DNA stage.
                                                                                     Last sequence update)
Last annotation update)
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Last annotation update)
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     96 AA.
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InterPro; IPR01788; RNA dep RNApol2.
InterPro; IPR007094; RNA_pol_FSvir.
Pfam; PP00978; RNA_dep_RNApol2; 1.
Pfam; PS0507; RDRP_POSITIUE; 1.
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seg
01-JUN-2002 (TrEMBLrel. 21, Last ann
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Best Local Similarity 28.00,
Local 8; Conservative
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     PRELIMINARY;
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MEDLINE=2153729; PubMed=11679669;

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Cherouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Cherouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Cherouani F., Couve E., de Daruvar A., Dehoux P.,

Butian K.-D., Feihi H., Garcia-del Portillo F., Garrido P.,

Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Mattournam A., Mata Vicente J., No B., Nodjari H.,

Nordeiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simes N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.0%; Score 38; DB 16; Length 92; 28.0%; Pred. No. 6.3e+02;
Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Complete proteome.
SEQUENCE 92 AA; 10656 MW; B1712506710528FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 AA; 11168 MW; CD748C4CE56E4A3A CRC64;
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"Genomics 77:43-49(2001).
EMBL; AJ303367; CAC33889.1; -.
InterPro; IPR000008; C2.
InterPro; IPR002149; LRI.
Pfam; PF00168; C2; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last seg
01-JUN-2002 (TrEMBLrel. 21, Last ann
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MEDLINE=21429112; PubMed=11543631;
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EMBL; AL591976; CAC98700.1; -. ·
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Best Local Similarity 28.0%;
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Matches 8; Conserv
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"Complete genome sequence of the alkaliphilic bacterium Bacillus "Complete genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL, APODIS19; BAB07231.1; -. EMBL, APODIS19; BAB07231.1; -. BAB1, BAB, 9454 MW; 471552D292B2A44F CRC64;
                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20515282; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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Pred. No. 5.56+02;
7; Mismatches 8; Indele 1:
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NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein BH3512.
01-MAY-1999 (TrEMBirel. 10, Created)
01-MAY-1999 (TrEMBirel. 10, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last annotation update)
Tyrosine kinase RYK (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DALINULMAMNIISK------EKKEIKWIGL 25
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Similarity 24.3%;
9; Conservative
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                   NCBI_TaxID=9031;
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Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin
Chen Z., Wen Y.;
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Pred. No. 6.6e+02;
R. Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 97;
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Similarity 43.8%; Score 38; DB 16; Length 97
7; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                                                    Pusobacterium nucleatum (subsp. nucleatum)
Bacteria; Fusobacteria; Pusobacterales; Fusobacteriaceae;
Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitting (100-2002) to the EMBL/GenBank/DDBJ databases. Submittal AE016(748; AA004880.1; -. Proteome. Hypothetical protein; Complete proteome. SEQUENCE 97 AA; 11165 MW; 8FB484B1968C4ECC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                      Last sequence update)
Last annotation update)
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Staphylococcus Bacteria; Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
                                                                                PRT;
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Best Local Similarity 32.0%;
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Matches 7; Conserv
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01-JUN-2002
01-JUN-2002
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RESULT 42

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Q9Y144 Q9Y144;

09Y144 ID 09

RESULT 43

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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1502;
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                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Small acid-soluble spore protein beta.
CPE1903.
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Q8XJ58
1D Q8XJ58
AT Q1.MAR-2.DT 01.MAR-2.DT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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Search completed: February 17, 2004, 10:56:24 Job time : 44.4752 secs

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GenCore version 5.1.6
Copyright (c) 1993. - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 17, 2004, 10:50:13; Search time 9.50495 Seconds (without alignments) 148.428 Million cell updates/sec Run on:

Title: Perfect score:

US-09-900-147-6 152 1 YDALNVLMAMNISKEKKEIKWIGLPTNSA 30 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

13973

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	TD	V089 FOWPV	YC53 ARCFU	Y246_METJA	VB11 VACCV	VB11_VACCC	VAPD HAEIN	BOFA_BACSU	RL29 SULTO	HLD STAAM	Y546 METJA	Y295_ARCFU	YDFK ECOLI	YNAE ECOLI	YQEI BACSU	YHBY ECOLI	TRPC_BACPU	COX2_LEPOC	COX2_LEPSP	FCEG MOUSE	Y511_BUCAP	RS24_THEAC	NU3M_NEUCR	RS16_STRA3	SECE_BACLI	YM32 MARPO	CSPA_RICCN	CSPA_RICPR		LEU2_HUMAN		1	- 1	Y117_NPVAC
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Gaps

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Length 65; 9; Indels

28.9%; Score 44; DB 1; llarity 31.8%; Pred. No. 8.1; Conservative 6; Mismatches 5

Query Match
Best Local Similarity
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2 DALNVLMAMNIISKEKKEIKWI 23 | : | : | : | : |: |: DFINTIMTVLTGKKESKQLSWL 43

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YC53_ARCFU
ID YC53_ARCFU STANDARD; PRT; 64 AA. AC 0.29015; DT 16-0CT-2001 (Rel. 40, Created)
DT 16-0CT-2001 (Rel. 40, Last sequence update)

P39230 bacteriopha P82708 bos taurus Q9ppy4 ureaplaama P58124 streptococc Q864019 streptococc Q12330 saccharomyc P51421 zea mays (m Q0699 bacillus su Q10365 schizosacch O6866 bacillus ce Q02406 bacitlus ce Q02406 bacitlus ce P11337 spiroplasma	65 AA.	ed) anguence update) annotation update) RNA stage; Poxviridae; Chordopoxvirinae;	BamHI-N fragment of fowlpox virus	JENCE FROM N.A. LINE-20193820; PubMed=10729156; LINE-20193820; PubMed=10729156; LINE-20193820; PubMed=10729156; Senome of fowlpox virus."; Senome of fowlpox virus."; Airol. 74:3815-3831(2000). SIMILARITY: BELONGS TO THE POXVIRUSES 12 FAMILY.	is produced through a col rmatics and the EMBL ou There are no restrictio ng as its content is i ved. Usage by and for See http://www.isb-sib.ch
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SPAC BPT4 RET5_BOVIN ACPH_UREPA RS16_STRPY RS16_STRPY RUS16_STRMY RUXE_YEAST RU32_MAIZE SECE_BACSU SECE_BACSU GEPD_BACCR V12J_BPT4 VG5_SPV4	PRT;	2.9	, 8782, aphy S., 4.3 kbp	0729156 Lu Z., us."; 0). THE PO	pyrigh e of B Insti utions is no agree @isb-s
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0 4 C 0 0 0 4 A 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	STANDARD;	מ הבינ	SEQUENCE FROM N.A. STRAIN=FP-9 / Isolate HP-440; STRAIN=EP-9 / Isolate HP-440; SPDIILE 5, Skinner M.A., Heaphy "Nucleotide sequence of the 4.3 k FP9."; Virus Genes 17:5-9(1998).	SEQUENCE FROM N.A. MEDLINE=20193820; PubMed=10729156; MEDLINE=20193820; PubMed=10729156; Affonso C.L., Tulman E.R., Lu Z., Z "The genome of fowlpox virus."; J. Virol. 74:3815-3831(2000)!- SIMILARITY: BELONGS TO THE POX	This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinformatics Institute. Use by non-profit institutions as low modified and this statement is not remodified and this statement is not remodified and this statement of not remodified and this statement of not remodified and this statement is not remodified and this statement is not remodified and this statement is not remodified and this statement of not send an email to license@isb-sib.ch] EMBL, AJ223385; CAA11292.1;
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222 222.0 222.0 222.0 221.1 211.7 211.7 211.7	ST	(Rel (Rel (Rel (Rel (Rel (Rel (Rel (Rel	M N.A. / Isolate H. / Isolate H. / Skinner M.A sequence of	3820, Tuln of fc :381; TY: H	S-PROT en the Swiss ean Bioli non-profi and this requires n email 23385; C7 23385; C7 65 AA;
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88888 8888 8888 8888 8888 8888 8888 8888	LT 1 FOWPV .V089 FOWPV 16-0CT-2001	1 2 2 8 8 9 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	SEQUENCE FROM N.A. STRAIN=FP-9 / Isolate HP MEDLINE=98451804; PubMed Pollitt E., Skinner M.A. "Nucleotide sequence of "Nucleotide sequence of FP9."; Virus Genes 17:5-9 (1998)	UENCE LINE=2 nso C. e genor Virol. SIMIL	This SWISS-PROT between the Swi the European Bio use by non-pro modified and thi entities require or send an email EMBL, AJ223385; EMBL, AJ223385; EMBL, AF198100;
6.6.6.6.6.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4	.7 1	16-OCT- 16-OCT- 16-OCT- Protein FPV089 Fowlpoxy Viruses Avipoxy NCBI_T3	SEQUEN STRAIN MEDLIN Pollit "Nucle PP9.";	SEQU MEDL Afon "The J. V	This Spetwee the Ethe Ethe Modified or Serici EMBL; EMBL;
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NCBI_TaxID=10254;
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ID VB11_VACCV
AC Q01229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake D.A., FitzGeraid L.M., Clayron R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,
Utterlack T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                     MEDLINE-9864934; PubMed-9388475; Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Kreinwick, Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D., Richardson D.L., Kerlavdge A.R., Graham D.B., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Kirness S., Reich C.I., McNail L.K., Badger J.H., Glodek A., Zhou L. Corton M.D., Spriggs T., Ariach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea, Euryarchaeota, Methanococci, Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                    Archaea; Euryarchãoota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 protein; Complete proteome.
64 AA; 7418 MW; CD6CF9F885F4FF15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 1;
Pred. No. 45;
4; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
  16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF1253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 AA
                                                                                                                          STRAIN=VC-16 / DSM 4304 / ATCC 49558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LNVLMAMNIISKEKKEIKWI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: : |: |: || ||||| |
42 LDKIEAVEEITKAKKEIKKI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001018; AAB90006.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein MJ0246.
                                                                                                                                                                                                                                                                                                                                       Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 50.0 tes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                              Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; D69406; D69406.
TIGR; AF1253; -
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
SEQUENCE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
                                                                                                                                                                                                                                                                                                   Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               057696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y246_METJA
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                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Klenk'H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91259063; PubMed-2045793; MEDLINE-91259063; PubMed-2045793; Smith G.L., Chan Y.S., Howard S.T.; "Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near the right inverted terminal repeat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccinia virus (strain WR).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                     Science 273:1058-1073(1996).
- SIMILARITY: STRONG, TO THE N-TERMINAL OF CHORISMATE MUTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGN: MUCLEY, MUCLEY PRODOZOU; Chorismate mut.
Pfam; PF01817; Chorismate mut; I.
PIRSP, PIRSP001501; Chor_mut_AroQ_pr; 1.
Hypothetical protein; Complete proteome.
SEGUENCE 99 AA; 11782 MW; 9759018D0A07E76C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 AA; 8184 MW; 372BE3DCE6AFAE07 CRC64;
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47.4%; Pred. No. 72;
tive 3; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.3%; Score 38.5; L
34.6%; Pred. No. 84;
tive 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LNVLMAMNIISKEKKEIK-WIGLPTN 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gen. Virol. 72:1349-1376(1991)
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4 DVTNVEDIINEIDREKEEI 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DALNVLMAMNIISKEKKEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 47.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U67480; AAB98234.1; -. PIR; G64330; G64330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, JQ1805, JQ1805.
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hes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sigma-K factor processing regulatory protein BOFA (Bypass-of-forespore
                                                                                  "Whole-genome random sequencing and assembly of Haemophilus influenzae
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Framer C.M., Smith H.O., Venter J.C.,
                                                                                                                                                              SEQUENCE OF 76-80.
MEDLINE=20137488; PubMed=10675023;
MEDLINE=20137488; PubMed=10675023;
MEDLINE=20137488; PubMed=10675023;
Gray C., Fountoulakis M.;
"Two-dimensional map of the protecome of Haemophilus influenzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=91088245; PubMed=2124672;
Alonso C., Shirahige K., Ogasawara N.;
"Molecular cloning, genetic characterization and DNA sequence analysis of the recM region of Bacillus subtilis.";
Nucleic Acids Res. 18:6771-6777(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 1; Length 91;
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the
subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70B23CDE28E083E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 AA
                                                                                                                                                                                                                                                                       Electrophoresis 21:411-429(2000).
-!- SIMILARITY: BELONGS TO THE VAPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96051385; PubMed=7584024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virulence; Complete proteome.
SEQUENCE 91 AA; 10543 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32728; AAC22108.1; -.
                                                                                                                            Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; HI0450; -.
Pfam; PF04605; VapD_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 1:1-14(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C64069; C64069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                            Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                          Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Appendix to 'The complete DNA sequence of vaccinia virus'."; Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 X 2 AA TANDEM REPEATS OF D-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 1; Length 88;
Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F81B3D279229AE02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 "The complete DNA sequence of vaccinia virus."; Virology 179:247-266(1990).
                                                                                                      (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Virulence-associated protein D.
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                                                               88 AA
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                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECURNCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7742800;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=91021027; PubMed=2219722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 DALNVLMAMNIISKEKKEI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gam
Pasteurellaceae, Haemophilus.
NCBI_TaxID=727;
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DVTNVEDIINEIDREKEEI
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88 AA; 9897 MW;
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                                                               STANDARD;
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tes 9; Conserv
                                                                                                                                                                                                                                                      Orthopoxvirus.
NCBI_TaxID=10249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLETE GENOME
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15-JUL-1999
                                                                                P21007;
01-FEB-1991
                                                                                                                         01-FEB-1991
16-OCT-2001
                                                                                                                                                                     Protein B11
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                                                               VACCC
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Gaps

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Indels

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VAPD OR

Matches

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ID VAPD HE
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OC BACTET
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4 LNVLMAMNIISKEKKEIKWIGL 25 | ::: : : | :||||: 11 LGLVILLFLSGSAAKPLKWIGI 32

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us-09-900-147-6.rsp

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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., RA Borrise R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., RA Chois S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Banizot F., Devine K.M., Dusterrhôft A., Ehrlich S.D., Emmerson P.T., Ra Fritz C., Fuliten M., Fulita Y., Fuma S., Galizzi A., Galleron P.T., RA Fritz C., Fuliten M., Fulita Y., Fuma S., Galizzi A., Galleron N., RA Fritz C., Fuliten M., Fulita Y., Fuma S., Galizzi A., Galleron N., RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Guiseppi G., Guy B.J., Hosono S., Hullow M., Klein C., RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., RA Kobayashi Y., Koetter P., Mizuno M., Mostl D., Nakai S., Noback M., Ra Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Noback M., Ra Persecan E., Pulit H., Mosuda S., Mauel C., Medigue C., RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Ra Pieger M., Ravolta C., Rocha B., Roche B., Rose M., Sadaie Y., RA Seto T., Scanlan B., Schleich S., Schroeter R., Scoffone F., Schleich S., Schroeter R., Scoffone F., Takagi T., Takagi T., Takamaru H., Weitzenegger T., RA Tosato V., Uchlyama S., Vandenbol M., Vannier F., Vassarctti A., Wandutt R., Waddler E., Wedler H., Weitzenegger T., RA Winters P., Wipat A., Yamamoch H., Waitzenegger T., RA Winters P., Wipat A., Yamamoch H., Waitzenegger T., RA Winters P., Wipat A., Yamamoch H., Waitzenegger T., RA Wohlda K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein B., Yoshikawa H., Danchin A., Tanchila H., Tahamara H., Danchin A., Tanka H., Waitzenegger T., Ramano K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein B., Yoshika H., Wandut B. S., Yoshika H., Yamamoch G., the Gram-positive bacterium Bacillus R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
MEDLINE-92250411; PubMed=1577688;
Ricca E., Cutting S.M., Losick R.;
"Characterization of bofA, a gene involved in intercompartmental
"cegulation of pro-sigma K processing during sporulation in Bacillus
subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (PROBABLE).
FF1DA14E6826B70E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
EXTRACELLULAR (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 174:3177-3184(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X17014; CAA34880.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D26185; BAA05259.1; -. EMBL; Z99104; CAB11799.1; -. PIR; B41869; B41869. Subtilist; BG10087; bofA.
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58 87
87 AA; 9010 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390:249-256(1997).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                         STRAIN-JCM 10545 / 7;
MEDLINE-21456156; PubMed=11572479;
MEDLINE-21456156; PubMed=11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Aokii K.-I., Masuda T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                        Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain?."; DNA Res. 8:123-140(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.3%; Score 37; DB 1; Length 88; 41.7%; Pred. No. 1.3e+02; tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9A5B120EB10382C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1991 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Delta-hemolysin precursor (Delta-toxin).
HLD OR SAV2035 OR SASO65.
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain N315), and
Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                               28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 50S ribosomal protein L29P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 AA.
                88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosomal protein; Complete proteome.
SEQUENCE 88 AA; 10277 MW; 9A5B120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF 00374; atypical; 1.
InterPro: IPR001854; Ribosomal L29.
Pfam, PF00831; Ribosomal L29; 7.
TIGRPAMS; TIGR00012; L29; 2.
PROSITE; PS00579; RIBOSOMAL L29; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP000982; BAB65412.1; -.
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                                                   28-FEB-2003 (Rel. 41, Created)
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                STANDARD;
                                                                                                                                      Sulfolobus tokodaii.
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nes 10; Conserv
                                                                                                                                                                                           NCBI_TaxID=111955;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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P01506;
                    SULTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Gaps

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Score 37; DB 1; Length 87; Pred. No. 1.2e+02; 7; Mismatches 9; Indels

h 24.3%; Similarity 27.3%; 6; Conservative

Query Match Best Local Similarity Matches 6; Conserv

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VARIANT
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                       SEQUENCE FROM N.A.

STRAIN=Mu50 / ATCC 700699, and N315;

MEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91126037; PubMed=2281085;
Raghunathan G., Seetharamulu P., Brooks B.R., Guy H.R.;
"Models of delta-hemolysin membrane channels and crystal structures.";
                                                                                                                                                                                                                                                                        hld,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: DELTA-TOXIN LYSES ERYTHROCYTES AND MANY OTHE MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                    STRAIN=Isolate GAL;
MEDLINE=96004766; PubMed=7565609;
Novick R.P., Projan S.J., Kornblum J., Ross H.F., Ji G.,
Novick R.P., Vandenesch F., Moghazeh S.;
"The agr P2 operon: an autocatalytic sensory transduction system in Staphylococcus aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The amino acid sequence of delta haemolysin purified from a canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=RN4220;
Bischoff M.;
"DNA for hld, agrB, and agrD genes of Staphylococcus aureus strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-80246463; PubMed-7398877;
Fitton J.E., Dell A., Shaw W.V.;
"The amino acid sequence of the delta haemolysin of Staphylococcus
                                                                                                                                                                                                                             STRAIN=NCTC 8325-4; MEDLINE=90158509; PubMed=2622452; Janzon L., Loefdahl S., Arvidson S.; alfactification and nucleotide sequence of the delta-lysin gene, adjacent to the accessory gene regulator (agr) of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fitton J.E., Hunt D.F., Marasco J., Shabanowitz J., Winston S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: ASSUMED TO INSERT AND OLIGOMERIZE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                     . Gen. Genet. 248:446-458(1995).
                                                                                                                                                                                                                                                                                                              Mol. Gen. Genet. 219:480-485(1989)
NCBI_TaxID=158878, 158879, 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'EBS Lett. 115:209-212(1980)
                                                                                                                                                                                        Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolate of S. aureus.";
FEBS Lett. 169:25-29(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins 8:213-225(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Canine variant;
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                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                   aureus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aureus."
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                                                                                                                                                                                                                                                                                                        DELTA-HEMOLYSIN.

PORYLATION (ABOUT 90% OF THE MOLECULES).

QO. -> A (IN CANINE STRAIN).

GDL. -> VEF (IN CANINE STRAIN).

W -> L (IN CANINE STRAIN).

ID -> AE (IN CANINE STRAIN).

ID -> AE (IN CANINE STRAIN).

T -> I (IN CANINE STRAIN).
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINES-96379999; Dubded=86808087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Serlawage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                         Pfam, PF05372; Delta lysin; 1.
Hemolysis; Formylation; Toxin; Transmembrane; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 1; Length 45;
Pred. No. 89;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3E6B661E0342CA01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 AA.
or send an email to license@isb-sib.ch)
                                    EMBL; AP003364; BAB58197.1; ALT_INIT.
EMBL, AP003135; BAB43122.1; ALT_INIT.
EMBL; X55543; CAA36780.1; ALT_INIT.
EMBL; AF230358; ARF43204.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67504; AAB98548.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5140 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein MJ0546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 23.7%;
Similarity 44.4%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VLMAMNIISKEKKEIKWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                      PIR; A01767; LESAD.
PIR; A89995; A89995.
PDB; 1DHL; 15-OCT-94.
PDB; 2DTB; 31-OCT-93.
PDB; 1DTC; 31-OCT-93.
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2190;
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Q57966;
01-NOV-1997 (
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16-OCT-2001
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Videa J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-RIZ / MG5655;
MEDLINE=97426617; Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasens J.D., Rode C.K., Rose D.J., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                              Bacherichia coli.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-i- SIMILARITY: STRONG, TO E.COLI YDFK.
                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; withe complete 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 1; Length 88;
Pred. No. 1.8e+02;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE000252; AAC74617.1; -.
PIR, C64909; C64909.
Ecodene; EQ1821; ydfK.
Hypothetical protein; Complete protecome.
BEQUENCE 88 AA; 10136 MW; 534806E2287CC6A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.UU-1998 (Rel. 36, Created)
15.UU-1998 (Rel. 36, Last sequence update)
15.SEP-2003 (Rel. 42, Last annotation update)
Hypothetical protein ynaE.
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                                                        Last sequence update)
88 AA
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PRT;
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                                   15-701-1998 (Rel. 36, Created)
15-701-1998 (Rel. 36, Last seq.
15-582-2003 (Rel. 42, Last anno
Hypothetical protein ydfk.
YDFK OR B1544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.7%;
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Best Local Similarity 44.1.
Best Local Similarity 69.1.
Si Conservative
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      STANDARD;
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                                                                                                                                                                                                   NCBI_TaxID=562;
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          YDFK ECOLI
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P76073;
                       P76154;
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Kienk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Kerlavage A.R., Graham D.E., Sutton G.G., Gill S.,
Kirkness E.F., Oudherty B.A., McKenney K., Adams M.D., Loftus B.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McMail L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Wasdman J.F., McDonald L., Utterback T.,
Sadow P.M., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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Pred. No. 1.5e+02;
2; Mismatches 8; Indels
                                                                                                                                                         Length 56;
                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales; Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                  PIR; B64368; B64368.
TIGR; MJ0546; -.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR, AF0295; -. Hypothetical proteome. Hypothetical protein; Complete proteome. SEQUENCE 74 AA; 8839 WW; ODCF5EF3B444B2F5 CRC64;
                                                                                                                   66CBFC395548BASD CRC64;
                                                                                                                                                              Score 36; DB 1; I
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                   23.7%; Sco...
35.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
                                                                                                     GLU-RICE
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                              4 LNVLMAMNII--SKEKKEIK 21
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LNIILGIKVIMLQKELEEVK 32
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PIR; G69286; G69286.
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                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created 16-0CT-2001 (Rel. 40, Last 81) 16-0CT-2001 (Rel. 40, Last and 16-0CT-2001 (Rel. 40, Last and 14) the second protein AF0295.
                                                                                                                          56 AA; 6460 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                 Query Match
Best Local Similarity 35...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaeoglobus fulgidus.
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Brunschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brunschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Disapel S., Exington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Alibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Akbayashi Y., Kootter P., Koningstein G., Krogh S., Kumano M.,
Abdyashi Y., Kootter P., Koningstein G., Krogh S., Kumano M.,
Abdyashi Y., Kootter P., Koningstein G., Krogh S., Kumano M.,
Akurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Akbayashi Y., Kootter P., Mizuno M., Moestl D., Nakai S., Noback M.,
Andina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rescort, A., Tacconi E., Schleich S., Schroeter R., Scoffone F.,
Schleich S., Schroeter R., Scoffone F.,
Schleich S., Schroeter R., Scoffone F.,
Schleich M., Taemakoshi A., Taragai T., Takahashi H., Takemaru K.,
A Rostothi M., Tamakoshi A., Taragai T., Varmier F., Vassarotti A.,
A Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
A Tosato V., Waller E., Wedler E., Wedler H., Weitzenegger T.,
A Tosato V., Wanier R., Wedler E., Wedler E., Wedler T.,
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STRAIN=168 / JH642;
MEDLINE=97124195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                        Score 36; DB 1; Length 88;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                         PIR; B64888; B64888.
ECGGEnt; EG1373; ynac
Hypothetical protein; Complete proteome.
SEQUENCE 88 AA; 10109 MW; 534B1813C77CC6A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 AA.
                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microbiology 142:3103-3111(1996)
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NIL--RNIFMKSKDTLKW 20
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                                                                                                                                                    EMBL; AE000234; AAC74457.1; -
                                                                                                                                                                                                                                                                                                        23.7%;
                                                                                                                                                                                                                                                                                                                                     44.48;
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                                                                                                                                                                                                                                                                                                                                                          8; Conservative
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                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P54454;
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YORI_BACSU
TYORI_BACSU
TYORI_BACSU
DT 01-0CT
DT 28-FEB
DE HYPOTH
DE HYPOTH
DE HYPOTH
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SPECIES-B.Coll; STRAIN-06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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"The complete genome sequence of Escherichia coli K-12.";
Science 27:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 96;
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53.3%; Pred. No. 1.9e+02;
ive 2; Mismatches 5; Indels
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Wang R., Kushner S.R.;
Sùbmitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D9BA3E935C161F54 CRC64;
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YHBY OR B3180 OR C3937 OR Z4542 OR EC84059 OR SF3220.
                                                                                                                                Nature 390:249-256(1997).
-!- SIMILARITY: BELONGS TO THE UPF0044 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
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TIGREAMS; TIGR00253; 1.
PROSITE; PS01301; UPF0044; 1.
Hypothetical protein; Complete proteome. SEQUENCE 96 AA; 10758 MW; D9BA3E935C
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NCBI_TaxID=562, 217992, 83334, 623;
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Escherichia coli 06,
Escherichia coli 0157:H7, and
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InterPro; IPR001890; UPF0044.
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Matches 8; Conservative
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01-NOV-1995
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Pfam; PF01985; UPF0044; 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157.";
Nucleic Acids Res. 30:4432-4441(2002).
-!- SIMILARITY: BELONGS TO THE UPF0044 FAMILY. STRONG, TO H.INFLUENZAE
                                                                                                                                                                                                                                                                                                                                                               [5]
SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Yasunaga T., Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genome comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES—S. flexner; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang Y., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Excensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                  SEQUENCE FROM N.A.

SPECIES=E.coli, STRAIN=0157:H7 / EDL933 / ATCC 700927;

SPECIES=E.coli, STRAIN=0157:H7 / EDL933 / ATCC 700927;

SPECIES=E.coli, STRAIN=01506551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Grotbeck E.J., Davis N.W., Lim A., Shao Y., Miller L.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

"Genome sequence of enterchaaemorrhagic Escherichia coli O157:H7.";

Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sparkowski J., Das A.;
"The nucleotide sequence of greA, a suppressor gene that restores
growth of an Escherichia coli RNA polymerase mutant at high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lemperature.";
Nucleic Acids Res. 18:6443-6443(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE000398; AAC76212.1; -.
101376; -; NOT ANNOTATED_CDS.
AE001676; AAN82377.1; -.
AE005546; AAG58314.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91057148; PubMed=2243801;
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PIR, F85981; F85981.
ECGGENe, EG12794; yhbY.
INCEPPO, IPRO01890; UPF0044.
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-!- CATALYTIC ACTIVITY: 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose 5-
-!- CATALYTIC ACTIVITY: 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose 5-
phosphate = 1-(indol-3-yl)glycerol 3-phosphate + CO(2) + H(2)O.
-!- PATHMAY: Tryptophan biosynthesis; fourth step.
-!- SIMILARITY: BELONGS TO THE TRPC FAMILY.
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01-NOV-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Indole-3-glycerol phosphate synthase (EC 4.1.1.48) (IGFS) (Fragment).
                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rivas M.V., Jarvis E.D., Rudner R.; "The structure of the trpE, trpD and 5' trpC genes of Bacillus
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Pred. No. 1.9e+02;
7; Mismatches 7; Indels
                                                                                            23.7%; Score 36; DB 1; Length 97; 35.3%; Pred. No. 2e+02; ive 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus pumilus (Bacillus mesentericus).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
       Probom; PD010559; UPP0044; 1.
TIGRPAMB; TIGR00253; TIGR00253; 1.
PROSITE; PS01301; UPP0044; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 97 AA; 10784 MW; 52B4F7AD4C203382 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 AA; 7688 MW; DFDDBEFC80E7BDE4 CRC64;
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Probour; PS001511; IGPS; 1.
Tryptophan biosynthesis; Lyase; Decarboxylase.
NON_TER 68 68
                                                                                                                                                                                                                                                                                             68 AA
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Rivas M.V., Jarvis E.D., Rudner R.;
Gene 94:141-143(1990)
                                                                                                                                                                                                                                                                                             PRT;
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1 MLNQIIARKKEHIQTLQLPVD 21
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                                                                                                                                                                                                23.0%;
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HAMAP; MF 00134; -; 1.
InterPro; IPR001468; IGPS.
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Best Local Similarity 33.33
Matches 7; Conservative
                                                                                                                                            6; Conservative
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Best Local Similarity
Matches 6; Conserv
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NCBI_TaxID=1408;
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TRPC_BACPU
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RESULT 17 COX2_LEPOC

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Cytochrome c oxidase polypeptide II (EC 1.9.3.1) (Fragment). COXII OR COII.
28-FEB-2003 (Rel. 41, Last annotation update)
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InterPro; IPR001205; Copper CuA.
InterPro; IPR002429; Cyt c_ox_2.
Pfam; PF02790; COX2_TM; I.
                                                                                                                                                     MEDLINE=92130804; PubMed=1663569;
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les 9; Conser
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63
72
72 AA;
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                                                                                                          NCBI_TaxID=7917;
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                                                       Mitochondrion.
                                                                                               Lepisosteus
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P20491;
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SEQÜENCE
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Matches
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à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                             SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Electron transport; Respiratory chain.

26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                               -i- COFACTOR: Copper A.
-i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                             Mitochondrion.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Semionotiformes, Lepisosteidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
8
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MITOCHONDRIAL MATRIX (POTENTIAL)
                                                                                  28-FBB-2003 (Rel. 41, Last annotation update)
Cytochrome c oxidase polypeptide II (EC. 1.9.3.1) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AABC3332F740FA32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 1;
Pred. No. 2e+02;
7; Mismatches
                                                                             Last sequence update)
Last annotation update)
                                     72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 LYIIVAMVSTKLTNKHILDSQEVBIVWTILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                 Lepisosteus oculatus (Spotted gar).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR001505; Copper_CuA.
InterPro, IPR002429; CYC, c_ox_2.
Pfam; PF02790; COX2_TM; I_
PROSITE; PS00078; COX2; PARTIAL.
                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M64898; AAB01464.1; -. EMBL; M64901; AAB01467.1; -.
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                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                     NCBI_TaxID=7918;
                                                                                                                                                                                                                                                                                                                                                                                                     + 2 H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COX2 LEPSP
P29656;
01-APR-1993
                                    LEPOC
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TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                                                                                                          Normark B.B., McCune A.R., Harrison R.G.;
Normark B.B., McCune A.R., Harrison R.G.;
"Phylogenetic relationships of neopterygian fishes, inferred from mitochondrial DNA sequences.";
Mol. Biol. Evol. 8:819-834(1991).
-! FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. Subunit 2 transfers the electrons from cytochrome c via its binuclear copper A center to the bimetallic center of the catalytic subunit 1.
--- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00078; COX2; PARTIAL.
Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c + 2 H(2)O.
-!- COFACTOR: Copper A.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
High affinity immunoglobulin epolion receptor gamma-subunit p(FCERI) (IgB Fc receptor gamma-subunit)
Lepisosteus spatula (Alligator gar) (Atractosteus spatula)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 1; Length 72;
Pred. No. 2e+02;
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(Rel. 25, Created) (Rel. 25, Last sequence update)

RESULT 18
COX2 LEPSP
ID COX2 L
AC P29656
DT 01-APR
DT 01-APR

Matches

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SEQUENCE FROM N.A.
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Q9HJ79;
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NU3M_NEUCR
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RS24 THEAC
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                                                                                                                                                                                           MEDLINE=22004549; PubMed=12009438; Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S., Tamas I., Klasson L., Canbaeck B., Moren N.A., Andersson S.G.E.; Mernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; "50 million years of genomic stasis in endosymbiotic bacteria."; Science 296:2376-2379 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
HIGH AFFINITY IMMUNOGLOBULIN EPSILON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                           SEQUENCE FROM N.A.

MEDLINE=89359361; PubMed=2527850;

Ra C., Jouvin M.H.E., Kinet J.-P.;

"Complete structure of the mouse mast cell receptor for IgE (FC epsilon RI) and surface expression of chimeric receptors

(rat-mouse-human) on transfected cells.";
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Pred. No. 2.5e+02;
3; Mismatches 7; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein BUS9511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 AA
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InterPro; IPR003110; ITAM.
PFam; PF02189; ITAM; 1.
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Best Local Similarity 44.4%;
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9652 MW;
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24
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86 AA;
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Q8K946;
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TRANSMEM
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@license.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.M., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 407:508-513(2000).
-!- SIMILARITY: BELONGS TO THE S24E FAMILY OF RIBOSOMAL PROTEINS:
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Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 1; Length 95;
Pred. No. 2.7e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.0%; Score 35; DB 1; Length 98;
40.9%; Pred. No. 2.8e+02;
ive 4; Mismatches 1; Indels
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InterPro; IPR001976; Ribosomal S24E.

Prodom; PF001282; Ribosomal S24e; 1.

Prodom; P0006052; Ribosomal S24E; 1.

PROSITE; PS00529; RIBOSOMAL S24E; 1.

Ribosomal protein; Complete protecome.

Ribosomal protein; Complete protecome.
                                                                                                                                                                                                                          EMBL; AE014125, AAM68054.1; -.
Pfam; PF04077; DBrH; ..
Hypothetical protein; Complete proteome.
SEQUENCE 95 AA, 10992 WW; 51E8A2023BE57141 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG-FEB-2003 (Rel. 41, Last sequence update) 30S ribosomal protein S24e. Thermonless OR TAL092.
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MEDLINE=20479972; PubMed=11029001;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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MEDLINE=22222988; PubMed=12200547;
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HAMAP; MF 0038
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P38381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE=86220159; PubMed=3011426; de Vries H., Alzner-Deweerd B., Breitenberger C.A., Chang D.D., de Vries H., Alzner-Deweerd B., Breitenberger C.A., Chang D.D., de Jones J.C., Rajbhandary U.L., "The Bis stopper mutant of Neurospora crassa: precise localization of deletion endpoints in mitochondrial DNA and evidence that the deleted DNA codes for a subunit of NADH dehydrogenase."; EMBO J. 5:779-785(1986).

-I. CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

-I. SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 3 FAMILY.
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STRAIN-NEMBLE / Serotype III;
STRAIN-NEMBLE / Serotype III;
MEDLINE-22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                      01-Nov-1997 (Rel. 35, Created)
01-Nov-1997 (Rel. 35, Last sequence update)
15-UUL-1999 (Rel. 35, Last amnotation update)
NADH-ubiquinone oxidoreductase chain 3 (EC 1.6.5.3) (Fragment).
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                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X03793; CAA27419.1; -.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
NON TER 52 52
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Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Pred. No. 1.7e+02;
6; Mismatches 11; Indels
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52 AA
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PRT;
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Best Local Similarity 30.00,
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STANDARD;
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                                                                                                                                                                                                                           Neurospora crassa.
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NEUCR
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ID RS16_STRA3
DT 15-SEP.DE 30S F115-SEP.DE 30S F125-SEP.DE 30S STREPT(OC STREPT(OC STREPT(OC STRAIN) RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX MEDLIN RX M
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Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daudherty S.C., Daboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
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MEDLINE=88139159; PubMed=3277943;
Dubnau E., Weir J., Nair G., Carter L. III, Moran C.P. Jr., Smith Bacillus sporulation gene spo0H codes for sigma 30 (sigma H).";
J. Bacteriol. 170:1054-1062(1988).
                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Sireptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.7%; Score 34.5; DB 1; Length 90; 35.0%; Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus licheniformis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDCA763D78007CBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1994 (Rel. 30, Last sequence update) 01-OCT-1994 (Rel. 30, Last annotation update) Preprotein translocase sec8 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Promiser Processing Ribosomal Si6; I. ProDom; PD003791; Ribosomal Si6; I. TIGRFAMs; TIGR00002; Si6; I. TIGRFAMs; TIGR00002; Si6; I. Ribosomal protein; Complete processes SEQUENCE 90 AA; 10282 MW; CDCA763D78007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP; MF_00385; -; 1.
InterPro; IPR000307; Ribosomal_S16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVLMAMNIIS-KEKKEIKWI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 NPLVAENQVTIKEERVLEWL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL766850; CAD47087.1; -. EMBL; AE014254; AAN00229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1994 (Rel. 30, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 35.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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(Rel. 41, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00313; CSD; 1.
PRINTS; PR00050; COLDSHOCK.
ProDom; PD000621; Cold_shock; 1.
                                                                                                                                                                                                                                                                                                                                                                       PIR, E97827; E97827.
InterPro; IPR002059; Cold_shock.
                                                                                                                                                                                                                                                                                                                                                         EMBL; AE008653; AAL03559.1; -.
              28-FEB-2003 (Rel. 41, Last an Cold shock-like protein cspA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.4%;
Similarity 38.1%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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STRAIN=Madrid E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                     Rickettsia conorii.
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=782;
                                        CSPA OR RC1021.
                                                                                          NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSPA_RICPR
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CSPA_RICPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMED outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion.

Bukaryopta, Virdiplantae, Streptophyta, Embryophyta, Marchantiophyta,
Bukaryota, Virdiplantae, Streptophyta, Embryophyta, Marchantiopsida, Marchantiidae, Marchantiales, Marchantiineae,
Marchantiacee, Marchantia.
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                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                            01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Hypothetical 7.2 kDa protein in ATPA-COX1 intergenic region (ORF 62)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM .N.A.
MEDLINE=22114051; PubMed=1731062;
MEDLINE=22114051; PubMed=1731062;
MAGA K., Yamato K., Ohta E., Nakamura Y., Takemura M., Nozato N.,
Akashi K., Kanegae T., Ogura Y., Kohchi T., Ohyama K.;
"Gene organization deduced from the complete sequence of liverwort
"Gene organization deduced from the complete sequence of plant
mitochondrial genome."
J. Mol. Biol. 223:1-7(1992).
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                                                                                                                                                            Length 59;
                                                                                                                                                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion, Hypothetical protein.
SEQUENCE 62 AA; 7231 MW; D98D55A9EF768E64 CRC64;
                                                                                                                      30 50 POTENTIAL.
59 AA; 6775 MW; BD40479D9FAS837B CRC64;
                             EMBL; M29694; -; NOT_ANNOTATED_CDS.
InterPro; IPR001901; SecE.
InterPro; IPR005807; SecE_bac.
Pfam; PP00584; SecE; 1
TIGREMB; TIGR00964; 3a0501606; 1.
PROSITE; PS01067; SECE_SEC61G; 1.
                                                                                                                                                         Score 34; DB 1; I
Pred. No. 2.4e+02;
7; Mismatches 8;
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                                                                                                                                                                                                                                                                                                   62 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
        send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LNVLMAMNIISKEKKEIKWIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LNTRFQLTLIPKENSNTEFVG 28
                                                                                                                                                                                                             4 LNVLMAMNIISKEKKEIKW 22
                                                                                                                                                                                                                             1 MGIIKFLKNVGKEMKKVTW 19
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Q92GVI;
28-FEB-2003 (Rel. 41, Created)
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                                                                                                                                                            22.4%;
Local Similarity 21.1%;
hes 4; Conservative
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                                                                                                                                                                                                                                                                                                    YM32 MARPO
P38474;
                                                                                                                                     SEQUENCE
                                                                                                                            TRANSMEM
                                                                                                                                                                Query Match
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CSPA_RICCN
ID CSPA_RI
AC Q92GVI
DT 28-FEB
                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00357; CSP; 1.
PROSITE; PS00352; COLD SHOCK; 1.
Transcription regulation; DNA-binding; Activator; Complete proteome.
                                                                                                                                                                                                                                                                                                                                           "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson S.G.B., Zomorodipour A., Anderson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; The genome sequence of Rickettsia prowazekii and the origin of mitochondria...
                                                                                                                                                                                      STRAIN=Malish 7;

BEDLINE=21442074; PubMed=11557893;

Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,

Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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Pred. No. 2.8e+02;
2; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN 7 67 CSD.
SEQUENCE 70 AA, 7771 MW; 822E9714229FE03A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
CSPA OR RP670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 MAMNIISKEKKEIKWIGLPIN 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MATNIVGK----VKWYNSTKN 17
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Gaps

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DOMAIN

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Einhorn S., Oscier D.; "Cloning of two candidate tumor suppressor genes within a 10 kb region on chromosome 13q14, frequently deleted in chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
High affinity immunoglobulin epsilon receptor gamma-subunit precursor (FCERI) (IgE Fc receptor gamma-subunit) (FC-epsilon RI-gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu Y., Corcoran M., Rasool O., Ivanova G., Ibbotson R., Grander D., Iyangar A., Barranova A., Kashuba V., Merup M., Wu X., Gardiner A., Mullenbach R., Poltaraus A., Hullstrom A.L., Juliusson G., Chapman R. Iller M., Cotter F., Gahrton G., Yankovsky N., Zabarovsky E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Leukemia associated protein 2 (Deleted in lymphocytic leukemia
DLEUZ OR LEUZ.
22.4%; Score 34; DB 1; Length 72; 36.8%; Pred. No. 2.9e+02; ive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 AA; 10196 MW; DIEE021072A0E03B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.4%; Score 34; DB 1; Len
                                                                                                                                                                                                                                                                                                                                                                            84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 15:2463-2473(1997).
-!- FUNCTION: MAY ACT AS A TUMOR SUPPRESSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 AA.
                                      Pred. No. 2.96 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0008181; F:tumor suppressor; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98055620; PubMed=9395242;
                                                                                                                                      6 VLMAMNIISKEKKEIKWIG 24
                                                                                                                                                                                                  21 LLLETGVISKLKSGVKILG 39
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                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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                                   Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                            HUMAN
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P20411;
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       Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                         RESULT 29
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                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P41016; 1050.
InterPro; IPR002059; Cold_shock.
Pfam: PF00313; CSD; 1.
PRINTS; PR00050; COLDSHOCK.
ProDom; PR000621; Cold_shock; 1.
SMART; SM00357; CSP; 1.
PROSTITS; P800352; COLD SHOCK; 1.
Transcription regulation; DNA-binding; Activator; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93062802; PubMed=1435726; Terbail R.; Erchauder S., Driessen A.J.M., Freudl R.; Erchauder S., Driessen A.J.M., Freudl R.; Cloning and molecular characterization of the secY genes from Bacillus licheniformis and Staphylococcus carnosus: comparative analysis of nine members of the SecY family."; Only Gen. Cenet. 235:147-152(1992).
-!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S KIBOSOWAL RNA.
-!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
   SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.4%; Score 34; DB 1; Length 70; 38.1%; Pred; No. 2.88+02; Nismarches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus licheniformis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7441 MW; 6DC3BA681492E6C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F49FBF2FB344903E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
50s_ribosomal protein L15 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00256; L15; 1.
Pfam; PF01305; Ribosomal L15; 1.
PROSITE; PS00475; RIBOSOMAL L15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001196; Ribosomal_L15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAMNIISKEKKEIKWIGLPTN 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MATNIVGK----VKWYNSTKN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosomal protein; rRNA-binding.
                                                                                                                                                                                                                                                                                                                                     EMBL; AJ235272; CAA15108.1; -. PIR; B71673; B71673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 AA; 7785 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RL15 BACLI
P35138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
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Gaps

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Length 84; Indels

SO TAWAR RANGE COLOR COL

Gарв

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Length 90;

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                                                                                                                                                                                                        22.4%; Score 34; DB 1; Length 90;
26.3%; Pred. No. 3.7e+02;
tive 7; Mismatches 7; Indels
                                                                                                                                                              Hypothetical protein; Complete proteome.
SEQUENCE 90 AA; 10501 MW; 4D9FF2FDB25E338F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 NVLMAMNIISKEKKEIKWI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55
                                                                                                                                                                                                                                                                                             : | : :: | ||:: | 72 INYIHFVSLTLKHKKQMTW 90
                                                                                                                                                                                                                                                                         4 LNVLMAMNIISKEKKEIKW 22
                                                                                                                               EMBL; AP001119; BAB13223.1; -. Pfam; PF04077; DsrH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|: | |: |: |: |: |
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                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal protein. SEQUENCE 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                            Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=114186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPSN OR RPS14.
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Y117_NPVAC
ID _Y117_NPVAC
                                                                                                                                                                                                                                                                                                                                                                                        RS14 CARRU
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  Q9AIF4;
                                                                                                                                                                                                                                                                                                                                                         RESULT 32
RS14_CARRU
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                                                       Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Tokyo 1998;
WEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome Bequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          symbiotic bacterium).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIGH AFFINITY IMMUNOGLOBULIN EPSILON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 86; Pred. No. 3.5e+02; 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (BY SIMILARITY). BD7B12E804311687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR GAMMA-SUBUNIT.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gE-binding protein; Receptor; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein BUS30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 AA
                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=89097258; PubMed=2521376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buchnera sp. APS.";
Nature 407:81-86(2000).
-i- SIMILARITY: STRONG, TO E.COLI YHEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L04306; -; NOT_ANNOTATED_CDS.
PIR; S02118; S02118.
INCENTED; IPRO03110; ITAM.
Pfem; PF02189; ITAM; 1.
SMO0077; ITAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | |: | : | | : 54 DIASREKSDAVYTGLNTRN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 NIISKEKKEIKWIGLPTNS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.4%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Query Match
Best Local Similarity 36.00.
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86
82
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24
45
62
62
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86 AA;
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DISULFID
SEQUENCE
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Y530_BUCAI
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                                                                                                                                                                                                                                                                             Carsonella ruddii.
Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21125546; PubMed=11222582; Moran N.A., Baumann P.; Clark M.A., Baumann D., Thao M.L., Moran N.A., Baumann P.; Clark M.A., Baumann L., Thao M.L., Moran of a Psyllid endosymbiont."; Ubegenerative minimalism in the genome of a Psyllid endosymbiont."; J. Bacteriol. 183:1853-1861(2001).

-I- FUNCTION: Known to be required for the assembly of 30S particles and may also be responsible for determining the conformation of the 16S rRNA at the A site (By similarity).

-I- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 AA; 11392 MW; 4BF942A9C3A61AD7 CRC64;
                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
30S ribosomal protein S14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 AA.
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InterPro; IPR001209; Ribosomal S14.
Pfam; PF00253; Ribosomal S14; 1.
PROSITE; PS00527; RIBOSOWAL_S14; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
95
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22 ALNVNMALRKIALLLKPDKEI 42
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                                                                                                                                                                                  Signal, Periplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                      RETS BOVIN
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE,
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                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                P82708;
                                                                                                                                                                                                                                                                                                                                                           RESULT 35
RETS_BOVIN
                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93188183; PubMed=8383243; Salick H.E., Stormo G.D., Dyson R.L., Alberts B.M.; "Analysis of five presumptive protein-coding sequences clustered between the primosome genes, 41 and 61, of bacteriophages T4, T2,
                                                                                                                                                          Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D., "The complete DNA sequence of Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriophage T4.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                           5
         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 11.0 Map protein in HE65-PK2 intergenic region.
Autographa californica nuclear polyhedrosis virus (AcMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 95;
Pred. No. 3.9e+02;
7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G. Mesyanzhinov V., Ruger W., Stidham T., Thomas E.; "Bacteriophage T4 genome analysis."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kai T., Ueno H., Otsuka Y., Morimoto W., Yonesaki T., "Gene 61.3 of bacteriophage T4 is the spackle gene.";
                                                                                                                                                                                                                                                                                                                                                                         95 AA; 10992 MW; 68897B745ECE51C6 CRC64;
                                                                                                                                                                                                          -!- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
MEDLINE=99348509; PubMed=10417260;
                                                                                                                                               MEDLINE=94303173; PubMed=8030224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||: | : :|::|:|
NVLLVPNAL--KKRDVKYI 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 NVLMAMNIISKEKKEIKWI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virol. 67:2305-2316(1993).
                                                                                                                                                                                                                                                                                                                                                                                                 22.4%;
                                                                                                                                                                                                                                                                                                                                     EMBL; L22858; AAA66747.1; -
                                                                                                                                                                                    polyhedrosis virus.";
Virology 202:586-605(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spackle protein precursor,
SP OR 61.3.
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 36.8
1es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                PIR; F72864; F72864.
Hypothetical protein.
SEQUENCE 95 AA; 10
                                                                                     Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=10665;
                                                                                               NCBI_TaxID=46015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPAC BPT4
P39230:
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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SPAC_BPT4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Virology 260:254-259(1999).
-1- FUNCTION: NOT KNOWN. MUTANTS ALLOW SURVIVAL OF LYSOZYME MUTANTS.
-1- SUBCELLULAR LOCATION: Periplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Folli C., Calderone V., Ottonello S., Bolchi A., Zanotti G., Stoppini M., Berni R.;
"Identification, retinoid binding and X-ray analysis of a human retinol-binding protein.";
Proc. Natl. Acad. Sci. U. S.A. 98:3710-3715(2001).
-!- FUNCTION: Intracellular transport of retinol.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARIY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٠.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Retinol-binding protein III, cellular (CRBP-III) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33.5; DB 1; Length 42; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 97;
Pred. No. 3.9e+02;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E0A5E5E076C97965 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 AA; 4892 MW; ACB4F1399FDD7F09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
SPACKLE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.0%; Scott 47.6%; Pred. No. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PS00214, FABP, FALSE NEG.
Vitamin A, Retinol-binding, Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P82980; 1GGL.
InterPro; IPR000463; Fatty acid BP.
InterPro; IPR000566; Lipocin_cyFRBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21173623; PubMed=11274389;
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                                                                                                                                                                                                                                                                                                                                             EMBL; S57514; AAB25710.1; -.
EMBL; AF158101; AAD42510.1; -.
PIR; C45681; C45681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 AA; 10994 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.4%;
41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00061; lipocalin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 MNIISKEKKEIK 21
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49 MNIVKRDRPEMK 60
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outbreaks.";
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                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                            Nature 407:757-762 (2000).

-!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid biosynthesis (By similarity).

-!- PATHWAY: De novo fatty acid biosynthesis.

-!- PTM: 4'-phosphopantetheine is transferrated from CoA to a specific serine of the apo-ACP-like protein (Potential).

-!- SIMILARITY: Contains I acyl carrier domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Fatty acid biosynthesis; Phosphopantetheine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHOPANTETHEINE (BY SIMILARITY) 3CDB655FBFA968C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
6
                                                                                                                                                                                                               Glass J.I., Lefkowitz B.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.;
                                                                                                                               Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 22.0%; Score 33.5; DB 1; Length 77; Local Similarity 35.7%; Pred. No. 3.7e+02; hes 10; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                       complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pyogenes (serotype M3), and.
Streptococcus pyogenes (serotype M18).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
30S ribosomal protein S16.
RPSP OR SPY0840 OR SPYM3_0567 OR SPS1287 OR SPYM18_0900.
                                                                       (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 AA
                                                77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 DALNV-----LMAMNIISKEKKEI 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERM; PF00550; pp-binding; 1.
PROSITE; PS50075; ACP DOMAIN; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR006163; Pp_bind.
Interpro; IPR006162; Ppantne_attach.
                                                                                                         carrier protein homolog (ACP).
                                                 PRT;
                                                                                                                                                                                             STRAIN=Serovar 3;
MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus.
NCBI TaxID=1314, 198466, 186103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 36
77 AA; 8750 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE002149; AAF30918.1;
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                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                        NCBI_TaxID=134821;
                                                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                                                                                                                       urealyticum.";
                                                                         28-FEB-2003
                                                 ACPH_UREPA
                                                                                                15-SEP-2003
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                                                                                      28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P58124;
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RS16_STRPY
ID _RS16_S
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STRAIN=SSI-1 / Serotype M3;
STRAIN=SSI-1 / Serotype M3;
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
Hayashi H., Hamada S.;
The genome of invasive Streptococcus pyogenes; a comparative analysis
of S. pyogenes SSI-1, SF370 and MGASS12.";
submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A.

STRAIN-SF370 / ATCC 700294 / Serotype M1;

STRAIN-SF370 / ATCC 700294 / Serotype M1;

STRAIN-SF370 / ATCC 700294 / Serotype M1;

STRAIN-SF370 / ATCC 700294 / Serotype M1;

MEDLINE-21192564;

PERTAIN-21192684; PubMed=11296256;

PERTAIN-1 J., McShan W.M., Ajdic D.J., Savic D.J., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Qian Y., Clifton S.W., Roe B.A., McLaughlin R.;

Tomplete genome sequence of an M1 strain of Streptococcus pyogenes.";

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=MGAS315 / Serotype M3;
STRAIN=FAGA31808; PubMed=12122206;
MEDLINE=2213808; PubMed=12122206;
Mammarella N.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Vessy L.G., Musser J.M., "Genome sequence and comparative microarray analysis of serotype I group A Streptococcus strains associated with acute rheumatic few
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDC5E92FEAAB660E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          emergence.";
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
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ProDom; PD003791; Ribosomal_S16; 1.
TIGRRAMs; TIGR00002; S16; 1.
PROSITE; PS00732; RIBOSOMAL_S16; FALSE_NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 90 Aa; 10252 MW; CDC5E92FEAAB6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          00385; -; 1.
IPR000307; Ribosomal S16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 NVLMAMNIIS-KEKKEIKWI 23
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Matches 8; Conservative
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Abelson J.;
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                                                                                                                                              SEQUENCE
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for scannercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=UALS9 / ATCC 700610 / Serotype C;
STRAIN=UALS9 / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UALS9, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Sm-E)
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.0%; Score 33.5; DB 1; Length 91; 33.3%; Pred. No. 4.4e+02; ive 7; Mismatches 6; Indels . 1;
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1-NOV-1997 (Rel. 35, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
Small nuclear ribonucleoprotein E (snRNP-E) (Sm protein E)
                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1E7329D1BDFF6EC2 CRC64;
                                                                                                                                                       15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
30S ribosomal protein S16.
Strenton
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                                                                                                                                              91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribosomal protein; Complete proteome SEQUENCE 91 AA; 10410 MW; 1E7329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE014928; AAN58580.1; -. HAMAP; MF 00385; -; 1. InterPro; IPR000307; Ribosomal S16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfan; PF00886; Ribosomal S16; T.
ProDom; PD003791; Ribosomal S16; 1.
TIGRFAMS; TIGR00002; S16; 1.
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                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 NPLVTENQVTLKEDRILEWLG 61
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MEDLINE=97075918; PubMed=8918241;
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   NPLVAENQITIKEDRVLEWL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 33.3%;
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                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus.
NCBI_TaxID=1309;
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                                                                                                                                              RS16 ST
QBDUN9;
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Cell. Biol. 20:7943-7954(2000).
-!- FUNCTION: Involved in pre-mRNA splicing. Binds and is required for the stability of sn-RNA U1, U2, U4 and U5 which contain a highly conserved structural motif called the Sm binding site. Involved in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Composition and functional characterization of the yeast spliceosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordonne R.; "" "Bordonne R.; "Functional characterization signals in yeast
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Stevens S.W., Ryan D.E., Ge H.Y., Moore R.E., Young M.K., Lee T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND RNA-BINDING.
MEDLINE-99298196; Pubmeda-1036684;
Salgado-Garrido J., Bragado-Nilsson E., Kandels-Lewis S., Seraphin
"Sm and Sm-like proteinis assemble in two related complexes of deep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE.
MEDLINE=97165029; PubMed=9012791;
Neubauer G., Gottschalk A., Fabrizio P., Seraphin B., Luehrmann R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Walke S., Bragado-Nilsson E., Seraphin B., Nagai K.; "Stoichiometry of the Sm proteins in yeast spliceosomal snRNPs supports the heptamer ring model of the core domain."; J. Mol. Biol. 308:49-58(2001).
                                               core
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                                           M
                                                                                                                                                                                                                                                                              Ayadi A., Bordonne R., Camasses A., Madania A., Poch O., Tarassov I.A., Winsor B., Martin R.P.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
Bordonne R., Tarassov I.A.; "The yeast SME1 gene encodes the homon
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND INTERACTION WITH SMX2 AND SMX3.
MEDLINE-98187616; PubMed-9528767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of the proteins of the yeast U1 smribonucleoprotein complex by mass spectrometry.";
Proc. Natl. Acad. Sci. U.S.A. 94:385-390(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     evolutionary origin.";
EMBO J. 18:3451-3462(1999).
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                                                                                                                                                                                                                                                STRAIN=S288c / FY1678;
                                                                                                                    Sene 176:111-117(1996)
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                                                                                                                                                                                                     FROM N.A
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                                                                             PIR., S67047.; SGT047.

SGD; S0005685; SME1.

GO; GO:0005685; SME1.

GO; GO:0008248; F: Pre-mRNA splicing factor activity; IPI.

GO; GO:0006371; P:mRNA splicing; IPI.

InterPro; IPR001163; snRNP_Sm.

Ffam; PF01423; Sm; 1.

SMART; SM00651; Sm; 1.

Nuclear protein; Ribonucleoprotein; mRNA splicing; mRNA processing; RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermarophyta, Magnoliophyta, Liliopaida, Poalee, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. HD5 X HD7;
STRAIN-CV. HD5 X D7;
STRAIN-CV. HD5 X D7;
SUBAIGE S.E.M., Vergine P., Dumas C.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE L32E FAMILY OF RIBOSOWAL PROTEINS.
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Pred. No. 2.4e+02;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             94 AA; 10375 MW; B76D72DA8456F3B5 CRC64;
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01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last annotation update)
60S ribosomal protein L32 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01655; Ribosomal L32e; 1.
ProDom; PD003823; Ribosomal L32E; 1.
PROSITE; PS00580; RIBOSOMAL_L32E; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interPro; IPR001515; Ribosomal_L32E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 MNIISKEKKEIKWIGLPTNSA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 MNVVIDEAVEI----PVNSA 65
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                   EMBL; X92449; CAA63198.1; -. EMBL; USS020; AAC49645.1; -. EMBL; Z75067; CAA99365.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 MAMNIISKEKKEI 20
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6 IAHNVSTKKRKEI 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.0°
Best Local Similarity 42.9
Matches 9; Conservative
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Matches 6; Conserv
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WEDLINE=21846401; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Rodouros W., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Rodries S., Goble A., Handin N., Harris D., Hidalgo J., Hodgeon G.,

Rodorey P., Moules T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Rodorey P., Moules S., Mangall K., Murphy L., Niblett D., Odell C.,

Rodorey P., Moules S., Mangall K., Murphy L., Niblett D., Odell C.,

Rodows K., O'Neil S., Mangall K., Murphy L., Niblett D., Odell C.,

Rodoward J., Simmonda M., Squares R., Squares S., Stevens K.,

Rodoward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

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Rodoward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Rodoward J., Volckaert J., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Roger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Rodfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mortier S.,

A Lodos M., Rochet M., Gaillardin C., Moore K., Hurst S.M.,

Locas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Rodoward J., Uowe T., McCombie W.R., Paulsen I., Potssburg S.L.,

Rodoward S., Barzell B.G., Nurse P.,

Rodoward J., Warsery D., Barzell B.G., Nurse P.,

Rodoward J., Warsery D., Barzell B.G., Nurse P.,

Rodoward J., Sucher F., Rodowski G., Potssburg S.D.,

Rodoward J., B., Rodowski G., Lelaure V., Worley P.,

Rodowski G.V., U
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Pfam; PF00584; SecB; 1.
TIGROPAS, TIGROD64; 3a0501806; 1.
PROSITE; PS01067; SECB SEC61G; 1.
Protein transport; Translocation; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                         21.7%; Score 33; DB 1; Length 59; llarity 21.1%; Pred. No. 3.3e+02; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                POTENTIAL. FS8F9D90EDE4DFC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C22E12.15 in chromosome I.
SPAC22E12.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 AA
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Hypothetical protein.
                                                                                                                                    59 AA; 6927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                          Local Similarity
tes 4; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 14579 / DSM 31;
STRAIN=ATCC 14579 / DSM 31;
MEDLINE=22608415; PubMed=12721630;
MEDLINE=22608415; PubMed=12721630;
Kapatral V., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman B., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.,
"Genome sequence of Bacillus cereus and comparative analysis with
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-!- INDUCTION: Expression is sigma K-dependent and negatively regulated by gerE.
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Pred. No. 3.3e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=226900, 1396;
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                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable spore germination protein gerPD.
GERPD OR BG1142.
Bacillus cereus (strain ATCC 14579 / DSM 31), and
                                                                                                                                                                                                                                                                                                      64 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN=ATCC 10876 / DSM 9378 / NRRL B-569;
MEDLINE=20179816; PubMed=10715007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 MAMNIISKEKK--EIKWIGLPTNS 29
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE017001; AAP08129.1; -. EMBL; AF053927; AAC08015.1; -.
                                 21.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sporulation; Germination.
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus anthracis.";
Nature 423:87-91(2003).
                                                                                                                                                         | ::||::|
3 KGKLKWVAVP 12
                                                                                                                             17 KKEIKWIGLP 26
.. Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus cereus.
                                                                                                                                                                                                                                                                                                      GEPD BACCR
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1 MNLNVVNRELKVGQIKMNGVSSSA 24

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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=93076002; PubMed=1446076;
Nivinskas R., Zajanckauskaite A., Raudonikiene A., Viteniene I.;
"The nucleotide sequence between genes 31 and 30 of bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                      Bacteriophage T4.
Viruses; dsbDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
                                                           01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
18-FEB-2003 (Rel. 41, Last annotation update)
18-FEB-2003 (Rel. 41, Last annotation update)
18-FEB-2003 (Rel. 41, Last annotation update)
18-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88832809; PubMed=2822658;
Renaudin J., Pascarel M.-C., Bove J.-M.;
Spiroplasma virus 4: nucleotide sequence of the viral DNA, regulatory signals, and proposed genome organization.";
J. Bacteriol. 169:4950-4961(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 36.8%; Pred. No. 3.7e+02;
Matches 7; Conservative 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;
"Bacteriophage T4 genome analysis.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spiroplasma virus 4 (SpV4).
Viruses; ssDNA viruses; Microviridae; Spiromicrovirus.
NCBI_TaxID=10855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 AA; 7252 MW; F6F53A9D21DFB4A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VG5 SPV4 STANDARD; PRT; 83 AA. P11337; 01-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 01-JUL-1989 (Rel. 11, Last annotation update) Gene 5 protein.
                               65 AA.
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 IISKEKKEIKWIGLPTNSA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 LISKVLPPFKWSGIQIKEA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, X60109; CAA42705.1; -.
EMBL, AF158101; AA042446.1; -.
PIR; S27147; S27147; S27147; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Seq. 2:405-409(1992).
                               STANDARD;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10665;
                                      BPT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
Y12J_BPT4
1D 712J6
DT 01-0CT
DT 01-0CT
DT 01-0CT
DT 01-0CT
DT 01-0CT
CN Y12J6
CN Y12J8
CN Y12J8
CN Y12J8
CN Y11J8
CN Y11J8
CN Y11J7
CN Y12J8
CN Y11J8
CN Y1J8
CN Y11J8
CN Y11J8
CN Y11J8
CN Y1J8
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                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                       Score 33; DB 1; Length 83;
Pred. No. 4.8e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                  83 AA; 9494 MW; F6E678B3CCF75A25 CRC64;
                                                                                                                                                             EMBL; M17988; -; NOT_ANNOTATED_CDS.
PIR; D29825; G5BPSV.
                                                                                                                                                                                                                                             21.7%;
66.7%;
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                          21 KWIGLP 26
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                                                                                                                                                                                                            SEQUENCE
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                    8888888888888
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Search completed: February 17, 2004, 10:57:04 Job time : 9.50495 secs

us-09-900-147-6.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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February 17, 2004, 10:50:13; Search time 18.1188 Seconds (without alignments) 159.230 Million cell updates/sec Run on:

US-09-900-147-6 152 1 YDALNVLMAMNIISKEKKEIKWIGLPTNSA 30

Perfect score: Sequence:

Scoring table:

283308 seqs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

37673 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
esult No.	Score	Query Match	Length	DB	ID	Description
1	43	28.3	78	7	G90530	hypothetical prote
7	42	27.6	61	N	159337	rane
ო	42	27.6	74	~	T37447	probable 8.5K prot
4	42	27.6	16	7	H90332	cal p
ß	42	27.6	96	~	B89941	
9	40	26.3	69	~	866650	proteinase inhibit
7	40	26.3	16	~	B90299	hypothetical prote
œ	40	26.3	16	N	B90331	_
6	40	26.3	90	~1	B81102	Ω
10	39	25.7	64	~	D69406	hypothetical prote
11	39	25.7	80	N	D97909	
12	39	25.7	92	7	AG1511	hypothetical lin06
13	٠	25.3	45	7	D81523	
14	ω.	25.3	66	Н	G64330	ືສ
15	38	25.0	72	7	JQ1805	B11R protein - vac
16	38		88	~	A42527	B11R protein - vac
11	38		91	Н	C64069	virulence-associat
18	38		92	~	AF1152	hypothetical 1mo06
19	•		83	~	H84088	hypothetical prote
20	7		95	~	T43125	
21	37	24.3	84	7	T47420	al
22	37		87	0	B41869	X O
23	37	24.3	88	~	H90329	partial transposas
24	37	٠:	96	~	E83815	hypothetical prote
52	36.5		69	N	T45696	
56	36	23.7	42	~	T07291	hypothetical prote
27	36	23.7	44	~	A89995	25
28	36	23.7	56	~	36	hypothetical prote
29	36	23.7	9	0	JC1386	homeotic protein E

hypothetical prote	nypornetical proce Rsal hypothetical hypothetical prote	SalF6R 8.8K protei hypothetical prote	hypothetical prote ynaE protein - Esc	ydfK protein - Esc dihydrodipicolinat	hypothetical 10.8 hypothetical prote		
AE3378 T48368	G69286 A24500 S33665	JQ1781 AC1217	AD1134 B64888	C64909 E69951	F65108 C91136	F85981	B95983
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36	9 9 9 3 9 9 7	36 36	36 36	36 36	36 36	36	36
30	3 B B 6	32 36	37 38	3 9 0 0	41	643	45

ALIGNMENTS

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Dypotherical protein MYPU 1510 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C; Species: Mycoplasma pulmonis (c;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Accession: G90530 C;Accession: G90530 A;Rither Res. 29, 2145-2153, 2001 A;Fitle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc A;Reference number: A9512; MUID:21267165; PMID:11353084 A;Recession: G90530 A;Retus: preliminary A;Molecule Type: DNA A;Residues: 1-78 cMNA A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.3%; Score 43; DB Best Local Similarity 45.0%; Pred. No. 33; Matches 9; Conservative 5; Mismatches
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LNVKLILDHISKNKFDKEWI 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Genetics:
A;Gene: MYPU 1510
A;Genetic code: SGC3
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mammary transforming protein - mouse (5gpecies: Mus musculus (house mouse) (2gpecies: Mus musculus (house mouse) (2gpecies: Mus musculus (house mouse) (2gpecies: Musul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999 (2gccssion: 159337 Parcession:
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-61 <RES>
A;Cross-references: GB:L31958; NID:g473909; PIDN:AAC37665.1; PID:g473910
C;Genetics:
A;Gene: MAT1

Length 61; Query Match 27.6%; Score 42; DB 2; Best Local Similarity 33.3%; Pred. No. 35; Matches 7; Conservative 9; Mismatches 3

Gaps 5. 3; Indels

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6 VLMAMNIISKEKKEIKWIGLP 26

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Length 96;

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hypothetical protein SSO7998 [imported] - Sulfolobus solfataricus transposon ISC1491 C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: B90299 [A;Accession: B90299] Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-N. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Plarett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. Albecription: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proceinase inhibitor BWI-1 - common buckwheat proceinase inhibitor BWI-1 - common buckwheat) C.Species: Fagopyrum esculentum (common buckwheat) C.Species: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-May-1997 C.Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-May-1997 B.Belozersky, M.A.; Dunaevsky, Y.E.; Musolyamov, A.X.; Egorov, T.A. FEBS Lett. 371, 264-266, 1995 #text. 371, 264-266, 1995 #text. 371, 264-266, 1995 #text. 366650; MulDi96013147; PMID:755606
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A;Gene: SSO7998
                   A;Accession: B89941
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-96 «KUR»
A;Cross-references: GB:BA000018; PID:g13701393; PIDN:BAB42687.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.3%; Score 40; DB 2; Length 76; 40.0%; Pred. No. 88; tive 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                         A;Gene: SA1423
C;Superfamily: Methanococcus jannaschii conserved hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.3%; Score 40; DB 2; Length 69; Best Local Similarity 40.9%; Pred. No. 79; Manatches 9; Indels Matches 9; Indels
A, Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                      Score 42; DB 2;
Pred. No. 58;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 DALNVLMAMNIISKEKKEIKWIGLP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AMNIISKEKKEIKWIGLPTNSA 30
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Best Local Similarity 40.0%;
Matches 10; Conservative
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A;Molecule type: protein
A;Residues: 1-69 <BEL>
C;Superfamily: eglin C
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Best Local Similarity
Matches 8; Conserv
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A;Residues: 1-76 <KUR>
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C; Species: Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C; Accession: H90332
R; She, Q: Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffitles, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Bubmitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Reterence number: A99139
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-76 < KUR>
A; Cesession: H90332
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
                                                                                                                                                                                         conserved hypothetical protein SA1423 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Species: 10-May_2001 #sequence_revision 10-May_2001 #text_change 02-Aug-2002
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27.6%; Score 42; DB 2; Length 76;
Best Local Similarity 40.0%; Pred. No. 44;
Matches 8; Conservative 7; Mismatches 5; Indels
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Best Local Similarity 52.6%; Pred. No. 43;
Matches 10; Conservative 2; Mismatches 7; Indels
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A;Experimental source: strain Ankara
C;Genetics:
A;Note: MVAL79R
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DKLTVVKAELVITQEKREVE 36
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7; Mismatches
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LDKIEAVEEITKAKKEIKKI 61
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32.0%;
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Best Local Similarity 41.21
Best Local 7; Conservative
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Best Local Similarity 50.0
Matches 10; Conservative
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Best Local Similarity
Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-92 <GLA>
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A;Molecule type: DNA
A;Residues: 1-80 <KUR>
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D69406
hypothetical protein AF1253 - Archaeoglobus fulgidus
CiSpecies: Archaeoglobus fulgidus
CiSpecies: Archaeoglobus fulgidus
CiSpecies: Archaeoglobus fulgidus
CiSpecies: Archaeoglobus fulgidus
CiSpecies: Archaeoglobus fulgidus
CiSpecies: Archaeoglobus fulgidus
CiSpecies: Tober-1997
CiAccession: D69406
Riklank, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
Riklank, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
Riklank, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
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B81102
C)Gooserved hypothetical protein NMB1264 [imported] - Neisseria meningitidis (strain MC58)
C)Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B81102
R;Tetclin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Sicience 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Accession: B81102
A;Status: preliminary
A;Molecule type: DNA
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B, strain MC58
hypothetical protein SSO8725 [imported] - Sulfolobus solfataricus transposon ISC1491
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: B90331
C;Accession: B90331
C;Accession: B90331
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C;Accession: B90332
C;Accession: A;Accession: C;Accession: A;Accession: B90333
C;Accession:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 1.1e+02;
8; Mismatches 9; Indels
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A;Experimental source: serogroup
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Matches 7; Conservative
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tes 8; Conserv
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A; Residues: 1-76 < KUR>
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A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo: A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69406
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E, R;Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M y, P.; Sun, P.M.; Winkler, M.B.
J. Bacteriol. 183, 5709-5717, 2001
A,Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Hitle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Experimental source: strain Clip11262
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C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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Pred. No. 1.5e+02;
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41.2%; Pred. No. 1.3e+02;
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Pred. No. le+02;
4; Mismatches
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virulence-associated protein vapD homolog H10450 - Haemophilus influenzae (strain Rd KW2/C) Species: Haemophilus influenzae (c) Species: Haemophilus influenzae (c) Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C; Accession: C64069 R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U32728; GB:L42023; NID:g1573425; PIDN:AAC22108.1; PID:g1573426; T1
C;Superfamily: virulence-associated protein vapD
R;Smith, G.L.; Chan, Y.S.; Howard, S.T.
J. Gen. Virol. 72, 1349-1376, 1991
A;Title: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right inv
A;Reference number: JQ1767; MUID:91259063; PMID:2045793
                                                                                                                                                                                                                              A; Cross-references: DDBJ:D11079; NID: 9222717; PIDN: BAA01841.1; PID: d1002317; PID: 9222756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIR protein - vaccinia virus (strain Copenhagen)
C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 08-Apr-1994
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ilarity 47.4%; Pred. No. 1.6e+02;
Conservative 3; Mismatches 7; Indels
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Pred. No. 2e+02;
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20 DVTNVEDIINEIDREKEEI 38
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Best Local Similarity 47.4%;
Matches 9; Conservative
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R; Johnson, G.P.
submitted to GenBank, June 1990
A; Reference number: A33172
A; Accession: A42527
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Matches 9; Conserv
                                                                                                                                                  A;Accession: JQ1805
A;Molecule type: DNA
A;Residues: 1-72 <SMI>
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A;Residues: 1-88 <JOH>
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C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 07-Mar-2003
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 07-Mar-2003
C;Accession: G64330
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reich, C.I.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.M.; A;Attlee: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Accession: G64330
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A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0930
                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: D81523
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Brunham, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Reference number: A81500; MUID:20150255; PMID:10684935
A; Accession: D81523
A; Rederence number: A81500; MUID:20150255; PMID:10684935
A; Rederence number: A81500; MUID:20150255; PMID:10684935
A; Rederence number: A81500; MUID:20150255; PMID:10684935
A; Rederence number: A81500; MUID:20150255; PMID:10684935
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A; Rederence number: A81500; MUID:20150255; PMID:10684935
A; Rederence number: A81500; MUID:20150255; PMID:10684935
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                                                                                                                                                                                                                                                                                 hypothetical protein CP0930 (imported] - Chlamydophila pneumoniae (strain AR39) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
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B11R protein - vaccinia virus (strain WR)
C;5pecies: vaccinia virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
C;Accession: JQ1805
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C.Superfamily: chorismate mutase of the AroQ class, prokaryotic type
C.Keywords: intramolecular transferase; isomerase
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Pred. No. 81;
4; Mismatches 8;
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                                                                    4 LNVLMAMNIISKEKKEIKWIGLPTN
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Best Local Similarity 43.5%;
Matches 10; Conservative
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hyporhetical protein T28A8.130 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C; Accession: T47420
R; Purnelle, B.; Boutry, M.; Goffeau, A.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X submitted to the Protein Sequence Database, March 2000
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C;species: Bacillus subtilis
C;date: 03-May-1994 #sequence_revision 27-Jan-1995 #text_change 15-Oct-1999
C;Accession: B41869; S13789; S66053; H69595
R;Ricca, E.; Cutting, S.; Losick, R.
B; Ricca, E.; Cutting, S.; Losick, R.
A;Title: Characterization of bofA, a gene involved in intercompartmental regulation of P; A;Reference number: A41869; MUID:92250411; PMID:1577688
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A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromd
A;Reference number: S65967; MUID:96051385; PMID:7584024
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R;Ogaṣawara, N.; Nakai, S.; Yoshikawa, H.
                                                                                                                                                                                                                                         1;
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                                                                                                                                                                          Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 2; Length 84; Pred. No. 2.7e+02; 8; Mismatches 7; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AL162691
A;Experimental source: cultivar Columbia; BAC clone T28A8
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A;Residues: 1-54,'G',56-87 <RIC>
R;Alonso, J.C.; Shirahige, K.; Ogasawara, N.
Nucleic Acids Res. 18, 6771-6777, 1990
A;Title: Molecular cloning, genetic characterization and A;Reference number: S13786; MUID:91088245; PMID:2124672
                                                                                                                                                                       Score 37.5; DB 2;
Pred. No. 2.6e+02;
0; Mismatches 7;
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                A; Experimental source: strain DPC3147
                                                                                                                                                                                                                                                                                                     9 AMNIISKEKKEIKWI-GLP 26
                                                                                                                                                                                                                                                                                                                                                        14 AQNTFEKEKKEDKIIQALP 32
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24.3%;
Best Local Similarity 28.6%;
Matches 6; Conservative
                                                                                                                                                                          Query Match 24.7%;
Best Local Similarity 57.9%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: Z24466
A;Accession: T47420
A;Status: preliminary
                                              C,Genetics:
A,Genome: plasmid pMRC01
A,Note: ORF00054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-84 <PUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-87 <ALO>
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A,Introns: 32/2; 50/3
A,Note: T28A8.130
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hypothetical lmo0622 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession. AFI152
B;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07231.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Puji, F.; Hira
Nucleic Acids Ree. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 20
Ty 3125
hypothetical protein - Lactococcus lactis plasmid pMRC01
C;Species: Lactococcus lactis
C;Species: Lactococcus lactis
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Date: 02-Jun-3000 #sequence_revision 02-Jun-2000
B;Dougherty, B.A.; Hill, C.; Weidman, J.F.; Richardson, D.R.; Venter, J.C.; Ross, R.P. Mol. Microbiol. 29, 1029-1038, 1998
A;Title: Sequence and analysis of the 60 kb conjugative, bacteriocin-producing plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:NC_003210; PIDN:CAC98700.1; PID:g16410011; GSPDB:GN00177
A;Experimental source: strain EGD-e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.0%; Score 38; DB 2; larity 28.0%; Pred. No. 2.1e+02; Conservative 8; Mismatches 10
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A,Residues: 1-95 <DOU>
A,Cross-references: EMBL:AE001272; PIDN:AAC56046.1
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nes 7; Conserv
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Matches 13; Conser
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A;Molecule type: DNA
A;Residues: 1-83 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-92 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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partial transposase ISC1190 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: H90329
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Changong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Jong, II.; Jeffries, A.C.; Sensen, C.W.; Van der Oost, J.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Reterence number: A99139
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 «KUR>
A;Cross_references: GB:AE006641; NID:g13814935; PIDN:AAK41895.1; GSPDB:GN00155
C;Genetics:
A;Genetics:
A;Gene: SSO8687
A;Cross-references: EMBL:D26185; NID:9467326; PIDN:BAA65259.1; PID:d1005801; PID:9467413
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G; Azevedo, V.; Berter
C; Broom, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Gapuano, V.; Carter, N.M.; Cho
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A;Authors: Poulger, D.; Pritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, M.; Pohl, T.M.; Portetelle
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
Rieger, M.; Rivolta, C.; Schroeter, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Accession: H69595
A;Accession: H69595
A;Accession: H69595
A;Accession: H69595
A;Accession: H69595
A;Crostiments: Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Crossinences: GBs.299104; GB:AL009126; NID:92632267; PIDN:CABII799.1; PID:e1181956;
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C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002
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24.3%; Score 37; DB 2; Length 87;
Best Local Similarity 27.3%; Pred. No. 2.8e+02;
Matches 6; Conservative 7; Mismatches 9; Indels
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50.0%;
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Best Local Similarity 50.0
Matches 9; Conservative
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C;Accession: E83915

R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and cinarian complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and cinarian complete genome sequence of the alkalis A;Reference number: A83045

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Arabidopsis thaliana (figecies: Arabidopsis thaliana (mouse-ear cress) (figecies: Arabidopsis thaliana (mouse-ear cress) (figecies: Arabidopsis thaliana (mouse-ear cress) (figecies: 04-Feb-2000 #sequence_revision 04-Feb-2000 #sequence_revision 04-Feb-2000 #scquence_revision 04-Feb-2000 (figer) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure) (figure
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C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May_1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 CHO>
A;Cross-references: EMBL:AL133298
A;Experimental source: cultivar Columbia; BAC clone F18L15
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36.0%; Pred. No. 3.1e+02;
iive 6; Mismatches 10;
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A;Molecule type: DNA
A;Residues: 1-42 <WAK>
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Matches 9; Conservative
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A;Residues: 1-60 <OLI>
A;Cross-references: EMBL:X66817
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Best Local Similarity
Matches 8; Conserva
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A;Introns: 30/1; 5
A;Note: F12E4.200
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                                                                                                                                                                                A;Cross-references: GB:U67504; GB:L77117; NID:g1591248; PIDN:AAB98548.1; PID:g1591251;
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A;Experimental source: strain N315
                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 44;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 2; I
Pred. No. 1.8e+02;
ilarity 47.1%; Pred. No. 1.8e+02; Conservative 3; Mismatches 6
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A;Map position: REV483625-483455
C;Superfamily: hypothetical protein MJ0546
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LNIILGIKVIMLQKELEEVK 32
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17 ISMAQDIISTIGDLVKWI 34
                                                               7 LMAMNIISKEKKEIKWI 23
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LFLIFFFSKKKKEIKQV
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Best Local Similarity
Best Local Similarity
Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-44 <KUR>
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Oct-1997 C;Accession: JC1386 R;Oliver, G;Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlic? A;Tile: Homeoboxes in flatworms. A;Tile: Homeoboxes in flatworms. A;Reference number: JC1386; MUID:93077050; PMID:1359988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: AE3378
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selvkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessr Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F12B4.200 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T48368
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; submitted to the Protein Sequence Database, March 2000
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A;Molecule type: DNA
A;Residues: 1-67 «KUPs
A;Cross-references: GB:AE008917; PIDN:AAL52192.1; PID:g17982973; GSPDB:GN00190
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein BMEI1011 [imported] - Brucella melitensis (strain 16M) c;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>
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A;Residues: 1-73 <BEV>
A;Cross-references: EMBL:AL162751
A;Experimental source: cultivar Columbia; BAC clone F12E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.7%; Score 36; DB 2; Le
Best Local Similarity 25.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 7; Mismatches 8;
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Pred. No. 3e+02;
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Gaps

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4; Indels

Length 77;

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A/Molecule type: DNA
A/Residues: 1-77 - CHAY>
A/Cross-references: EMBL:D13409; NID:g217776; PIDN:BAA02674.1; PID:d1003179; PID:g2168168
A/Note: the authors translated the initiation codon GTG for residue 1 as Val
C/Genetics:
A/Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salred 8.8K protein - vaccinia virus (strain WR and Ankara)
Galred 8.8K protein - vaccinia virus
Galred 8.8K protein - vaccinia virus
Galred 9.93 #sequence revision 30-Sep-1993 #text_change 18-Feb-2000
GiAccession. JG1781; 1040897; T37429
R.Smith, G.L.; Chan, Y.S.; Howard, S.T.
J. Gen. Virol. 72, 1349-1376, 1991
A.Title: Nucleotide sequence of 42kbp of vaccinia virus strain.WR from near the right inv.
A.Recession. JG1781
A.Rocession. JG1781
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MyResidues: 1-79 eBLA>
MyResidues: 1-79 eBLA>
MyResidues: 1-79 eBLA>
MyResidues: 1-70 eBLA>
MyResidues: 1-70 eBLAD: MD:9335761; PIDN:AAA48310.1; PID:9335765
MyResidues: 1-70 eBLAD: MyResidues: F.G.; Dorner, F.
R;Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
R;Antoine, G.; Scheiflinger, March 1997
MyBescription: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strair:
A;Reference number: Z20877
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c;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001
S;Accession: AC1217
R;Glaeer, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Disjones, L.M; Karet, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Macok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
23.7%; Score 36; DB 2; I
Best Local Similarity 35.3%; Pred. No. 3.5e+02;
Matches 6; Conservative 7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                Score 36; DB 2; I
Pred. No. 3.5e+02;
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A;Molecule type: DNA
A;Residues: 1-78 <ANT>
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A,Experimental source: strain Ankara
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54.5%;
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DVLLAQSVAVEEAKDVK
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Best Local Similarity 54.5
Matches 6; Conservative
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31 VPWYGLPTQLA 41
    A;Status: preliminary
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G69286
hypothetical protein AF0295 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: G69286
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Natures 390, 384-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Atference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69286
A;Scratus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-74 «KLE>
A;Access-references: GB:AE001084; GB:AE000782; NID:92689407; PIDN:AAB90939.1; PID:9265034
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C;Species: Neisseria gonorrhoeae
C;Species: Neisseria gonorrhoeae
C;Date: 30-Unn-1988 #sequence_revision 30-Jun-1988 #text_change 23-Mar-1995
C;Accession: A24500
R;Correia, F.F.; Inouye, S.; Inouye, M.
J. Bacteriol. 167, 1009-1015, 1986
A;Title: A 26-base-pair repetitive sequence specific for Neisseria gonorrhoeae and Neiss A;Reference number: A91818; MUID:86304144; PMID:3091577
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Query Match 23.7%; Score 36; DB 2; Length 73; Best Local Similarity 37.5%; Pred. No. 3.3e+02; Matches 6; Conservative 5; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 23.7%; Score 36; DB 2; I
Local Similarity 47.4%; Pred. No. 3.3e+02;
hes 9; Conservative 2; Mismatches 8
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                                                                                                                                                                                     13 ISKEKKEIKWIGLPTN 28
                                                                                                                                                                                                                                            32 IAWQEMRKKWVGDPSN 47
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A; Residues: 1-75 < COR>
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CiAccession: C64909
Riblatiner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, C.J.; 1453-1462, 1997
A; Feference number: A64720; MUID:97426617; PMID:9278503
A; Accession: C64909
A; Astatus: nucleic acid sequence not shown; translation not shown
A; Molécule type: DMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: E69951

R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc C; Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chol A.; Ehrlich, S.D.; Brenillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chol A.; Ehrlich, S.D.; Brenillet, C.; Fritz, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chol A.; Atuthors: Foulgar, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerr A.; Atuthors: Foulgar, D.; Friz, C.; Fujita, M.; Fujita, K.; Lapidus, A.; Gallerr A.; Henaut, J.; Hawood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Atuthors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogiwara, A.; Odega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteclelle Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sakowska, A.; Sekowska, A.; Sekowska, A.; Sekowska, A.; Togato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A; Hitle: The complete genome sequence of the Gram-positive bacterium Bacillus subrilis. A; Accession: E69951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-88 <BLAT>
A;Cross-references: GB:AE000252; GB:U00096; NID:g2367119; PIDN:AAC74617.1; PID:g1787826;
A;Experimental source: strain K-12, substrain MG1655
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-96 <KUN>
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C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0652
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Č;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
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              Pred. No. 4e+02;
                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ydfK protein - Escherichia coli (strain K-12)
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NIL--RNIFMKSKDTLKW 20
                                                                                                                                            5 NVLMAMNIISKEKKEIKW 22
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              44.48;
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                                                        8; Conservative
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Best Local Similarity
--ham 8; Conserve
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Matches 8; Conserv
         Best Local Similarity
Matches 8; Conserv
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: B6488
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Imo0475 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: Ab1134
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Jonanguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Simoes, N.; Tierez, A.; Vozquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74457.1; PID:g1787639;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1217
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-79 < GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99217.1; PID:gl6410555; GSPDB:GN00177
C;Genetics: A;Keeilues: atrain EGD-e
A;Gene: lmo1139
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-80 «GLA>
A; Residues: 1-80 «GLA>
A; Cross-references: GB:NC_003210; PIDN:CAC98554.1; PID:g16409851; GSPDB:GN00177
A; Experimental source: strain EGD-e
C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics
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43.8%; Pred. No. 3.6e+02;
tive 3; Mismatches 6; Indels
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Pred. No. 3.6e+02;
5; Mismatches 4;
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Best Local Similarity 43.8°
Matches 7; Conservative
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Matches

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hypothetical protein PHS020 - Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Mg-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C;Accession: H71158
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekint R;Kawarabayasi, Y.; Sawada, M.; Horikawa, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic and A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reterence number: A71000; MUID:98344137; PMID:9679194
A;Sterus: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-97 KAMA.
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A;Rotecule type: DNA
A;Residues: 1-98 × KURA
A;Residues: 1-98 × KURA
A;Cross-references: GB:AL591985; PIDN:CAC49530.1; PID:g15141017; GSPDB:GN00167
A;Cross-references: GB:AL591985; PIDN:CAC49530.1; PID:g15141017; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
B;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, C.; Finan, R.W.; Jones, T.
L:; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Wong, K.; Yeh, K.A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: GB:AP000002, NID:g3236129; PIDN:BAA29557.1; PID:d1030500, PID:g325687, A;Experimental source: strain OT3
A,Rote: this accession replaces an interim accession for a sequence replaced by GenBank
                                     A;Accession: F85581
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <STO
A;Cross-references: GB.AE005174; NID:g12517792; PIDN:AAG58314.1; GSPDB:GN00145; UWGP:Z454
A;Experimental source: strain O157:H7, substrain BDL933
C;Genetics:
C;Genetics:
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0652
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Best Local Similarity 36.0%; Pred. No. 4.5e+02;
Matches 9; Conservative 2; Mismatches 14; Indels
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23.7%; Score 36; DB 2; Length 97;
Best Local Similarity 35.3%; Pred. No. 4.5e+02;
Matches 6; Conservative 6; Mismatches 5; Indele
A; Reference number: A85480; MUID:21074935; PMID:11206551
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A,Gene: PHS020
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A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Roberliminary
A; Molecule type: DNA
A; Reperimental source: strain (o157:H7, substrain RIMD 0509952
C; Genelics:
C; Genelics:
C; Genelics:
C; Genelics:
C; Genelics:
C; Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0652
                                                                                                                                                                                                                                                                                                               Pubblic Repetical 10.8 kD protein in ftsj-grea intergenic region - Escherichia coli (strain K Chypothetical 10.8 kD protein in ftsj-grea intergenic region - Escherichia coli (Chate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002 C. Acte: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002 C. Acterior F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; Residues: 1-97 callAT> A; 
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C;Species: Escherichia coli
C;Date: 16-Feb_2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
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C,Accession: F85981
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew R;Perna, N.T.; Plunkett III, G.; Burland, Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
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RESULT 42

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A; Reference number: A96039; MUID:21368234; PMID:11474104
A; Contents: annotation
C; Genetics:
A; Gene: SMb21004
A; Gene: SMb21004
A; Genew: plasmid
Query Match
Best Local Similarity 55.6%; Pred: No. 4.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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Search completed: February 17, 2004, 10:58:18 Job time : 19.1188 secs

18 KEIKWIGLP 26 :|:|| |:| 3 EEVKWRGVP 11

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, OM protein February 17, 2004, 10:50:13; Search time 4.22772 Seconds (without alignments) 159.230 Million cell updates/sec Run on:

US-09-900-147-7 31 Title: Perfect score:

1 ALNVLMA 7 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

37673 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	25	80.6	53	2	D83832	hypothetical prote
7	25	80.6		~	S41828	
m	24	77.4	20	~	S77603	ccoH protein - Par
4	24	77.4		~	G64767	
ß	24	77.4		7	A90684	
9	24	77.4		~	E85534	
7	24	77.4	98	N	S24920	ñ
80	24	77.4	98	N	T11449	NADH2 dehydrogenas
6	23	74.2	51	7	E95849	hypothetical prote
10	23	74.2	96	٦	F71843	
11	23	74.2	96	7	800119	cal pro
12	22			~	803819	
13	22	71.0		~	A97862	proline/betaine tr
14	22	71.0		~	866332	protein kinase AK1
15	22	71.0	63	~	C34514	MHC class II histo
16	22	71.0		7	AI0225	probable membrane
17	22	71.0		~	AI2346	hypothetical prote
	22	71.0		~	A61623	juvenile-hormone e
19	22	71.0	77	7	A36817	ORF X protein - hu
	22	71.0	82	~	T17912	hypothetical prote
	22	71.0		~	D97870	
	22	71.0		~	339696	ywcE protein - Bac
23	22	71.0		7	T14135	NADH2 dehydrogenas
24	22	71.0		7	D97717	hypothetical prote
25	22			Н	QXB04L	
56	22			7	T10980	
27	22	71.0		~	T11058	NADH2 dehydrogenas
28	22	71.0	98	~	JC5794	elongin C - fruit
29	21	67.7	36	N	C70211	hypothetical prote

alpha-internexin - hypothetical prote	conserved hypothet probable small nuc gene SPHAR protein	hypothetical prote hypothetical prote	0	hypothetical prote hypothetical prote	hypothetical prote probable snrnp PAB	probable small nuc replication licens	hypothetical prote
PN0624 T16930	A69337 H90118 I38244	H90804 E91196	D86043 E85613	H98064 AH0390	AC2335 B75106	D71028 S52172	E85664
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57	63 63	65 65	65 65	66 71	72	75	80
67.7	67.7 67.7 67.7	67.7	67.7	67.7	67.7	67.7	67.7
21	21 21 21	21	22	2 2	2 2	21	21
30	8 8 8 8 8 8	32 36	37 38	9. 9.0	4 4 2 4 2	4 4 4 4	45

ALIGNMENTS

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C;Accession: D83832
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-53 <STO>
                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05179.1; GSPDB:GN001
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                         C,Species: Bacillus halodurans
C,Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
hypothetical protein BH1460 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 29;
0; Mismatches
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Similarity 85.7%;
6; Conservative
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Best Local Similarity
Matches 6; Conserv
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ALMVLAA 21 1 ALNVLMA 7 RESULT 2 δ 엄

A;Molecule type: DNA A;Residues: 1-98 <ARN> A;Cross-references: EMBL:X72204; NID:g414126; PIDN:CAA51003.1; PID:g575317

A;Accession: S41828

A; Gene: NADH4L

C;Genetics:

A; Genome: mitochondrion A; Genetic code: SGC1

A;Start codon: GTG C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c

80.6%; Score 25; DB 2; Length 98; Query Match

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Aggoday

yaiE protein [similarity] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)

Cispecies: Bacherichia coli
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Cispecies: Asunaga, T.; Rulara, S.; Shiba, T.; Hattori, M.; Yokoyama, K.; Han, C.G.;
Rihayashi, T.; Asunaga, T.; Rulara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genor
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Recession: A90684
A; Retarus: preliminary
A; Robolccule type: DNA
A; Residues: 1-94 cHAX>
A; Robolccule type: DNA
A; Residues: 1-94 cHAX>
A; Cross-references: GB:BA000007; PIDN:BAB33864.1; PID:gl3359898; GSPDB:GN00154
A; Genetics:
C; Genetics:
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yilE protein [similarity] - Escherichia coli (strain 0157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Nov-2001
C;Accession: E85534
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, II, Lim, L.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE005174; NID:g12513234; PIDN:AAG54737.1; GSPDB:GN00145; UWGP:Z046
A;Experimental source: strain 0157:H7, substrain EDL933
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Pred. No. 96;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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A; Residues: 1-98 <ARN>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-94 <STO>
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C;Species: Paracoccus denitrificans
C;Species: Paracoccus denitrificans
C;Species: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: S77603
R;Ge Gier, J.W.; Schepper, M.; Reijnders, W.N.M.; van Dyck, S.J.; Slotboom, D.J.; Warne, R;Ge Gier, J.W.; Schepper, M.; Reijnders, W.N.M.; van Dyck, S.J.; Slotboom, D.J.; Warne, Mol. Microbiol. 20, 1247-1260, 1996
A;Atitle: Structural and functional analysis of aa(3)-type and cbb(3)-type cytochrome c A;Reference number: 877603
A;Reference number: 877603
A;Recession: 877603
A;Recession: 877603
A;Residues: nucleic acid sequence not shown; translation not shown
A;Residues: 1-50 cDEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:U34353; NID:gl002874; PIDN:AAC44521.1; PID:gl002883
A,Experimental source: strain Pd1222
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
C,Genetics:
A,Gene: ccoH
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Pred. No. 96;
1; Mismatches 0; Indels
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Pred. No. 48;
1; Mismatches 1; Indels
                     Indels
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Pred. No. 57;
1; Mismatches
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83.3%;
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71.48;
  83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
                          5; Conservative
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51 ALNVLL 56
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MNVLMA 11
       Similarity
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       Best Local
Matches
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Indels

Length 51;

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C;Accession: F71843
R;Alm, R.A.; Ling, D.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Tres, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathx A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Variety: strain J99
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                             cytochrome c553 precursor - Helicobacter pylori (strain J99)
                                                                                                        DB ,
                                                                                                                   Score 23; DB Pred. No. 88; 1; Mismatches
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hypothetical protein C - Proteus vulgaris
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                                                                                                                   74.2%;
71.4%;
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                                                                                                                                                                       5; Conservative
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-96 <ARN>
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A, Residues: 1-96 <COL>
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        C;Genetics:
A;Gene: SMb20061
A;Genome: plasmid
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R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A; Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A; Reference number: A95842; MUDD:21396508; PMID:11481431

A; Accession: B95849

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-51 <KUR>
A; Residues: 1-51 <KUR>
A; Residues: 1-51 <KUR>
A; Residues: 1-51 <KUR>
A; Residues: 1-51 <KUR
A; Residues: 1-51 <KUR
A; Residues: Relation 1021, megaplasmid pSymB
B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, A; Hyman, R. W.; Jones, T.
B; Hyman, R. W.; Jones, T.
C; Hyman, R. W.; Jones, T.
C; Science 293, 668-672, 2001

A; Mathors: Kahn, D.; Kahn, M.L.; Kahnan, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A.; A; Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T11449
R;Arnason, U.; Gullberg, A.; Janke, A.
Mol. Biol. Bvol. 14, 762-768, 1997
A;Title: Phylogenetic analysis of mitochondrial DNA suggest a sister group relationship A;Reference number: Z17272; MUID:97357423; PMID:9214749
A;Accession: T11449
A;Cross-references: GB:X61145; NID:g12772; PIDN:CAA43447.1; PID:g12779
A;Note: submitted to the EMBL Data Library, August 1991
C;Genetics:
C;Genetics:
A;Genome: mitochondrion
A;Genome: code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - nine-banded armadillo mitochono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: NADH4L
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: mitochondrion Dasypus novemcinctus (nine-banded armadillo)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 1e+02;
2; Mismatches 0; Indels
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66.7%; Pred. No. 1e+02;
ive 2; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-98 <ARN>
                                                                                                                                                                                                                              77.4%;
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Best Local Similarity 66...
A: Conservative
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Matches 4; Conservative
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LNIIMA 11
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MNILMA 11
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A;Cross-references: GB:AE001542; GB:AE001439; NID:g4155739; PIDN:AAD06721.1; PID:g4155742;
A;Experimental source: strain J99
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Eur. J. Biochem. 167, 481-488, 1987
A;Title: Nucleotide sequence and comparative analysis of the frd operon encoding the fume
d-linked ampC cephalosporinase gene.
A;Reference number: S00107; MUID:88004470; PMID:3308458
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C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 14-Apr-2003
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                                                                                                                                           C;Superfamily: cytochrome c6; cytochrome c6 homology
C;Superfamily: cytochrome c6; cytochrome c6 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-96/Product: cytochrome c553 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X06151; NID:g45907; PIDN:CAA29511.1; PID:g45910 C;Superfamily: [NiFe]-hydrogenase maturation chaperone
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                                                                                                                                                                                                                                                                                                   F:20-92/Domain: cytochrome c6 homology <CYC>
F:29,32/Binding site: heme (Cys) (covalent) #status predicted
F:33/Binding site: heme iron (His) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 74.2%; Score 23; DB 1; Length 96; Similarity 100.0%; Pred. No. 1.8e+02; 5; Conservative 0; Mismatches 0; Indels
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Pred. No. 1.8e+02;
0; Mismatches 1;
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C34514

WHC class II histocompatibility antigen, 2 - baboon (fragment)

WHC class II histocompatibility antigen, 2 - baboon (fragment)

C;Species: Papio sp. (baboon)

C;Species: 22-Uun-1990 #sequence_revision 22-Uun-1990 #text_change 12-Jul-1996

C;Accession: C34514

C;Accession: C34514

Broc. Natl. Acad. Sci. U.S.A. 86, 9986-9990, 1989

Proc. Natl. Acad. Sci. U.S.A. 86, 9986-9990, 1989

A;Title: Ancient roots for polymorphism at the HLA-DQalpha locus in primates.

A;Title: Ancient roots for polymorphism at the HLA-DQalpha locus in primates.

A;Feference number: A34512; MUID:90099387; PMID:2533578

A;Feference number: A34514

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trashylocenel type: DNA

A;Residues: 1-63 < GYL-

C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
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probable membrane protein YPO1852 [imported] - Yersinia pestis (strain CO92)
C;Species Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: A10225
E;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; Antherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Altitle: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Gene: AK19
A;Introns: 30/1
A;Introns: 30/1
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase
C;Keywords: AfP; phosphotransferase; protein kinase
P;1-56/Domain: protein kinase homology (fragment) <KIN>
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C;Species: Nostoc sp. PCC 7120
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Pred. No. 2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              71.0%; Score 22; DB 2; Length 56;
80.0%; Pred. No. 1.7e+02;
tive 1; Mismatches 0; Indels
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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A;Molecule type: DNA
A;Residues: 1-65 <KUR>
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proteins: Arabidopsis thaliana (mouse-ear cress)
C;Species: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 24-Sep-1999
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 24-Sep-1999
C;Accession: 856632; 858268
R;Thuemmler, F; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes A;Reference number: 866312
A;Accession: 866332
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A; Residues: 1-56 <THU>
A; Cross-references: EMBL:X86964; NID:g928903; PIDN:CAA60527.1; PID:g928904
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22; DB 2; Length 54;
Pred. No. 1.7e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                          Proteus vulgaris (fragment)
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71.4%;
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Matches 5; Conservative
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S66332
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C;Accession: D97870 "Courselow Survey 2001 #Text_change 30-Sep-2001
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ron A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ywcE protein - Bacillus subtilis

N;Alternate names: hypothetical protein ipa-41r

C;Species: Bacillus subtilis
C;Date: 07-0ct-1999 #sequence_revision 26-May-1995 #text_change 15-0ct-1999
C;Accession: 38966; H70052
R;Glaser, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu, P. A.; Rapoport, G.; Danchin, A.

Mol. Microbiol. 10, 371-384, 1993
A;Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fr
A;Reference number: S39655; MuID:95020537; PMID:7934828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D97870
oxidoreductase homolog RC1364 [imported] - Rickettsia conorii (strain Malish 7)
C,Species: Rickettsia conorii
C,Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: AE006914; PIDN: AAL03902,1; PID: 915620509; GSPDB: GN00173
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                                                                                                                                                                                                 hypothetical protein a409R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Molecule type: DNA
A;Residues: 1-82 <GRA>
A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96777.1
A;Experimental source: specific host Chlorella strain NC64
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 82;
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Pred. No. 2.6e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.0%; Score 22; DB 2; I 66.7%; Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                              C;Accession: T17912
R;Graves, W.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
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66.7%;
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                  LINVAMA 33
                   2 LINVLAMA 7
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A;Molecule type: DNA
A;Residues: 1-86 <KUR>
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                                                                  28
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: A12346
R;Accession: A12346
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Accession: A13346
A;Accession: A13346
A;Accession: Preliminary
A;Accule type: DNA
A;Residues: 1-68 «KUR»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Valaitis, A.P.
Insect Biochem. Mol. Biol. 22, 639-648, 1992
A;Title: Use of concanavalin A in the purification of juvenile hormone esterase from the
A;Reference number: A61623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORF X protein - human papillomavirus type 41
C;Species: human papillomavirus type 41
A;Note: host Homo sapiens (man)
A;Note: host Homo sapiens (man)
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 08-Oct-1999
C;Accession: A36817
R;Hirt, L.; Hirsch-Behnam, A.; De Villiers, E.M.
Virus Res. 18, 179-190, 1990
A;Reference number: A43550
A;Reference number: A43550
A;Accession: A36817
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A;Experimental source: strain PCC 7120
C;Genetics: a814328
A;Gene: a814328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Lymantria dispar (gypsy moth)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A;Molecule type: DNA
A;Residues: 1-77 <HIR>
A;Cross-references: EMBL:X56147; NID:g60942; PIDN:CAA39620.1; PID:g60951
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Pred. No. 2.1e+02;
1; Mismatches 1; Indels
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.0%; Score 22; DB 2; Length 69; 66.7%; Pred. No. 2.2e+02; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A61633
A;Status: preliminary
A;Molecule type: protein
C;Superfamily: alkaline phosphatase
C;Keywords: carboxylic ester hydrolase; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.0%;
71.4%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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45 ALELLMA 51
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49 AMNVVM 54
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R; Valaitis, A.P.
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Gaps

D.; ROL

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Gaps

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Length 95;

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NADMIZ dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - pig mitochondrion C.Species: mitochondrion Sus scrofa domestica (domestic pig)
C.Species: mitochondrion Sus scrofa domestica (domestic pig)
C.Spate: 16-101-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C.Accession: T10980; T11878
R.Jin, C.S.; Liu, C.Y.; Sun, Y.L.; Chang, L.C.; Cheng, I.C.; Yang, P.C.; Mao, S.J.T.; Hu& Submitted to the RMEL Data Library, November 1997
A.Bescription: Complete nucleotide sequence of the porcine mitochondrial genome.
A.Reference number: Z17237
A.Accession: T10980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADEZ dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - bovine mitochondrion NADEZ dehydrogenase (ubiquinone oxidoreductase chain 4L CADECISE mitochondrion Bos primigenius taurus (cattle) (cippecies: mitochondrion Bos primigenius taurus (cattle) (cippecies: mitochondrion Bos primigenius taurus (cattle) (cippecies: 18-Aug-1982 #sequence_revision. 18-Aug-1982 #text_change 03-Jun-2002 (cippecies: 18-Aug-1982 #sequence_revision. 18-Aug-1982 #text_change 03-Jun-2002 (cippecies: 18-Aug-1982 #sequence District Complete sequence of bovine mitochondrial DNA. Conserved features of the mammal A; Title: Complete sequence of bovine mitochondrial DNA. Conserved features of the mammal A; A; Reseiducts A00429 A; MUD: 83010260; PMID: 7120390 A; Reseiducts type: DNA A; Reseiducts type: DNA A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A; Reseiducts (mitocatter) A; A;
          A)Status preliminary, translated from GB/EMBL/DDBJ
A)A)Status preliminary, translated from GB/EMBL/DDBJ
A)A)Clecule type: DNA
A)Residues: 1-98 «LIN»
A)ACOGES ** references: EMBL:AF034253; NID:94958951; PID:94958960; PIDN:AAD34193.1
B, Gross ** references: EMBL: Data Library, February 1999
Submitted to the EMBL Data Library, February 1999
Submitted to the Complete mitochondrial DNA sequence of the pig (Sus scrofa).
A, Reference number: Z17370
A, Reference number: X17370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE006914; PIDN:AAL02678.1; PID:g15619183; GSPDB:GN00173 C;Genetics: A;Gene: RC0140
30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
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Pred. No. 3.2e+02;
3; Mismatches 0; Indels
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66.7%; Pred. No. 3.1e+02;
iive 2; Mismatches 0;
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Best Local Similarity 50.0%;
Matches 3; Conservative
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MNIMMA 11
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALNVIM 6
                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <KUR>
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                                           A; Molecule type: DNA
A; Residues: 187 (GLA)
A; Residues: 187 (GLA)
A; Residues: 187 (GLA)
A; Cross-reference: RBBL:X73124; NID:g413923; PIDN:CAA51597.1; PID:g413965
A; Cross-reference: RBBL:X73124; NID:g413923; PIDN:CAA51597.1; PID:g413965
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, Julian, S.D.; Ememerson, P.T.; Entian, C.V.; Capuano, V.; Carter, N.M.; Ch. Carter, D.; Eritz, C.; Fujita, K.D.; Erington, J.; Pabret, C.; Ferrari, E. N.; Buthors: Pollger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, A; Authors: P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, K.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mauda, S.; Maucel, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mauda, S.; Maucel, A; Authors: Schleich, S.; Schroeter, R.; Roche, B.; Rose, F.; Sekiguchi, V.; Seto, T.; Scrollon, Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Seron, T.; Seron, A, Authors: Schlikawa, H.F.; Zumance, M.; Yasumoto, K.; Yata, K.; Yoshida, R.; Alathors: Yoshikawa, H.F.; Zumancein, B.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama, A; Residues: 1-8 Tomolecule type: DNA
A; Residues: 1-8 Tomolecule cof the Gram-positive bacterium Bacillus subtilis. A; Residues: 1-8 Tomolecule type: DNA
A; Residues: 1-8 Tomolecule cof the Gram-positive bacterium scillus subtilis. A; Cross-references: GB: 299123; GB: ALO09126; NID:g2636240; PIDN: CABI5839.1; PID:e1186312; A; Gene: Yock
C.; Gene: Yock
C.; Rockerican
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Cispecies: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
CiAccession: T14135
CiAccession: T14135
Bubmitted to the EMBL Data Library, November 1995
A;Description: Mitochondrial DNA analysis of the systematic relationships within the Per A;Reference number: Z17885
A;Reference number: Z17885
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-89 s-HOGA
A;Residues: 1-89 s-HOGA
A;Residues: 1-89 s-HOGA
A;Residues: 1-89 s-HOGA
A;Residues: 1-89 s-HOGA
A;Residues: 1-80 s-HOGA
A;Residues: 1-80 s-HOGA
A;Residues: 1-80 s-HOGA
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C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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hypothetical protein RC0140 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
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C;Genetics:
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Pest Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels
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Best Local Similarity 66.7
Matches 4; Conservative
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62 AVNVIVA 68
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C, Superfami
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Riffaser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Aturer 390, 580-586, 1937.
A,Authors: Smith, H.O.; Venter, J.C.
A,Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A,Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE000790; NID:g2690224; PIDN:AAC66298.1; PID:g2690297; TIGR:BBA35
A;Experimental source: strain B31
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C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999
C;Accession: RN0624
T;Tanaka, J; Ogawara, M.; Ando, S.; Shibata, M.; Yatani, R.; Kusagawa, M.; Inagaki, M. Biochem. Biochhys. Res. Commun. 196, 115-123, 1993
A;Title: Phosphorylation of a 62kD porcine alpha-internexin, a newly identified intermed A;Reference number: RN0624; MUID:94029981; PMID:8216281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 1-18;19-28;29-45;46-57 <TAN>
C;Comment: This intermediate filament protein polymerizes to form filament itself, in vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: C70211
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
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C;Species: Caenorhabditis elegans
C;bate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Jun-2000
C;Accession: T16930
R;Du, Z.
                                                                                                                                                                                                                                                                                                                                   hypothetical protein BBA35 - Lyme disease spirochete plasmid A/lp54
C.Species: Borrelia burgdorferi (Lyme disease spirochete)
C.Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
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Pred. No. 1.9e+02;
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            Length 98;
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Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 1;
            71.0%; Score 22; DB 2; I
71.4%; Pred. No. 3.2e+02;
                                                                      1; Mismatches
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C, Keywords: brain; intermediate filament
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86 ALELLMA 92
                                 Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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               Query Match
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Biochem. Biophys. Res. Commun. 241, 334-340, 1997
A;Title: Molecular cloning of DNAs encoding the regulatory subunits of elongin from Sacd A;Reference number: UC5792; MUID:98086352; PMID:9425272
A;Accession: UC5794
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
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A;Cross-references: DDBJ:AB007693; NID:g2780364; PIDN:BAA24287.1; PID:g2780365
C;Comment: This protein binds to each other in the absence of elongin A to form a binary or induction of elongin A activity.
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-98 «URS»
A;Residues: 1-98 «URS»
A;Generics:
C;Genetics:
A;Genee: MADH4L
A;Genee: mitochondrion
A;Geneet code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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R;Hiendleder, S.; Lewalski, H.; Wassmuth, R.; Janke, A.
J. Mol. Bvol. 47, 441-448, 1998
A;Title: The complete mitochondrial DNA sequence of the domestic sheep (Ovis aries) and A;Reference number: Z17245; MUID:98440761; PMID:9767689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain 4L - sheep mitochondrion C; Species: mitochondrion Ovis orientalis aries, Ovis ammon aries (domestic sheep) C; Date: i6-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
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A;Experimental source: strain Merinolandschaf; liver
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C;Species: Drosophila melanogaster
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 17-Nov-2000
C;Accession: JC5794
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C;Superfamily: elongin C
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Best Local Similarity 50.0
Matches 3; Conservative
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Best Local Similarity 50.0
Matches 3, Conservative
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MNIMMA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Genome: mitochondrion
A;Genetic code: SGC1
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6 MNIIMA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LIVLIMA 7
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A; Residues: 1-98 <HIE>
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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C;Accession: 138244
R;Digweed, M.; Gunthert, U.; Schneider, R.; Seyschab, H.; Friedl, R.; Sperling, K.
R;Digweed, M.; Gunthert, U.; Schneider, R.; Seyschab, H.; Friedl, R.; Sperling, K.
Mol. Cell. Biol. 15, 305-314, 1995
A;Title: Irreversible repression of DNA synthesis in Fanconi anemia cells is alleviated by A;Reference number: 138244; MUID:95098005; PMID:7799938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein EC81408 [imported] - Becherichia coli (strain O157:H7, substrain RI. C;Species: Escherichia coli C;Species: Escherichia coli C;Accession: H90804 (C;Accession: H90804 (R;Andrashi, T; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. G;Ryhayashi, N.; Yasunaga, T.; Ruhara, N.; Yasunaga, T.; Ruhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A;Trile: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypochetical protein EC84541 [imported] - Escherichia coli (strain O157:H7, substrain R. S. Species Escherichia coli (S. Species Escherichia coli (C. Species Escherichia coli (C. Species IS-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 (C. S. S. Species Escherichia) (C. S. S. Species Espino, E.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:BA000007; PIDN:BAB34831.1; PID:913360868; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross references: EMBL: X82554; NID: 9575271; PIDN: CAA57901.1; PID: 9575272
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        Length 63;
                                                                                        0; Indels
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80.0%; Pred. No. 3.5e+02;
tive 1; Mismatches 0;
            67.7%; Score 21; DB 2; I
80.0%; Pred. No. 3.5e+02;
ive 1; Mismatches 0;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 57.1.
Best Local 4; Conservative
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                     Query Match
Best Local Similarity 80.03
Matches 4; Conservative
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9 ALDILIA 15
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-65 <HAY>
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23 MNVLM 27
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A; Residues: 1-63 <RES>
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E91196
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Cionserved hypothetical protein AF0697 - Archaeoglobus fulgidus
Cionserved hypothetical protein AF0697 - Archaeoglobus fulgidus
Cionserved hypothetical protein Archaeoglobus fulgidus
Cionserved hypothetical protein No. 10. Dec-1997 #text_change 29-Sep-1999
CiAccession: A69337
Riklenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
Riklenk, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: A69337
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-61 < KLB>
A;Cross-references: GB:AE001056; GB:AE000782; NID:92689379; PIDN:AAB90542.1; PID:9264991
C;Superfamily: hypothetical protein MJ0546
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 < DOU>
A;Cross-references: GB:AF083031; NID:g13794269; PIDN:AAK39646.1; GSPDB:GN00152
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Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
submitted to the EMBL Data Library, October 1995
A, Description: The sequence of C. elegans cosmid T23F2.
A, Reference number: Z18608
A, Reference number: L18630
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-57 < VDUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.7%; Score 21; DB 2; I
ilarity 50.0%; Pred. No. 3.1e+02;
Conservative 3; Mismatches 0;
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C;Superfamily: conserved hypothetical protein b2666
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17 ALNLLL 22
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Matches 3; Conserv
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A, Genome: nucleomorph
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C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: H98064
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blassczak, L.; Burgett, S.; DeHoff, B.S.; E e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M y, P.; Sun, P.M.; Winkler, M.E.
A; D Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
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A; Title: Genome sequence of Persinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AC2335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AE007317; PIDN: AAL00349.1; PID: 915459210; GSPDB: GN00174
                                                                                                                                                                                                                                                                                          hypothetical protein spr1545 [imported] - Streptococcus pneumoniae (strain R6)
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
         Gaps
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            Indels
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66.7%; Pred. No. 3.7e+02;
iive 2; Mismatches 0;
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         3; Mismatches
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         4; Conservative
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ALDILIA 15
                                                                       1 ALNVLMA 7
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-66 <KUR>
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A; Residues: 1-71 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Accession: H98064
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         Matches
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D86043
unknown protein encoded within prophage CP-933L [imported] - Escherichia coli (strain Ol
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001
C;Accession: D86043
R;Perra, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Reference number: A85480; MUID:21074935; PMID:11206551
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res; 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91196
A;Accession: E91196
A;Etatus: pre-liminary
A;Molecule type: DNA
A;Residues: 1-65 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37964.1; PID:g13364016; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-65 <STO>
A;Cross-references: GB:AE005174; NID:g12518429; PIDN:AAGS8808.1; GSPDB:GN00145; UWGP:Z5C
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Z1225 [imported] - Escherichia coli (strain O157:H7, substrain EDL9 (5.) Species Escherichia coli (5.) Species Escherichia coli (5.) Species Escherichia coli (5.) Pate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 (5.) Accession: E85613 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 (5.) Arperna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A.; Aritles Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551
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A,Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                  67.7%; Score 21; DB 2; Length 65; 57.1%; Pred. No. 3.6e+02;
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Matches 4; Conservative
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ALDILIA 15
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Best Local Similarity
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ALDILIA 15
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Matches 4; Conserv
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A; Residues: 1-65 <STO>
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Length 75;

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Search completed: February 17, 2004, 10:58:19
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C;Genetics:
A;Gene: Z1663
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C; Species Pyrococcus abyssi
C; Species Pyrococcus abyssi
C; Species Pyrococcus abyssi
C; Species Pyrococcus abyssi
C; Accession: B75106
R; Anonormous, Genoscope
Submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struth Reservance number: A75001
A; Recent and P75106
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-75 < KAW
A; Residues: 1-75 < KAW
A; Residues: 1-75 < WAW
A; Resperimental source: strain Orsay
C; Genetics:
C; Superimental source: strain Orsay
C; Superimental source: SNP2 protein
C; Superimental source: SNP2 protein
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A;itle: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
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A, Residues: 1-75 «KAM»
A, Cross-references: GB: AP000006; NID: G3236133; PIDN: BAA30628.1; PID: G3257945
A, Experimental source: strain OT3
A, Experimental source: strain OT3
A, Note: this accession replaces an interim accession for a sequence replaced by GenBank
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:2159285; PMID:11759840
A;Recession: AC2335
A;Reteria preliminary
A;Residues: 1-72 < KUR>
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: D71028
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Pred. No. 4.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                           Length 72;
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Pred. No. 4.1e+02;
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C,Superfamily: yeast SNP2 protein
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Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   67.7%;
83.3%;
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Matches 5, Conservative
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38 LAVVLA 43
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57 LNKLMA 62
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injournerment processions account and the sequence revision 16-Feb-2001 #text_change 14-Sep-2001 C;Species Escherichia account procession: E85664
C;Accession: E85664
E;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Experna, N.T.; Plunkett III, G.; Burland, V.; Mai, B.; Dimalanta, E.; Potamousis, K.; Apodaca, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Recession: E85664
A; Residues: DNA
A; Rosidues: 1-80 <STO>A; Rosidues: 1-80 <STO>A; Rosidues: BNA
A; Residues: 1-80 <STO>A; Rosidues: Brain O157:H7, substrain EDL933
A; Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                              Figure 1 icensing factor MCM3 - barley (fragment)
NyAlternate names: DNA polymerase alpha-associated protein P1; minichromosome maintenance.
NyAlternate names: DNA polymerase alpha-associated protein P1; minichromosome maintenance; Species: Hordeum vulgare (barley)
C;Species: Hordeum vulgare (barley)
C;Date: O'-May-1995 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999
C;Accession: S52172
R;Sabelli, P.A.; Burgess, S.R.; Young, M.; Tye, B.K.; Shewry, P.R.
R;Sabelli, P.A.; Burgess, S.R.; Young, M.; Tye, B.K.; Shewry, P.R.
A;Description: A maize homologue of yeast proteins required for the initiation of DNA reg.
A;Reference number: S52172
A;Accession: S52172
A;Accession: S52172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A;Residues: 1-78 <SAB>
A;Cross-references: EMBL: Z29369; NID: g609018; PIDN: CAA82557.1; PID: g609019
C;Comment: The complex of six MCM proteins is one of several proteins that must be bound
Ephosphorylated and dissociate from the chromatin.
C;Complex: The predominant form is a heterohexamer of MCM2, MCM3, MCM5, MCM6, and C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: part of the replication licensing system that permits DNA replication to C;Superfamily: human replication licensing factor MCM3; MCM homology C;Keywords: cell cycle control; DNA replication initiation; nucleus; phosphoprotein P;1-78/Domain: MCM homology (fragment) <MCM>
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Pred. No. 4.6e+02;
3; Mismatches 0; Indels
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Pred. No. 4.4e+02;
1; Mismatches 0; Indels
                                                           0; Indels
67.7%; Score 21; DB 2; I 66.7%; Pred. No. 4.2e+02;
                                                                  2; Mismatches
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Best Local Similarity 66.79
Matches 4; Conservative
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38 LNVVLA 43
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1: /cgn2 6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2 6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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18: /cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
19: /cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
17: /cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
18: /cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
19: /cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
10: /cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
11: /cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:

Description	Sequence 7, Appli Sequence 11, Appl	Sequence 5, Appli	Sequence 3, Appli	Sequence 16, Appl	Sequence 6, Appli	Sequence 1, Appli	Sequence 10, Appl	Sequence 15, Appl	Sequence 8, Appli	Sequence 58, Appl	Sequence 824, App	Sequence 824, App	Sequence 89, Appl	Sequence 89, Appl
SUMMARIES	US-09-900-147-7 US-09-900-147-1	US-09-900-147-5	US-09-900-147-3	US-09-900-147-16	US-09-900-147-6	US-09-900-147-1	US-10-214-188-10	US-09-900-147-15	US-10-044-359-8	US-09-820-893-58	US-09-925-299-824	US-09-925-299-824	US-09-853-161-89	US-09-852-659A-89
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; Sequence 11, Application US/09900147; Patent No. US20020103121A1

RESULT 2 US-09-900-147-11

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Sequence 35481, A Sequence 35481, A Sequence 4982, Ap Sequence 538, App Sequence 538, App Sequence 538, App Sequence 20049, A Sequence 41818, A Sequence 41818, A Sequence 412, App Sequence 412, App Sequence 501, App Sequence 501, App Sequence 626, App Sequence 636, App Sequence 636, App Sequence 636, App Sequence 976, App Sequence 1076, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11219, App Sequence 11211, App Sequence 11211, App Sequence 11211, App Sequence 11211, App Sequence 11311, App Seq
US-09-852-797-89 US-09-864-761-35481 US-09-864-761-35481 US-09-738-626-4982 US-10-74-860-538 US-10-74-860-538 US-10-029-386-29049 US-10-029-386-29049 US-09-900-147-2 US-09-900-147-2 US-09-900-147-4 US-09-900-147-4 US-09-900-147-4 US-09-864-761-41818 US-09-864-761-41818 US-09-864-761-4531 US-10-024-652-142 US-10-024-652-142 US-10-024-652-976 US-10-024-652-976 US-10-024-652-976 US-10-024-652-976 US-10-024-652-976 US-10-024-652-976 US-10-024-652-1219 US-10-024-652-1219 US-10-024-652-1219 US-10-024-652-1279 US-10-024-652-1279 US-10-024-652-1383
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ALIGNMENTS

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APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
CURRENT PILICATION NUMBER: US/09/900,147
CURRENT APPLICATION NUMBER: La 2001-07-09
FRIOR APPLICATION NUMBER: RABLIER APPLICATION NUMBER: 09/308,935
FRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27
FRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
IENGTH: 7
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Sequence 7, Application US/09900147
Patent No. US20020103121A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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CURRENT APPLICATION NUMBER: US/09/900,147
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US-09-900-147-5

Sequence 5. Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lesantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE REFERENCE: 620-67

CURRENT PILING DATE: 2001-07-09

PRIOR PILING DATE: EARLIER PILING DATE: 1999-05-27

PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR PILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 16
                           PAPPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Lasantha R
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 200-07
CURRENT APPLICATION NUMBER: US/09/900,147
CURRENT PILING DATE: 2001-07-09
PRIOR PILING DATE: EARLIER PILING DATE: 1999-05-27
PRIOR PILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATCHT NOS: 18
SEQ ID NO 11
SEQ ID NO 11
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Patent No. US20020103121A1
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
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ORGANISM: Artificial Sequence
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US-09-900-147-16

Sequence 16, Application US/09900147

Sequence 16, Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT FILING DATE: EARLIER APPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: EARLIER PILING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16

LENGTH: 19
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US-09-900-147-16
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Sequence 6, Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935

PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
PRIOR PILING DATE: BABLIER FILING DATE: 1999-05-27
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
LENGTH: 19
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11arity 100.0%; Pred. No. 2.2;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity luv.
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ALNVLMA 13
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Matches 7; Conserv
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US-09-900-147-6
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; Sequence 8, Application US/10044359
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| 52 ALNVLMA 58
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US-09-900-147-15
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US-10-044-359-8
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Fatent No. US20020103121A1

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

CURRENT APPLICATION NUMBER: US/09/900,147

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935

FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935

FRIOR FILING DATE: BARLIER PLING DATE: 1999-05-27

FRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOSTWARE: PATENTIN VET. 2.1
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                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-900-147-6
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                                                                                                                                                                                                                       100.0%; Score 31; DB 10; Length 30; 100.0%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                      0; Indels
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HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 6 LENGTH: .30
                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/10214188
; Publication No. US20030022260A1
; GENERAL INPORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: VIRGINIA COUNTRY: U.S.A.
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US-10-214-188-10
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US-09-900-147-1
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LENGTH: 37
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Sequence 15, Application US/09900147

Patent No. US20020103121A1

GENERAL INFORMATION:

PAPLICANT: La Thangue, Nicholas B

PPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

PILE REPERBNCE: 200-67

CURRENT FILING DATE: 2001-07-09

PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR PILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 15

LENGTH: 19
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Pred. No. 17;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 10:
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Best Local Similarity 85.
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Best Local Similarity 100.
Matches 7; Conservative
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RESULT 13
US-09-925-299-824
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US-09-853-161-89
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Pred. No. 54;
2; Mismatches 0; Indels
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85.7%; Pred. No. 65;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 824, Application US/09925299;
Sequence 824, Application US/09925299;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PA102
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US-09-820-893-58
Sequence 58, Application US/09820893
Fatent No. US20202076705A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REPERENCE: PZ033P1
CURRENT PILING DATE: 2001-03-30
PRIOR PPLICATION NUMBER: 09/531,119
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 140
SOFTWARE: PALENTING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 140
SOFTWARE: PALENTING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 140
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; LOCATION: (41)
; OTHER INFORMATION: Xaa equals stop translation
US-09-820-893-58
Publication No. US20020160454A1
GENERAL INFORMATION:
APPLICANT: Hoerman, Rafael
APPLICANT: Hoerman, Rafael
APPLICANT: Hoerman, Sachel
TITLE REPERBNCE: BA1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2002-01-11
PRIOR PILING DATE: 2002-01-11
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SORTHARE: Microsoft Office 97
SERIOTH SE
                                                                                                                                                                                                                                                                                                                                                                                    87.1%;
71.4%;
                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Hottentotta judaica
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Best Local Similarity 85.77
Local 6, Conservative
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ORGANISM: Homo sapiens
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13 AMNVMMA 19
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US-09-925-299-824
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FEATURE:
NAME/KEY: SITE
LOCATION: (36)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-824
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                                                                                                                                                                                                                                               NAME/KEY: SITE
CCATION: (36)
COTHEN INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-824
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3%; Score 26; DB 9; Length 90;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
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; Patent No. US20020076756A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: 28 Human Secreted Proteins
; TITLE OF INVENTION: 28 Human Secreted Proteins
; CURRENT PEPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
CURRENT APPLICATION NUMBER: US/09/925,299;
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-02
PRIOR PILING DATE: 1999-03-12
NUMBER: OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 824
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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44 ALNILM 49
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44 ALNILM 49
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FEATURE:
NAME/KEY: SITE
LOCATION: (11)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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US-09-189
US-09-189
US-09-189
Sequence 89, Application US/09852797
Patent No. US20020172994A1
GENERAL INFORMATION:
I APPLICANT Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ001-05-11
PRIOR PLING DATE: 2001-05-11
PRIOR PLING DATE: 2001-05-05
PRIOR PLING DATE: 1998-09-11
PRIOR PLING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
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                                   PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 6/057,765
PRIOR PILING DATE: 1997-09-05
PRIOR PILING DATE: 1997-09-06
PRIOR PILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 89
LENGTH: 87
               APPLICATION NUMBER: 60/048,189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Patent No. US20020077287A1

GENERAL INFORMATION:

JAPPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins

FILE REFERENCE: PS703P4

CURRENT APPLICATION NUMBER: US/09/852,659A

CURRENT PILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 06/265,583

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-09-12

PRIOR APPLICATION NUMBER: 60/040,762

PRIOR PILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30
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R FILING DATE: 2001-02-02
R APPLICATION NUMBER: 09/152,060
R FILING DATE: 1998-09-11
R FILING DATE: 1998-09-12
R FILING DATE: 1998-03-12
R APPLICATION NUMBER: 60/040,762
R APPLICATION NUMBER: 60/040,710
R FILING DATE: 1997-03-14
R FILING DATE: 1997-03-14
R APPLICATION NUMBER: 60/040,710
R RILING DATE: 1997-03-14
                                                               PRIOR FILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR PRILING DATE: 1997-05-30
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R APPLICATION NUMBER: 60/040,710

R RELING DATE: 1997-03-14

R APPLICATION NUMBER: 60/050,934

R APPLICATION NUMBER: 60/050,934

R RILING DATE: 1997-05-30

R FILING DATE: 1997-05-30

R APPLICATION NUMBER: 60/048,100

R APPLICATION NUMBER: 60/048,357

R RILING DATE: 1997-05-30
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Best Local Similarity 71.*
5. Conservative
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ORGANISM: Homo sapiens
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US-09-852-659A-89
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          FEATURE:
OTHER INFORMATION: MAP TO AB020871.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 2.0
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.0
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN PLACEMY, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN PLACEMY, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN PLACEMY, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACEMY, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN PLACEMY, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN PLACEMY, SIGNAL = 3.6
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sequence 4982, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                    Conservative
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US-10-106-698-7834
ORGANISM: Homo sapiens
                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
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         FEATURE:
MAMB/KEY: SITE
LOCATION: (11)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                            ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-852-797-89
                                                                                                                                               Gaps
                                                                                                                    Query Match

80.6%; Score 25; DB 10; Length 87;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels
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                                                            NAME/KEY: SITE
LOCATION: (86)
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2 LINVLMA 7
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; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION:
; FILE REFERENCE: PC008
; CURRENT FAPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 538
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Pred. No. 2.9e+02;
1; Mismatches 0; Indels
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC008C2
CURRENT APPLICATION NUMBER: US/10/212,872
CURRENT FILING DATE: 2002-08-07
Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 1198
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.4%; Score 24; DB 9; Length 65; 66.7%; Pred. No. 3e+02;
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT PILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENT NOTE: 2000-08-03
SOFTWARE: PATENT NOTE: 2000-08-03
SOFTWARE: PATENT NOTE: 2000-08-03
SOFTWARE: PATENT NOTE: 2000-08-03
SOFTWARE: PATENT NOTE: 2000-08-03
                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4982
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Best Local Similarity 66...
4; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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28 LNIIMA 33
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US-09-764-860-538
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-212-872-538
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                                                                                   77.4%; Score 24; DB 12;
66.7%; Pred. No. 3e+02;
tive 2; Mismatches 0
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APPLICATION WUMBER: 60/226,868
FILING DATE: 2000-08-22
APPLICATION NUMBER: 60/216,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/225,267
FILING DATE: 2000-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/251,869
FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/235,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-07-07
                                                                                                           4; Conservative
TYPE: PRT 'ORGANISM: Homo sapiens
                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (3)
                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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28 LNIIMA 33
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09-29 : 60/224,5 08-14 : 60/220,9)7-26 : 60/241, 10-20	: 60/249, 11-17	: 60/236, 09-29	: 60/241, 10-20	: 60/244, 11-01	: 60/225, 08-14	: 60/236, 09-29	: 60/251, 12-08	60/251,	60/229,	60/234,	60/229,	60/229,	9-01 60/229,	9-01 60/229,	9-05	9-08 60/229,	9-05	19-29	0-02	R: 60/237, -10-02	60	166	9	0-0	-10-02 R: 60/240,	-10-20 R: 60/239,	10-13	10-13	10-20	60/24 11-08	R: 60/246, -11-08	: 60	11.6	5.1	-08-	-08-
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FILING DATE: APPLICATION FILING DATE: APPLICATION		APPLICATION FILING DATE	S m	APPLICATI FILING DA	APPLICATI FILING DA	APPLICATI	APPLICATI	APPLICATI	APPLICATION	PPLI	APPLICAT	APPLICATION	PILING DA	FILING DA	FILING DA	FILING DA	FILING DA	FILING D	FILING D	APPLICAT PILING D	APPLICAT	APPLIC	APPLIC	APPLIC	FILING	FILING	FILING	FILING	FILING	FILING	APPLICA	APPLICA PILING	APPLICA	APPLICA	APPLICA	FILING	FILING
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PRIOR APPLICATION NUMBER: 60/225,213
PRIOR FILING DATE: 2000-08-12
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PRIOR FILING DATE: 2000-08-13
PRIOR FILING DATE: 2000-08-14
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PRIOR PLING DATE: 2000-10-08
PRIOR PLING DATE: 2000-11-17
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
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US-9-864-761-41818
US-9-864-761-41818
Sequence 41818, Application US/09864761
Fatent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Penn, Pavid K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT FILING DATE: 2000-05-24
FRIOR PELICATION NUMBER: US 60/207,456
FRIOR APPLICATION NUMBER: US 60/203,366
FRIOR APPLICATION NUMBER: US 60/203,366
FRIOR PILING DATE: 2000-10-04
FRIOR PILING DATE: 2000-10-04
FRIOR PILING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: PCT/US01/00666
FRIOR PILING DATE: 2001-01-30
FRIOR PILING DATE: 2001-01-30
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Fatent No. US20020103121A1
GENERAL INFORMATION:
Fatent No. US20020103121A1
GENERAL INFORMATION:
Fatent No. US20020103121A1
GENERAL INFORMATION:
Fatent Name of Internation of Internation Experies antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: 08/09/900,147
CURRENT FILING DATE: 2001-07-09
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
FRIOR PILING DATE: RARLIER FILING DATE: 1996-12-20
FRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
                                                                                                                                                     Gaps
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                                                                                           Length 96;
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; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8 US-10-029-386-29049
                                                                                           Score 24; DB 12; I
Pred. No. 4.5e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.2%; Score 23; DB 10; ilarity 100.0%; Pred. No. 7e+05; Conservative 0; Mismatches 0
                                                                                           Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Best Local Similarity
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13 VNVLMA 18
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Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Harizel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 29049
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| Ratent No. US20020151681A1
| Patent No. US20020151681A1
| GENERAL INPORMATION:
| APPLICANT: Craig Roosen,
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REPREBNCE: PA101
| CURRENT APPLICATION NUMBER: US/09/925,300
| CURRENT FILING DATE: 2001-08-10
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1890
| SOFTWARE: PatentIN Ver. 2.0
| SEQ ID NO 1456
                                                          77.4%; Score 24; DB 15; Length 65; 66.7%; Pred. No. 3e+02; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.4%; Score 24; DB 10; Length 71; 66.7%; Pred. No. 3.3e+02; tive 2; Mismatches 0; Indels
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN FERTL LIVER, SIGNAL = 1.5
   ; PRIOR FILING DATE: 2000-09-08
                                                                                        Best Local Similarity 66.7
Matches 4; Conservative
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Matches 4; Conservative
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ORGANISM: Homo sapiens
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35 LNIIMA 40
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28 LNIIMA 33
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US-10-029-386-29049
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NAME/KEY: SITE
                                                                Query Match
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US-09-864-761-45731

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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.67

US-09-064-761-45731
                                IndelB
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PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION UNMER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vere: 1.1
SEQ ID NO 45731
Pred. No. 1.4e+02;
0; Mismatches 0;
100.08;
                                    5; Conservative
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ORGANISM: Homo sapiens
   Best Local Similarity
                                                                                                         3 NVLMA 7
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                                       Matches
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; Sequence 4, Application US/09900147
; Patent No. US2002013121A1
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas B
; APPLICANT: La Thangue, Nicholas B
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; TITLE OF INVENTION: Poblide antagonists of DP transcription factors
; TILLS REFERENCE: 200-07-09
; FILLS REFERENCE: 200-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
; PRIOR FILLNG DATE: BARLIER FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2

OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EST_HUMAN HIT: AW131202.1, EVALUE 5.00e-04
US-09-864-761-41818
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FLING DATE: 2001-01-30
PRIOR FLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 41018
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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US-09-900-147-4
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ઠે В 74.2%; Score 23; DB 10; Length 20;

Query Match

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APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
FILE REPRENCE: 51158-20025.00
CURRENT APPLICATION NUMBER: US/10/24,652
CURRENT APPLICATION NUMBER: 60/256,210
PRIOR APPLICATION NUMBER: 60/256,210
PRIOR APPLICATION NUMBER: 60/256,210
PRIOR PLING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2598
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Aya
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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0
                                                                                                                                                             Score 22; DB 12; Length 9;
Pred. No. 7e+05;
2; Mismatches 0; Indels
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    SOFTWARE: FastSEQ for Windows Version 4.0
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Afar, Daniel E.H.
Hubert, Rene S.
Mitchell, Steve Chappell
Levin, Elana
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 348, Application US/10024652
Publication No. US20030219738A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 412, Application US/10024652
Publication No. US20030219738A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hubert, Rene S.
Mitchell, Steve Chappell
Levin, Elana
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Faris, Mary
Afar, Daniel E.H.
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APPLICANT: Challita-Eid, Pia M.
                                                                                                                                                                  Query Match 71.0
Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: homo sapien
US-10-024-652-348
                                                                       TYPE: PRT
CORGANISM: homo sapien
US-10-024-652-142
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Best Local Similarity
Matches 4; Conserv
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1 AVNVIM 6
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
FILE REPERBENCE: 51158-20025.00
CURRENT APPLICATION NUMBER: US/10/024,652
PRIOR APPLICATION NUMBER: 60/256,210
PRIOR FILING DATE: 2000-12-15
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Associate Asya
TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
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                                                   Gaps
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Pred. No. 7e+05;
2; Mismatches 0; Indels
74.2%; Score 23; DB 9; Length 26; 83.3%; Pred. No. 1.9e+02; ive 0; Mismatches 1; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
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CURRENT APPLICATION NUMBER: US/10/024,652
CURRENT FILING DATE: 2002-06-28
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Afar, Daniel E.H.
Hubert, Rene S.
Mitchell, Steve Chappell
Levin, Elana
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PRIOR APPLICATION NUMBER: 60/256,210
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2598
                                                                                                                                                                                                                                                                                                                                                                                                                             Hubert, Rene S.
Mitchell, Steve Chappell
Levin, Elana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 142, Application US/10024652; Publication No. US20030219738A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                          ; Sequence 27, Application US/10024652; Publication No. US20030219738A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   APPLICANT: Agensys, Inc
APPLICANT: Agensys, Inc
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Agensys, Inc
APPLICANT: Challita-Eid, Pia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.0%;
66.7%;
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Best Local Similarity 66.7
Matches 4; Conservative
                                              Conservative
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ORGANISM: homo sapien
Query Match
Best Local Similarity
Matches 5; Conserv
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AVNVIM 7
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US-1U-U44-b52-b2b

Sequence 626, Application US/10024652

Sequence 626, Application US/10024652

Sequence 626, Application Wollows

Subblication No. 1200303019738A1

SERVERAL INFORMATION:

APPLICANT: Agensys, Inc

APPLICANT: Afar, Daniel E.H.

APPLICANT: Mitchell, Steve Chappell

APPLICANT: Levin, Elana

APPLICANT: Levin, Elana

APPLICANT: Levin, Raren So.

APPLICANT: Raitano, Arthur B.

APPLICANT: Molect, Raren Jane Meyrick

APPLICANT: Saitano, Arthur B.

APPLICANT: Saitano, Arthur B.

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NOLeic Acid and Encoded Zinc

TITLE OF INVENTION: Detection of Cancer

TITLE OF INVENTION: Detection of Cancer

TITLE OF INVENTION: Detection of Cancer

TITLE OF INVENTION: Detection of Cancer

TITLE OF INVENTION: UNDERE: 2002-06-28

TITLE REFERENCE: 21188-20025.00

CURRENT PILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 2598

SOFTWARE: FastSEQ for Windows Version 4.0

TRACTH: 9
                                                                                                           APPLICANT: JANCOUNTES, Aya
APPLICANT: JANCOUNTES, Aya
TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
FILE REPRENCE: 51158-20025.00
CURRENT APPLICATION NUMBER: US/10/024,652
CURRENT PILING DATE: 2002-06-28
PRIOR FILING DATE: 2000-12-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.0%; Score 22; DB 12; Length 9; 66.7%; Pred. No. 7e+05; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 2598
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 501
LENGTH: 9
Mitchell, Steve Chappell
Levin, Blana
Morrison, Karen Jane Meyrick
Raitano, Arthur B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 36
US-10-024-652-636
; Sequence 636, Application US/10024652
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CORGANISM: homo sapien
US-10-024-652-626
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CORGANISM: homo sapien
US-10-024-652-501
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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1 AVNVIM 6
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APPLICANT:
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APPLICANT: Afar, Daniel E.H.
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mariano, Karen Jane Meyrick
APPLICANT: Mariano, Athur B.
APPLICANT: Markobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
TITLE OF INVENTION: Detection of Cancer
TITLE OF INVENTION: Detection of Cancer
TITLE OF INVENTION: Detection of Cancer
TITLE OF INVENTION: Detection of Cancer
TITLE OF INVENTION: 1002-06-28
TITLE OF INVENTION: DOSC-06-28
TITLE OF INVENTION NUMBER: 06/256,210
RRIOR APPLICATION NUMBER: 06/256,210
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Pred. No. 7e+05;
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                      TITLE OF INVENTION: Detection of Cancer FILE REFERENCE: 51158-20025.00
CURRENT APPLICATION NUMBER: US/10/024,652
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/256,210
PRIOR APPLICATION NUMBER: 60/256,210
NUMBER OF SEQ ID NOS: 2598
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 412
LENGTH: 9
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Publication No. US20030219738A1
GENERAL INFORMATION:
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E.H.
APPLICANT: Hubert, Rene S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Agensys, Inc
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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US-10-024-652-444
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: homo sapien
US-10-024-652-412
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1 AVNVIM 6
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2 AVNVIM 7
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US-10-024-652-501
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APPLICANT: Afar, Daniel E.H.
APPLICANT: Afar, Daniel E.H.
APPLICANT: Afar, Daniel E.H.
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Matchell, Steve Chappell
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
FILE REFERENCE: 51158-2002.00
FILE REFERENCE: 51158-2002.00
CURRENT APPLICATION NUMBER: 60/256,210
FRIOR FILING DATE: 2000-12-15
FRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2598
SOUTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Nucleic Acid and Encoded Zinc

TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and

TITLE OF INVENTION: Detection of Cancer

FILE REFERENCE: 51158-20025.00

CURRENT APPLICATION NUMBER: US/10/024,652

CURRENT FILING DATE: 2002-06-28

PRIOR PPLICATION NUMBER: 60/256,210

PRIOR FILING DATE: 2000-12-15
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Pred. No. 7e+05;
2; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 977
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Mitchell, Steve Chappell
Levin, Blana Morrison, Karen Jane Meyrick
Raitano, Arthur B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 977, Application US/10024652
Publication No. US20030219738A1
GENERAL INFORMATION:
                                                                                                                                                   Sequence 976, Application US/10024652
Publication No. US20030219738A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Challita-Eid, Pia M.
Faris, Mary
Afar, Daniel E.H.
                                                                                                                                                                                                                               APPLICANT: Agensys, Inc
APPLICANT: Challita-Eid, Pia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.0%;
66.7%;
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CORGANISM: homo sapien
US-10-024-652-976
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ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
     |:||:|
1 AVNVIM 6
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3 AVNVIM
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ababovits, Aya
TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
TITLE OF INVENTION: Detection of Cancer
FILE REFERENCE: 51158-20025.00
CURRENT APPLICATION NUMBER: 08/10/024,652
CURRENT FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2598
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 926
LENGTH: 9
                                                                                                                                                                                                                                                                         APPLICATE: Jakobovits, Aya

TITLE OF INVENTION: Nucleic Acid and Encoded Zinc

TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and

TITLE OF INVENTION: Detection of Cancer

FILE REFERENCE: 51158-20025.00

CURRENT APPLICATION NUMBER: US/10/024,652

CURRENT FILING DATE: 2002-16-28

PRIOR PAPLICATION NUMBER: 60/256,210

PRIOR FILING DATE: 2000-12-15
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Afar, Daniel E.H.
Hubert, Rene S.
Mitchell, Steve Chappell
Levin, Blana
Morrison, Karen Jane Meyrick
Raitano, Arthur B.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 636
LENGTH: 9
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APPLICANT: Challita-Bid, Pia M.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E.H.
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Levin, Elana
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Publication No. US20030219738A1
GENERAL INFORMATION:
                                                  Agensys, Inc
Challita-Eid, Pia M.
n No. US20030219738A1
FORMATION:
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Best Local Similarity 66.7
Matches 4; Conservative
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US-10-024-652-926
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Best Local Similarity
Matches 4; Conserv
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AVNVIM 9
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APPLICANT: MOTTION, Karen Jane Meyrick
APPLICANT: MoTTION, Karen Jane Meyrick
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovite, Aya
TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
FILE REFERENCE: 51158-20025.00
CURRENT APPLICATION NUMBER: US/10/024,652
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/256,210
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2598
SOFTWARE: PastSEQ for Windows Version 4.0
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pred. No. 7e+05;
2; Mismatches 0; Indels
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PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2598
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1219
IENGTH: 9
TYPE: PRT
ORGANISM: homo sapien
US-10-024-652-1219
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Raitano, Arthur B.
Jakobovits, Aya
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Publication No. US20030219738A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
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Mitchell, Steve Chappell
Levin, Elana
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Mitchell, Steve Chappell
Levin, Elana
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APPLICANT: Challita Eid, Pia M.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E.H.
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66.7%;
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US-10-024-652-1272
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Best Local Similarity
Matches 4; Conserv
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AVNVIM 9
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TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
FILE REPRENCE: 51158-2005.00
CURRENT APPLICATION NUMBER: US/10/024,652
CURRENT APPLICATION NUMBER: 60/256,210
PRIOR PILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2598
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1076
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Pred. No. 7e+05;
2; Mismatches 0; Indels
                                                  71.0%; Score 22; DB 12; Length 9; 66.7%; Pred. No. 7e+05; ive 2; Mismatches 0; Indels
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Hubert, Rene S.
Mitchell, Steve Chappell
Levin, Elana
Morrison, Karen Jane Meyrick
Raitano, Arthur B.
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CURRENT FILING DATE: 2002-06-28
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Raitano, Arthur B.
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Publication No. US20030219738A1
GENERAL INFORMATION:
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APPLICANT: Challitae Eid, Pia M.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E.H.
APPLICANT: Michell, Steve Chappell
APPLICANT: Michell, Steve Chappell
APPLICANT: Levin, Elans
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
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66.7%;
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                4; Conservative
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US-10-024-652-1076
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1 AVNVIM 6
                                                       Query Match
Best Local Similarity
Matches 4; Conserv
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AVNVIM 7
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             US-10-024-652-977
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ORGANISM:
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APPLICANT: Morrison, Karen Jane Meyrick

APPLICANT: Mariano, Arthur B.

APPLICANT: Astrano, Arthur B.

APPLICANT: Astrano, Arthur B.

TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and TITLE OF INVENTION: US.10/024,652

TITLE OF INVENTION: Detection of Cancer TITLE OF INVENTION: US.10/024,652

FILE REFERENCE: 511S8-2002-06-28

PRIOR PAPLICATION NUMBER: 2002-06-28

PRIOR PLING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 2598

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1383

LENGTH: 9
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Best Local Similarity 66.7
Matches 4; Conservative
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CORGANISM: homo sapien
US-10-024-652-1383
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TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
TITLE OF INVENTION: Detection of Cancer
FILE REFERENCE: 51158-20025.00
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/10/024,652
PRIOR APPLICATION NUMBER: 60/256,210
PRIOR APPLICATION NUMBER: 60/256,210
PRIOR PLING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2598
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1311
  TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
FILE REPERRNCE: 51158-2002-06
CURRENT APPLICATION NUMBER: US/10/024,652
CURRENT APPLICATION NUMBER: 06/256,210
PRIOR PILING DATE: 2002-06-28
SUPRING APPLICATION NUMBER: 60/256,210
PRIOR FILING DATE: 2000-12-15
SUPRING APPLICATION WINGER: 06/256,210
PRIOR FILING DATE: 2000-12-15
SUPRING APPLICATION WINGER: 06/256,210
PRIOR FILING DATE: 2000-12-15
SUPRING APPLICATION WINGOWE VERSION 4.0
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Afar, Daniel E.H.
Hubert, Rene S.
Mitchell, Steve Chappell
Levin, Blana
Morrison, Karen Jane Meyrick
Raitano, Arthur B.
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Publication No. US20030219738A1
GENERAL INFORMATION:
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APPLICANT: Challita-Eid, Pia M.
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Best Local Similarity 66.7
Matches 4; Conservative
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ORGANISM: homo sapien
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; ORGANISM: homo sapien
US-10-024-652-1279
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Best Local Similarity
Matches 4; Conserv
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AVNVIM 7
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US-10-024-652-1383
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0; Indels

DB 12;

Score 22; DB 12 Pred. No. 7e+05; 2; Mismatches

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Sequence 11, Appl
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                                                                           February 17, 2004, 10:50:13; Search time 5.05941 Seconds (without alignments) 58.540 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-308-935-3

US-09-308-935-3

US-09-308-935-1

US-09-308-935-1

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US-08-184-185-18

US-08-186-188-14

US-08-308-935-2

US-08-308-935-3

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Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
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seq length: 100
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No.
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                 Sequence 7, Application US/09308935

Sequence 7, Application US/09308935

Patent No C268334

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Petide antagonists of DP transcription factors
FILE REFERENCE: 620-67

CURRENT FILING DATE: 1999-05-27

EARLIER APPLICATION NUMBER: PCT/GB97/03506

EARLIER FILING DATE: 1997-12-22

EARLIER FILING DATE: 1996-12-20

SARIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 7

LENGTH: 7

LENGTH: 7
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US-09-308-935-9
US-08-725-459B-11
US-08-725-459B-13
US-08-725-459B-75
US-08-725-459B-75
US-08-725-459B-76
US-08-725-459B-76
US-08-725-459B-76
US-08-725-459B-76
US-08-725-459B-76
US-08-725-459B-78
US-08-725-459B-18
US-08-725-459B-19
US-08-725-459B-19
US-08-725-459B-49
US-08-725-459B-49
US-08-725-459B-49
US-08-725-459B-49
US-08-725-459B-47
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Fatent No. 6269334
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
TILE COF INVENTION: Peptide antagonists of DP
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT FILING DATE: 1999-02-27
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: GB 9626589.7
SARLIER PAILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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100.0%;
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Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: protein US-09-078-596-13
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TOPOLOGY: linear
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) MOLECULE TYPE: protein
US-08-428-131-13
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Best Local Similarity
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STRANDEDNESS: si
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JETUREAL INFORMATION:
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JETUREAL INFORMATION:
JETURE OF INVENTION: Deptide antagonists of DP transcription factors
JITLE OF INVENTION: Peptide antagonists of DP transcription factors
JITLE OF INVENTION: Peptide antagonists of DP transcription factors
JETLE REFERENCE: 620-67
JETLE REFERENCE: 620-67
JETLE REFERENCE: 1999-05-27
JETLE REFING DATE: 1999-05-27
JETLING DATE: 1997-12-22
JETLING DATE: 1997-12-22
JETLING DATE: 1996-12-20
JETLING DATE: 1996-12-20
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                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-11
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Sequence 13. Application US/08428131
Sequence 13. Application US/08428131
Sequence 13. Application US/08428131
Sequence 13. Application Factor DP-1
TITLE OF INVERTION: Transcription Factor DP-1
AUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESSE: 14
CORRESPONDENCE ADDRESS: 14
STREET: 1100 No. 5863757th Glebe Road, 8th Floor CITY: Arlighia
SCOUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
COMPUTER: PLAN PC Compatible
COMPUTER: IN PC Compatible
COMPUTER: PLAN PC Compatible
COMPUTER: PLAN PC Compatible
COMPUTER: PRESPONDENCE PC-DOS/MS-DOS
SOFTWARE: PRECENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 31; DB 3; Length 16; 100.0%; Pred. No. 0.58; 1.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 7; Conservative 0; Mismatches 0; Indels
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Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
SOFTWARE: Patentin Ver. 2.1
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|S ALNVLMA 11
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                           SEQ ID NO 11
LENGTH: 14
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CLASSIPPICATION:
CLASSIPPICATION:
PRIOR APPLICATION NUMBER: US/08/428,131
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-0U1-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEFRENCE; (703) 816-4100
TELEFAX: (703) 816-4100
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APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 117-181
REPERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
INFORMATION POR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 maino acids
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10 ALNVLMA 16
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Patent No. 6268334.

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: La Thangue, Nicholas B

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

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TITLE OF INVENTION: Peptide antagonists of DP transcription factors

TITLE OF INVENTION: Peptide anta
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Patent No. 626834

FRENERAL INFORMATION:
FRENERAL INFORMATION:
FILL BAPLICANT: Bandara, Lasantha R

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILL REFERENCE: 620-67

CURRENT APPLICATION NUMBER: US/09/308,935

CURRENT PILING DATE: 1999-05-27

FARLIER PILING DATE: 1997-12-22

FARLIER PILING DATE: 1997-12-22

FARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE PATENT VET. 1806-12-20
   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-3
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   0; Indels
   0; Mismatches
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LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
7; Conservative
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6 ALNVLMA 12
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ALNVLMA 13
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US-09-308-935-16
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Matches
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US-09-308-935-1
Sequence 1, Application US/09308935
Patent No. 626834
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas B
APPLICANT: La Thangue, Nicholas B
TITLE OF INVENTION: Peptide antagonists of DP transcription factors
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT PILING DATE: 1999-05-27
EARLIER PILING DATE: 1997-12-22
EARLIER PILING DATE: 1997-12-22
MUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
FENCINE APPLICATION NUMBER: CB 9626589.7
FENCINE APPLICATION NUMBER: CB 9626589.7
FENCINE APPLICATION NUMBER: CB 9626589.7
FENCINE APPLICATION NUMBER: CB 9626589.7
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FENCINE APPLICATION NUMBER: CB 9626589.7
FENCINE APPLICATION NUMBER: CB 9626589.7
FENCINE APPLICATION NUMBER: CB 9626589.7
                                                                                                       APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTED.
FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT APPLICATION NUMBER: US/09/308,935
CURRENT APPLICATION NUMBER: US/09/103506
EARLIER APPLICATION NUMBER: ET/0897/03506
EARLIER FILING DATE: 1999-02-27
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARRE: PALENT NOWER: CB 9626589.7
EARLIER FILING DATE: 1996-12-20
NUMBER: OF SEQ ID NOS: 18
SEQ ID NO 6
IENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 31; DB 3; Length 30; Best Local Similarity 100.0%; Pred. No. 1.2; Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 6, Application US/09308935
Patent No. 6268334
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                 100.0%; Score 31; DB 3; Length 72; 100.0%; Pred. No. 3; tive 0; Mismatches 0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAK: (703) 816-4000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                     NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REBERENCE/DOCKET NUMBER: 117-
TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 816-400
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: peptide
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TOPOLOGY: linear
MOLECULE TYPE: protein
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STRANDEDNESS:
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Patent No. 5863757

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5863757th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIPE: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-JUN-1995
CLASSIFICATION STATE
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. CTAWford
RECISTRATION NUMBER: 117-181
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: T2 amino acids
TYPE: amino acids
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Sequence 11, Application US/09078596

Patent No. 6150116

GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6150116th Glebe Road, 8th Floor
CITY: Arlington
STRATE: Virginia
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 23-UDN-1995
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Best Local Similarity 100.
Matches 7; Conservative
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STRANDEDNESS: single
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MOLECULE TYPE: protein
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13 ALNVLMA 19
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LOCATION: (11)

TOCATION: (11)

TOTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids to TRATURE:

NAME/KEY: SITE

LOCATION: (86)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-152-060-89
                                                                                                                                                                                                                                                                                         Score 25; DB 4; Length 87;
Pred. No. 84;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIR:
US/08/484,493
PILING DAIE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Occhiodoro, Teresa
APPLICANT: Bielicki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08484493
Patent No. 5728381
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
REFRENCE/DOCKET NUMBER: 8416;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                            80.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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STRANDEDNESS: si
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TELEFAX: 5
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APPLICANT: La Thangue, Nicholas B
APPLICANT: Bandara, Lasantha R
TITLE OF INVENTION:
FILE REPRENCE: 620-67
CURRENT APPLICATION NUMBER: US/09/306,935
CURRENT FILING DATE: 1999-65-27
CURRENT FILING DATE: 1999-65-27
EARLIER PLICATION NUMBER: PCT/GB97/03506
EARLIER PILING DATE: 1997-12-22
EARLIER PILING DATE: 1997-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTION OF 2: 1
SEQ ID NO 15
LENGTH: 19
TYPE: PRT
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.1%; Score 27; DB 3; Length 19; 85.7%; Pred. No. 5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
IIILE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P1.US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/152,060
                                                                                 RESULT 13
US-09-308-935-15
; Sequence 15, Application US/09308935
; Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 89, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
52 ALINVLIMA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALNALMA 13
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Gaps .; 0

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Query Match

77.4%; Score 24; DB 2; Length 25;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                            CORRESPONDERS:
ADDRESSE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,212
FILING DATE:
CLASSIFICATION 435
PRICH APPLICATION HUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
RECISTRATION NUMBER: 31,346
REPERENUE/AGENT INFORMATION:
TELEPHONE: 516-742-4343
TELEPHONE: 516-742-4343
TELEPHONE: 516-742-4343
TELEPHONE: 516-742-4366
TELEFAX: 530 901 SANS UR
INFORMATION POR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: LING ACIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Clements Donald S
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: IDTRONATE 2-SULFATASE
NUMBER OF SEGUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
APPLICANT: Occhiodoro, Teresa
APPLICANT: Bielicki, Julie
APPLICANT: Bielicki, Julie
APPLICANT: Clements, Peter R
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Sequence 5, Application US/09249003
; Patent No. 6153188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-09-249-003-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPRY: USA

ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SUCTAME: PAPLICATION DATA:
APPLICATION NUMBER: US/08/484,494
FILING DATE: 10-7-DEC-1992
ATTORNEY AGENT INFORMATION:
NAME: Digiqlio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416Z
TELECOMMUNICATION INFORMATION:
TELEPANING POCKET NUMBER: 16-742-436
TELECOMMUNICATION INFORMATION:
TELEPANING POR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TWENT TELECTION ACIDS
LENGTH: 25 amino acids
TWENT TELECTION ACIDS
TELECTION TO SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                         APPLICANT: Wilson, Peter J
APPLICANT: Wilson, Charles P
APPLICANT: Morris, Charles P
APPLICANT: Ancon, Donald S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STRATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08345212
Patent No. 5932211
GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
                                                                                                                                                            US-08-484-494-5
; Sequence 5, Application US/08484494
; Patent No. 5798239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 77.4 Best Local Similarity 83.3 Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-484-494-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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STRANDEDNESS: Bil
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US-08-345-212-5
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Length 25;
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| Sequence 14, Application US/08194338
| Patent No. 5474898
| GENERAL INFORMATION:
| APPLICANT: Fraeer, John C. APPLICANT: McCombie, William R. TITLE OF INFURITION: OCTOPAMINE RECEPTOR NUMBER OF SEQUENCES: 16
| ADDRESSEE: Knobbe, Martens, olson and Bear STREET: 620 Newport Center Drive, Sixteenth Floor CITY: Newport Beach STREET: CA. CATAMATICE. CA. STREET: CA. STREET: CA. STREET: CA. CATAMATICE. CA. STREET: CA. CATAMATICE. CA. STREET: CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. CA. CATAMATICE. C
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAMME: ISTABLSON, NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001DV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-6176
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.4%; Score 24; DB 4;
83.3%; Pred. No. 36;
Live 1; Mismatches
                                                                                                                                                   REFERENCE DOCKET NUMBER: 8416Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                 ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
        FILING DATE: 17-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-685-844-5
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wilson, Peter J
Morris, Charles P
Anson, Donald S
Occhiodoro, Teresa
Bielicki, Julie
Clements, Peter R
Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDURONATE 2-SULFATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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APPLICATION NUMBER: 07/991,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                             PILING DATE:
CLASSIFICATION NOMBER: US/US/LAS/UGS
PILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991,973
FILING DATE: 17-DEC-1992
ATTONERY/ABENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416Z
TELECOMMUNICATION INFORMATION:
TELEPAX: S16-742-4343
TELEFAX: S16-742-4343
TELEFAX: S10-742-4365
TELEFAX: S10-742-4365
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Patent No. 6541254
GENERAL INFORMATION:
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STATE: New York
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Best Local Similarity 83.3
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-09-249-003-5
                                                                                COMPUTER READABLE FORM:
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US-09-685-844-5
COUNTRY:
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Sequence 33, Application US/08811492;
Patent No. 5834247;
GENERAL INFORMATION:
APPLICANT: PERLER, FRANCINE B.
APPLICANT: APACK, WILLIAM E.
APPLICANT: XU, MILG-QUN
APPLICANT: YU, MING-QUN
APPLICANT: NODGES, ROBERT A.
APPLICANT: NOREN, CHRISTOPHER J.
                                                                                                                                                                                                                                                                               Sequence 33, Application US/08004139B Patent No. 5496714
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 42188
TELECOMMUNICATION INFORMATION:
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(617) 523-6440
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Best Local Similarity 100.
Matches 5; Conservative
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INFORMATION FOR SEQ ID NO:
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      5; Conservative
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STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                 3 NVLMA 7
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                                                                                                                               1 NVLMA
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STREET: 13
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US-08-004-139B-33
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             Matches
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Sequence 2, Application US/09308935

Patent No. 626834

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: La Thangue, Nicholas B

APPLICANT: La Thangue, Nicholas B

FILE REFERENCE: 620-67

CURRENT APPLICATION WUMBER: US/09/308,935

CURRENT APPLICATION WUMBER: EVT/GB97/03506

EARLIER APPLICATION WUMBER: EVT/GB97/03506

EARLIER FILING DATE: 1999-05-27

EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-308-935-2
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                                                                                                     Score 24; DB 1; Length 63; Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.2%; Score 23; DB 3; Length 9; 100.0%; Pred. No. 2.5e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                      1; Indels
                                                                                                                                                                             1; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                               Query Match 77.4
Best Local Similarity 71.4
Matches 5; Conservative
      ; FRAGMENT TYPE: internal US-08-194-338-14
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Best Local Similarity
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APPLICANT: COMB, DONALD G.
APPLICANT: PERLER, FRANCINE B.
APPLICANT: AU, MING-QUN
APPLICANT: AU, MING-QUN
APPLICANT: JACK, WILLIAM E.
APPLICANT: JACK, WILLIAM E.
TITLE OF INVENTION: PRODUCTION
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 22;
53;
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APPLICATION NUMBER: US/08/004,139B
FILING DATE: 09-DEC-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 1; Pred. No. 53; 0; Mismatches
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22 amino acids
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SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: un
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Best Local Similarity
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APPLICANT: CHONG, SHAORONG S.C.
APPLICANT: ADAM, ERIC
APPLICANT: ADAM, ERIC
APPLICANT: SOUTHWORTH, MAURICE
TITLE OF INVENTION: MODIFIED PROTEINS, METHODS OF THEIR
TITLE OF INVENTION: PRODUCTION AND METHODS FOR PURIFICATION OF TARGET
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 155
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER RAOD
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                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC\ DOS/MS\\ DOS
SOFTWARE: IBM PC compatible
OPERATING SYSTEM: PC\ DOS/MS\\ DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US\08\811,492
FILING DATE: 29-DEC.1995
FILING DATE: 29-DEC.1995
FILING DATE: 29-DEC.1995
CLASSIFICATION NUMBER: US\08\496,247
FILING DATE: 28-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US\08\496,247
FILING DATE: 03-000-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US\08\496,247
FILING DATE: 03-000-1993
CLASSIFICATION NUMBER: US\08\406,139
FILING DATE: 03-000-1993
CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: US\08\406,139
FILING DATE: 03-000-1993
CLASSIFICATION: 435
ATCASSIFICATION: 
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100.0%; Pred. No. 53;
iive 0; Mismatches (
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PCT-US96-10545A-33
SEQUENCE 33, Application PC/TUS9610545A
SEQUENCE 33, Application PC/TUS9610545A
PEPLICANT: COMB, DONALD G.
APPLICANT: PERLER, FRANCINE B.
APPLICANT: JACK, WILLIAM E.
APPLICANT: HODGES, ROBERT A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 22 amino acida
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
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unknown
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                                                                                                                                                                                                                                                                                                                          CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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TITLE OF INVENTION WOLFELD POTEINS AND METHODS OF THEIR

ITTLES OF INVENTION WOLFELD POTEINS AND METHODS OF THEIR

INTERIOR OF SEQUENCES: 77

COMPETED SECURITY STATES AND WILLIAMS, NEW ENGLAND BIOLASS, INC.

STREET: 22 TOZES END.

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-9
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71.0%; Score 22; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 1; Indels
                                                                          Length 11;
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: CONAWAY, RONALD C.
APPLICANT: CONAWAY, JOAN W.
TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPANIOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,459B
FILING DATE: 04-OCT-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HANSEN, EUGENIA S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/COCKET NUMBER: 11146/07501
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 11:
SEQUENCE CRARACTERISTICS:
LENGTH: 13 amino acids
TUTENTALE AMINO ACIDS
TELENGTH: 13 amino acids
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Elongin C"
                                                                            3;
                                                                          71.0%; Score 22; DB 100.0%; Pred. No. 42; ive 0; Mismatches
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STREET: 717 N. HARWOOD, SUITE 3400
CITY: DALLAS
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                                                                                                                                                                                                                                                                                                       US-08-725-459B-11
; Sequence 11, Application US/08725459B
; Patent No. 6084068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                 Query Match 71.0
Best Local Similarity 100.
Matches 5; Conservative
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; CTHER INFORMATION:
; CTHER INFORMATION:
US-08-725-459B-11
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1 ALELLMA 7
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Better No. 6.580370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PLING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4216
LENGTH: 67
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US-09-308-935-9
IS-09-308-935-9
Sequence 9, Application US/09308935
Sequence 9, Application US/09308935
Sequence 9, Application US/09308935
Sequence 9. Application US/09308935
Sequence No. 6268334
Sequence No. 6268334
Septicant: La Thanque, Nicholas B
APPLICANT: La Thanque, Nicholas B
APPLICANT: La Thanque, Nicholas B
APPLICANT: La Thanque, Nicholas B
SPLICANT: Peptide antagonists of DP transcription factors
FILE REPRENCE: 620-67
CURRENT APPLICATION NUMBER: 02/0308
SEALLER FILING DATE: 1999-05-27
EARLIER FILING DATE: 1997-12-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NO 9
SERVIEW NUMBER: PatentIN Ver. 2.1
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Pred. No. 1.8e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    Score 23; DB 3; Length 40;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                   1; Mismatches
                         CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 197 56 975.7
PRIOR FILING DATE: 1997-12-20
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PAtentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus epidermidis
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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15 LNILMS 20
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6 LNVLIA 11
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US-09-134-001C-4216
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Query Match
Best Local Similarity 71.4%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 1: Indels
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Patent No. 5792634
GENERAL INFORMATION:
APPLICANT: Conaway, Ronald C.
APPLICANT: Conaway, Joan W.
APPLICANT: Bradsher, John N.
TITLE OF INVENTION: RNA POlymerase Transcription Factor NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                        Sequence 75, Application US/08725459B
Patent No. 6084068
GENERAL INFORMATION:
APPLICANT: CONAWAY, RONALD C.
APPLICANT: CONAWAY, JOAN W.
TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIDLEY & AUSTIN
STREET: 717 N. HARWOOD, SUITE 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING DATE: US/08/725,459B FILING 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 717 N. HP
CITY: DALLAS
STATE: TX
COUNTRY: US
ZIP: 75201-6507
                  10 ALELLMA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || :|||
12 ALELLMA 18
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CITY: Dallas
                                                                                                                                                                                    RESULT 32
US-08-725-459B-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-524-757-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
TITLE OF INVENTION: PEPTIDES FOR THE TREATMENT OF SYSTEMIC LUPUS TITLE OF INVENTION: ERYTHEMATOSUS FILE REPERENCE: 56040-A-PCT-US CURRENT APPLICATION NUMBER: US/09/399,494 CURRENT FILING DATE: 1999-09-20 NUMBER OF SEQ ID NOS: 22 SOFTWARE: PATENTIN Ver. 2.1 SEQ ID NO 19 LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22; DB 3; Length 21;
Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08725459B
Fatent No. 6084068
GENERAL INFORMATION:
APPLICANT: CONNAMY, RONALD C.
APPLICANT: CONNAMY, JOAN W.
TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIDLEY & AUSTIN
STREET: 717 N. HARWOOD, SUITE 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US

ZIP: 75201-6507

ZIP: 75201-6507

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,459B
FILING DATE: 04-0CT-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HANSEN, EUGENIA S.
REGISTRATION NUMBER: 31,966
REFERENCE/POCKET UNBER: 31,966
RELECOMMUNICATION INFORMATION:
TELEPHONE: 214-991-3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "amino acids 91-112 of
Elongin C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: not relevant not relevant
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57.1%;
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 57.1
Matches 4; Conservative
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COTHER 
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STRANDEDNESS: not
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ALNITLA 15
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                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: mouse
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US-08-725-459B-13
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Gaps

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SS: not relevant
not relevant
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40 ALELLMA 46
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US-08-152-721B-22
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| Sequence 8, Application US/09217293
| Sequence 8, Application US/09217293
| Patent No. 6337181
| GENERAL INFORMATION:
| APPLICATION: A METHOD OF SPECIFYING VACCINE COMPONENTS FOR VIRAL TITLE OF INVENTION: QUASISPECIES
| TITLE OF INVENTION: QUASISPECIES
| TITLE OF INVENTION: QUASISPECIES
| TITLE OF INVENTION: QUASISPECIES
| CURRENT APPLICATION NUMBER: US/09/217,293
| CURRENT FILING DATE: 1998-12-21
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NOS: 9
| SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa1 is HY, Xaa2 is KE; Xaa3 is SRk; Xaa4 is DE;
COTHER INFORMATION: Xaa5 is SN
OTHER INFORMATION: Capital letters indicate advantageous variants and
OTHER INFORMATION: Lowercase letters indicate possibly advantageous
OTHER INFORMATION: variants (see detailed description)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
CUNTER: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/524,757

FILING DATE: 29-MOV-1994

FILING DATE: 129-MOV-1994

FILING DATE: 30-MOV-1994

FILING DATE: 30-MOV-1993

ATFORNEY/AGENT INFORMATION:

NAME: Harre, John A. A. STELEPHOME: (214) 339-4600

TELEPHOME: (214) 339-4600

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 29-mino acids

mund: amino acids
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TYPE: PRT
ORGANISM: Influenza A virus
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18 ALELLMA 24
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; Sequence 22, Application US/08152721B
; Patent No. 596215
; GENERAL INFORMATION:
    APPLICANT: Livingston, David M.
    APPLICANT: Livingston, David M.
    APPLICANT: Ewen, Wark E.
    TITLE OF INVENTION: Related Polypeptides
    TITLE OF INVENTION: Related Polypeptides
    NUMBER OF SECHENCES: 31
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: CHOATE, HALL & STEWART
    STREET: 53 State Street
    CITY: Boston
US-08-725-459B-76
US-08-725-459B-76
US-08-725-459B-76
US-08-725-459B-76
US-08-725-459B-76
US-08-725-459B-76
US-08-725-459B-76
US-08-725-459B-76
US-08-725-72-72
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OTHER INFORMATION: /note= "amino acids 61-112 of
OTHER INFORMATION: Blongin C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.0%; Score 22; DB 3;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1
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GENERAL INTECTATION: DETECTOR Et al.
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLBIC ACID AND THERAPEUTICS
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT FILING DATE: 1999-06-04
CURRENT PELICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5729
LENGTH: 63
TYPE: PRT
CRENT SHIPS: PRT
CREATION: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5689055
; GENERAL INPORMATION:
MAPPLICANT: Mayerowitz, Elliott M.
APPLICANT: Chang, Caren
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
TITLE OF INVENTION: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 3400 Embarcadero Center, Suite 3400
CUTY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                Score 22; DB 3; Length 56;
Pred. No. 2.5e+02;
1; Mismatches 1; Indels
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Elongin C"
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66.7%; Pred. No. 2.8e+02;
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; Sequence 5729, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 39
US-08-530-010-18
; Sequence 18, Application US/08530010
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: Patentin Release #1
                                                                                                             STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                 TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                           56 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                        LOCATION: 1.56
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                     NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                   || :|||
44 ALELLMA 50
                                                                                             TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                              1 ALNVLMA 7
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Matches 4; Conserv
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46 LNLIMA 51
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                                                                           LENGTH:
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Pred. No. 2.4e+02;
1; Mismatches 1; Indels
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Sequence 50, Application US/08725459B
Patent No. 6084068
GENERAL INFORMATION:
APPLICANT: CONAWAY, RONALD C.
APPLICANT: CONAWAY, JOAN W.
TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS; NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,721B
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         NAME: Pasternack Esq., Sam
REGISTRATION NUMBER: 29,576
REPERENCE/DOCKET NUMBER: 181411-011DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SIDLEY & AUSTIN
STREET: 717 N. HARWOOD, SUITE 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: HANSEN, EUGENIA S.
REGISTRATION NUMBER: 31,966
REFRENCE/DOCKET NUMBER: 1114
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 71.0%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; IMMEDIATE SOURCE:
; CLONE: RB region 3
US-08-152-721B-22
STATE: PL.
COUNTRY: USA
... 02109-2891
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || |:||
46 ALEVVMA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALIVVLMA 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 717 R
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; Sequence 18, Application US/08714524D
; Patent No. 6294716
; GENERAL INFORMATION:
; APPLICANT: Meyerowitz, Elliott M
; APPLICANT: Chang, Caren
; APPLICANT: Bleecker, Anthony B
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
; FILE REPRENCE: a-57515-4
; CURRENT APPLICATION NUMBER: US/08/714,524D
; CURRENT PLING DATE: 1996-09-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
: LENGTH: 67
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US-08-725-459B-49
Sequence 49, Application US/08725459B
; Patent No. 6084068
; GENERAL INFORMATION:
; APPLICANT: CONAMAY, RONALD C.
APPLICANT: CONAMAY, JOAN W.
; TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SIDLEY & AUSTIN
STREET: 717 N. HARWOOD, SUITE 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h Similarity 100.0%; Pred. No. 3e+02; 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                   Length 67;
                                                                                                                                                                                                                                  0; Indels
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APPLICATION NUMBER: US/08/725,459B FILING DATE: 04-OCT-1996
                                                                                                                                                                                      Score 22; DB 2;
; Pred. No. 3e+02;
                                                                                                                                                                         71.0%; Scor.
100.0%; Pred. No. scor.
0; Mismatches
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STATE: TX
COUNTRY: US
ZIP: 75201-6507
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04-OCT-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HANSEN, EUGENIA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Escherichia coli
US-08-714-524D-18
                           67 amino acids
                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 5; Conservative
SEQUENCE CHARACTERISTICS
                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
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US-08-714-524D-18
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US-08-484-101B-18
; Sequence 18, Application US/08484101B
; Sequence 18, Application US/08484101B
; Patent No. 5824868
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO TITLE OF INVENTION: ETHYLENE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS: 5
; STREET: 3400 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; CITY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.0%; Score 22; DB 1; Length 67; 100.0%; Pred. No. 38+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: C-LOSYMS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,101B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US94/
FILING DATE: 01-JUL-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/086,555
FILING DATE: 01-JUL-1994
CLASSIFICATION NUMBER: US 08/086,555
FILING DATE: 01-JUL-1993
CLASSIFICATION NUMBER: 31,801
REFERENCE/POCKET NUMBER: A-57515-2/RFT
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 398-3249
INFORMATION FOR SEQ ID NO: 18:
                                                                    FILING UNIE:

PRIOR APPLICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,555
FILING DATE: 01-JUL-1993
ATTORNEY AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57515/RFT
TELEPONE (15) 781-1989
TELEPONE (415) 398-3249
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE (415) 398-3249
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE (415) 398-3249
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,010
FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.
Matches 5; Conservative
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MOLECULE TYPE: peptide
US-08-530-010-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 ALNVL 40
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Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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Matches 5; Conservative
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82 ALELLMA 88
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78 ALELLMA 84
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US-08-725-459B-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-725-459B-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.0%; Score 22; DB 3; Length 84; Best Local Similarity 71.4%; Pred. No. 3.8e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: CONAWAY, RONALD C.
APPLICANT: CONAWAY, JOAN W.
TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUMTRY: US

ZIP: 75.01-65.07

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,459B
FILING DATE: US-04-0CT-1996
CLASSIFICATION: 530
ATYORNEY/AGENT INPORMATION:
NAME: HANSEN, EUGENIA S.
REGISTRATION NUMBER: 31,966
REFERENCE/POCKET NUMBER: 31,966
REFERENCE/POCKET NUMBER: 11146/07501
TELEPHONE: 214-981.3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "amino acids 29-112 of
Elongin C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "amino acids 23-112 of
Elongin C"
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 11146/07501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SIDLEY & AUSTIN
STREET: 717 N. HARWOOD, SUITE 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 43
US-08-725-459B-48
; Sequence 48, Application US/08725459B
; Patent No. 6084068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: 214-981-3400
INPORMATION FOR SEQ ID NO: 48: SEQUENCE CHARACTERISTICS: LENGTH: 90 amino acids TYPE: amino acid STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                         TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO: 49
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS: not relevan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAME/KEY: Peptide
LICCATION: 1..90
CHER INFORMATION: /
CTHER INFORMATION: BOTHER INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: Peptide
; LOCATION: 1..84
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-725-459B-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :|||
72 ALELLMA 78
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Devery Match

Outery Match

Outery Match

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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 Gaps
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 Query Match
Pest Local Similarity 71.4%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
NUMBER OF SEQUENCES: 79

CORRESPONDENCE ADDRESS:
ADDRESSEE: SIDLEY & AUSTIN
STREET: 717 N. HARWOOD, SUITE 3400
CITY: DALLAS
CITY: DALLAS
STATE: TX
COUNTRY: US
ZIDPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,459B
FILING DATE: 04-OCT-1996
CLASSIFICATION : 31,966
REFERENCE/DOCKET INFORMATION:
NAME: HANSEN, EUGENIA S.
RECIETRATION NUMBER: 31,966
REFERENCE/DOCKET INFORMATION:
TELEPHONE: 214-981-3300
TELEPHONE: 214-981-3400
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
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TYPE: amino acids
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TYPE: amino acids
TYPE: applicative TYPE: applicative TYPE: amino acids
 FEATURE:

NAME/KEY: Peptide

LOCATION: 1..98

OTHER INFORMATION: /note= "amino acids 15-112 of orner information: blongin C"

US-08-725-459B-46
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Search completed: February 17, 2004, 10:59:42 Job time : 6.05941 Bec8

1 ALNVLMA 7 || :||| 86 ALELLMA 92

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us-09-900-147-7.rspt

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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February 17, 2004, 10:50:12; Search time 9.91089 Seconds (without alignments) 182.261 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-900-147-7 31 1 ALNVLMA 7 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

830525 seqs, 258052604 residues Searched:

146963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 23:\* Database :

1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\*
7: sp\_mhc:\*
8: sp\_orden:\*
11: sp\_ordent:\*
11: sp\_vortebrate:\*
12: sp\_virus:\*
13: sp\_virus:\*
14: sp\_unclassified:\*
15: sp\_arcteriap:\*
16: sp\_bacteriap:\*
17: sp\_archeap:\*
16: sp\_bacteriap:\*
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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 $\frac{1}{2} \int_{\mathbb{R}^{n}} dx = \frac{1}{2} \int_{\mathbb{R}^{n}} dx = \frac{1}{2}$ 

## SUMMARIES

|               |       | ф              |                          |    |        |                    |
|---------------|-------|----------------|--------------------------|----|--------|--------------------|
| Result<br>No. | Score | Query<br>Match | Query<br>Match Length DB | DB | ID     | Description        |
|               | 25    | 80.6           | 53                       | 16 | 09KCV9 | O9kcv9 bacillus ha |
| 7             | 24    | 77.4           | 50                       | 7  | 051684 | O51684 paracoccus  |
| ٣             | 24    | 77.4           | 56                       | Ŋ  | 09UAC6 | Oguace mesobuthus  |
| 4             | 24    | 77.4           | 64                       | 16 | OBNOT3 | Ognat3 corynebacte |
| Ŋ             | 24    | 77.4           | 74                       | 10 | O9ZRT2 | 09zrt2 triticum ae |
| 9             | 24    | 77.4           | 98                       | œ  | 021582 | O21582 scotinomys  |
| 7             | 23    | 74.2           | 51                       | 16 | 092XA1 | O92xal rhizobium m |
| 80            | 23    | 74.2           | 59                       | Ŋ  | O9W5W3 | O9w5w3 drosophila  |
| σ             | 23    | 74.2           | 74                       | 17 |        | O9hhq1 halobacteri |
| 10            | 23    | 74.2           | 16                       | 11 |        | O70322 mus musculu |
| 11            | 23    | 74.2           | 81                       | 16 |        | 09cnl3 pasteurella |
| 12            | 23    | 74.2           | 90                       | 7  |        | P72475 streptococc |
| 13            | 23    | 74.2           | 95                       | 16 | QBKCM5 | Q8kcm5 chlorobium  |
| 14            | 23    | 74.2           | 98                       | æ  | Q9MES8 | O9mes8 physeter ca |
| 15            | 23    | 74.2           | 98                       | œ  | Q8W9B6 | Q8w9b6 vombatus ur |
| 16            | 23    | 74.2           | 98                       | œ  | 021588 | 021588 ochrotomva  |

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Query Match 80.6%; Score 25; DB 16; Length 53; Best Local Similarity 85.7%; Pred. No. 1.3e+02; Matches 6; Conservative 0; Mismatches 1; Indels

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| 021593 reithrodont 021541 bolomys lac 02bm46 euperipatoi 02bm45 euperipatoi 02bm45 euperipatoi 02bm47 streptococc 02mch4 streptococc 025616 proteus vul 032618 rickettsia 038984 arabidopsis 096bx7 homo sanien | Q8dv25 streptococc Q8zf6 yershia pe Q9yi43 gallus gall Q8yp72 anabaena sp Q8rzpl oryza sativ Q84212 human papil Q92A41 morganella Q92A61 paramecium Q98461 paramecium Q92693 rickettsia Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9588 peromyscus Q9589 peromyscus Q9590 satisticalia | ENTS       | ; 53 AA.<br>ed)<br>sequence update)                         | annotation update)<br>Bacillaceae, Bacillus.                                                                                   | N.A. JCM 9153; 82; PubMed=11058132; 820r K., Takaki Y., Maeno G., Sasaki R., Masui N., a C., Takaki Y., Ogasawara N., Kuhara S., me sequence of the alkaliphilic bacterium Bacillus genomic sequence comparison with Bacillus subtilis."; Res. 28:4317,4331(2000). ** BABO5179-1; rotein; Complete proteome. AA; 5537 WW; 2F97204707F6EE46 CRC64;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
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| 021593<br>021541<br>0298846<br>0998845<br>086887<br>08P015<br>09P015<br>092628<br>038984<br>038984                                                                                                              | Q8DV25<br>Q8ZF66<br>Q8ZF66<br>Q8XF143<br>Q8RZF1<br>Q8RZF1<br>Q9ZH4112<br>Q9SZF83<br>Q9SZF83<br>Q9SZF83<br>Q8GZC8<br>Q8GZC8<br>Q8KYQ9<br>Q8JFQ9<br>Q93FQ9                                                                                                                                                                                                                                                                                                                                                                                                                        | ALIGNMENTS |                                                             | Last anno<br>ales; Bac                                                                                                         | 73;<br>fed=11058132;<br>Adamura Y., Maen<br>akamura Y., Ogasaw<br>nnce of the alkali;<br>sequence compari;<br>54317-4331(2000).<br>Complete proteome<br>37 Mw; 2F97204707.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
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|                                                                                                                                                                                                                 | 22222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |            | T 1<br>9<br>09KCV9<br>09KCV9;<br>01-0CT-2000<br>01-0CT-2000 | 01-WAR-2002 (TrEMBLre<br>Hypothetical protein<br>BH1460.<br>Bacillus halodurans.<br>Bacteria; Firmicutes;<br>NCBI_TaxID=86665; | UENCE FI<br>LINE=201<br>ami H.,<br>i F., H.<br>i F., H.<br>incomplete<br>odurans<br>leic Ac.<br>L, APOO.<br>Othetic                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 114<br>118<br>119<br>119<br>129<br>129<br>129<br>129<br>129                                                                                                                                                     | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |            | SUL                                                         |                                                                                                                                | REAL SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF S |

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 1 ALNVLM 6
 NCBI_TaxID=4565;
 Nakagawa S.;
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 01-MiY-2000 (TrEMBLrel. 13, Created)
01-MiY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Bmp-03 neurotoxin precursor.
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Bukaryota, Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
NCBL_TaxID=34649;
 Paracoccus denitrificans.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.
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 Score 24; DB 5; Length 56;
Pred. No. 2.4e+02;
1; Mismatches 1; Indels
 77.4%; Score 24; DB 2; Length 50; 71.4%; Pred. No. 2.2e+02; ive 1; Mismatches 1; Indels
 SEQUENCE FROM N.A.
Wu J.J., Dai L., Chi C.W.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF0730631; AAD473777.1; -.
HSSP; Q9NJP7; IDU9.
 4BB7C73200798CDF CRC64;
 CONTY.

01-OCT-2002 (TrEMBLrel. 22, Created)

01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

Hypothetical protein Cgl1341.
 Last sequence update)
Last annotation update)
 POTENTIAL.
BMP-03 NEUROTOXIN.
 56 AA
 Created)
 PRT;
 Query Match 77.4%;
Best Local Similarity 71.4%;
Matches 5; Conservative
 SEQUENCE 56 AA; 5940 MW;
 01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
 Best Local Similarity 71.4
Matches 5; Conservative
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13 AMNVTMA 19
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23 AVNVFMA 29
 1 ALNVILMA 7
 1 ALNVLMA 7
 Neurotoxin; Signal
 SEQUENCE FROM N.A.
 NCBI_TaxID=266;
 CcoH (Fragment)
 STRAIN=Pd1222;
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 "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005278; BAB98734.1;
Hypothetical protein; Complete protecome.
SEQUENCE 64 AA; 7524 MW; 2B9CBEBC70EA2897 CRC64;
 "Chromosomal location and genetic mapping of the mismatch repair gene homologs MSH2, MSH3 and MSH6 in rye and wheat."; Genome 42:1255-1257(1999).

EMBL; AJ131671; CAA10479.1; -.

InterPro; IRRO00432; Muts.C.

Prom; PRO0488; Muts.C; 1.

Probom; PR001263; Muts.C; 1.

SMART; SM00534; MUTSac; 1.
 Korzun V., Boerner A., Siebert R., Malyshev S., Hilpert M., Kunze R.,
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
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Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
 Score 24; DB 10; Length 74;
Pred. No. 3.2e+02;
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 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADH dehydrogenase subunit 4L.
 Last sequence update)
Last annotation update)
 77.4%; Score 24; DB 16;
83.3%; Pred. No. 2.8e+02;
iive 1; Mismatches 0;
 98 A.A.
 74 AA
 SEQUENCE FROM N.A.
STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
 Created)
 PRT;
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 77.4%;
 01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (TrEMBLrel. 19,
 STRAIN=cv. Chinese Spring;
PubMed=10659795;
 Conservative
 PRELIMINARY;
 5; Conservative
 PRELIMINARY;
 MSH2 protein (Fragment). MSH2.
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RA MAGININE-ZUISBOUGE, PUNDEGE-1073132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Gucrog R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Batland R.C., Bazeri E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Dril J.P., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,

RA Beson K.Y., Basu A., Baxendals J., Bayraktaroglu L., Beasley E.M.,

RA Berry J.M., Cawley S., Dallke C., Davengoll L., Boasley E.M.,

RA Berry J.M., Cawley S., Dallke C., Davengort L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleiter B., Durbin K.J., Boulder A., Deng Z., Mays A.D., Dav I. D., Dun P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleiter M.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

Jalai M., Kalush F., Karpen G.H., Ke Z., Kunp D., Lai Z.,

Liuk X., Mattei B., McIntosh T.C., McLeod M.P., Morberson D.,

RA Harris N.L., Levitsky A.A., Li J. J., Li S., Liang Y., Lin X.,

RA Merkluov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Barzolo M., Pittman G.S., Pan S., Pollard J., Mosleon D.L.,

RA Reinert K., Remington K., Sunders R.D., Vang S., Yang D.,

RA Reinert K., Remington K., Sunders R.D., Vang S., Yang S.,

RA Barzolo M., Pittman G.S., Pan S., Pollard J., Wang S., Yang S.,

RA Barnert K., Remington K., Saunders R.D., Vang S., Yang S.,

RA Harris S.M., Woodage T., Worley K.C., Wu D., Yang S., Yang R.,

RA Harris S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho G.A.,

RA Zheng X.H., Zhong F.N., Zhong M., Zhong S., Zhu S., Smith H.O.,

Ra Zheng X.H., Zhong F.N., Zhong W., Zhong S., Zhu S., Smith H.,

Ra Cherce S.B7:2185-2195 (2000)
 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Psphydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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Pred. No. 4.5e+02;
0; Mismatches 1; Indels
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Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 74 AA.
 Created)
 MEDLINE=20196006; PubMed=10731132;
 FlyBase; FBgn0040055; CG14474.
SEQUENCE 59 AA; 6824 MW: 3
 Science 287:2185-2195(2000).
EMBL; AE002612; AAF45482.1; -
 74.2%;
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Best Local Similarity 83.3
Matches 5; Conservative
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 CG14474 protein.
 01-MAR-2001
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 SEQUENCE
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MEDLINE=21396508; PubMed=11481431;
MEDLINE=21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
Golding B., Puehler A.;
"The complete sequence of the 1,683-kb psymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium mellioti.";
Proc. Natl. Acad. Sci. US.A. 98:9889-9894 (2001).
EMBL, ALGO3642; CAC48461.1; -.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 51 AA; 5923 MW; OCC8242997150D7B CRC64;
 Gaps
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 SEQUENCE FROM N.A.
MEDLINE=98152303; PubMed=9491603;
Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
"Molecular systematics and paleobiogeography of the South American
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 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
 74.2%; Score 23; DB 16; Length 51; 71.4%; Pred. No. 4e+02;
 Length 98;
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 98 AA; 10742 MW; F297223A06492F8A CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RB0061.
 Score 24; DB 8; I
Pred. No. 4.1e+02;
 RB0061 OR SMB20061.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
 59 AA.
 51 AA
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 1; Mismatches
 Scotinomys teguina (Alston's brown mouse).
 01-MAY-2000 (TrEMBLrel. 13, Created)
 PRT;
 Mol. Biol. Evol. 15:35-49(1998).
EMBL; UB3828; AB487245.1; -.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
 sigmodontine rodents.";
Mol. Biol. Evol. 15:35-49(1998).
 Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1.
 77.48;
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Best Local Similarity 71.*
5. Conservative
 Local Similarity 66.7 nes 4; Conservative
 PRELIMINARY;
 PRELIMINARY;
 33 ALNLLFA 39
 1 ALNVLMA 7
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6 MNILMA 11
 SEQUENCE FROM N.A.
 2 LNVLMA 7
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 NCBI_TaxID=382;
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 Mitochondrion
 Scotinomys
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 Q9W5W3
 092XA1
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RESULT 7
092XA1
10 092XA1
AC 092XA1
DT 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-

RESULT 8 09W5W3 ID 05 AC 05 DT 01

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Matches

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Gaps

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Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
 Query Match
Best Local Similarity 71...
S; Conservative
 Ouery Match
Best Local Similarity 57.1.
A; Conservative
 PRELIMINARY;
 PRELIMINARY;
 ||::|||
67 ALSLLMA 73
 1 ALNVLMA 7
 31 AINLLMS 37
 [1]
SEQUENCE FROM N.A.
 1 ALNVLMA 7
 SEQUENCE FROM N.A.
 Streptococcus.
NCBI_TaxID=1309;
 Fragment) .
 QBKCM5
 P72475
P72475;
 RESULT 13
 RESULT 12
 P72475
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SEQUENCE FROM N.A.

MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMedline N., Sprogna J.,

Swartzell S., Weiler K., Cruz R., Danson W.J., Hough D.W.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Meddocks D.G., Jablonski P.E., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freites T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

"Genome sequence of Halobacterium species NRC-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 Gaps
 Gaps
 Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
 ö
 Pasteurella multocida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 ö
 74.2%; Score 23; DB 11; Length 76; 83.3%; Pred. No. 5.8e+02; tive 1; Mismatches 0; Indels
 74.2%; Score 23; DB 17; Length 74; 83.3%; Pred. No. 5.6e+02; ive 1; Mismatches 0; Indels
 Stuart R.O., Pavlova A., Nigam S.K.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF045562; AAC05261.1; --
MGD; MGI:1921354; Abcb6.
 Halobacterium sp. (strain NRC-1).
Plasmid pNRC200.
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriacee; Halobacterium.
 76 AA; 8600 MW; 7D614DBE4333E26A CRC64;
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PMPOthetical protein PM0415.
 Complete proteome. 74 AA; 8286 MW; 5D045F8E606B6FC5 CRC64;
 01.5UG-1998 (TrEMBLrel. 07, Created)
01.5UG-1998 (TrEMBLrel. 07, Last sequence update)
01.0CT-2002 (TIEMBLrel. 22, Last annotation update)
 81 AA.
 76 AA.
 PRT;
 PRT;
 ABC transporter (Fragment)
ABCB6 OR 1200005B17RIK.
 Query Match
Best Local Similarity 83.3.
From Si Conservative
 Local Similarity 83.3
 PRELIMINARY;
 PRELIMINARY;
 |||||:
6 ALNVLV 11
 ||||:|
47 LNVLVA 52
 1 ALNVLM 6
 SEQUENCE FROM N.A.
 2 LINVLIMA 7
 NCBI_TaxID=10090;
 NCBI_TaxID=64091;
 SEQUENCE
 Query Match
 Plasmid;
SEQUENCE
 070322;
 070322
 RESULT 11
 RESULT 10
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 Gaps
STRAIN=Pm70;

MEDLINE=21145866; PubMed=11248100;

MAY B.J., Zhang C., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

MAY B.J., Zhang C., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

MCOmplete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL, AE006077; AACX2499.1; --

EMBL, AE006077; ACCADIACE proteome.

SEQUENCE 81 AA; 9432 MW; 0FB82498E5351973 CRC64;
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 PSEQUENCE FROM N.A.

C STRAIN-GS-5 Kuramiteu;

A Peruzzi F., Piggot P.J., Daneo-Moore L.;

E Manited (OCT-1996) to the EMBL/GenBank/DDBJ databases.

L Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

R InterProj IPRO339; ABC_transporter.

R ProDom; PD000006; ABC_transporter.

R PROSTIE; PS00211; ABC_TRANSPORTER; 1.

R PROSTIE; PS00211; ABC_TRANSPORTER; 1.

I NON TER 90 90

SEQÜENCE 90 AA; 9857 MW; 3F92DE952FE38647 CRC64;
 Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
Chlorobium.
NCBI_TaxID=1097;
 74.2%; Score 23; DB 16; Length 81; 57.1%; Pred. No. 6.1e+02; tive 3; Mismatches 0; Indels
 Score 23; DB 2; Length 90;
Pred. No. 6.8e+02;
2; Mismatches 0; Indels
 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
High affinity branched chain amino acid transport protein
 Streptococcus mutans.
Bacteria, Firmicutes; Lactobacillales, Streptococcaceae,
 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein CT1389.
 95 AA.
 PRT;
 74.28;
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MEDLINE-21592585; PubMed=11734900;
Janke A., Magnell O., Wieczorek G., Westerman M., Arnason U.;
"Phylogenetric analysis of 188 rRNA and the mitochondrial genomes of
the wombat, Vombatus ursinus, and the spiny anteater, Tachyglossus
aculeatus: Increased Support for the Marsupionta Hypothesis.";
J. Mol. Evol. 54.71-80(2002).
EMBL, AJ34826; CAC83113.1; --
InterPro; IPR001133; Oxidared 4L.
InterPro; IPR001214; Oxidared4L.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 [1] SEQUENCE FROM N.A. MEDINES-9491603; MEDINES-9415133; PubMed-9491603; Engel S.R.; Hogan K.M., Taylor J.F., Davis S.K.; Molecular systematics and paleobiogeography of the South American
 Mitochondrion.
Sukaryota Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Vombatidae, Vombatus.
NCBI_TaxID=29139;
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 ;
 Length 98;
 Length 98;
 0; Indels
 0; Indels
 Ochrotomys nuttali (Golden mouse) (Peromyscus nuttali)
 98 AA; 10655 MW; E15DFB15EC4219CA CRC64;
 98 AA; 10728 MW; DAE4B4DE0EEA713C CRC64;
 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 Score 23; DB 8; 1
Pred. No. 7.3e+02;
2; Mismatches 0;
 74.2%; Score 23; DB 8; I 57.1%; Pred. No. 7.3e+02;
 98 AA.
 98 AA
 3; Mismatches
 PRT;
 PRT;
 Mol. Biol. Evol. 15:35-49(1998).
EMBL; UB3830; AAB87209.1; -.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
 ursinus (Common wombat).
 Pfam; PF00420; oxidored q2; 1.
ProDom; PD000359; Oxidred4L; 1.
 Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1.
 NADH dehydrogenase subunit 4L.
 74.28;
 Query Match
Best Local Similarity 57.1.
 4; Conservative
 PRELIMINARY;
 PRELIMINARY;
 sigmodontine rodents.";
 :||::||
5 SLNLIMA 11
 1 ALNVLMA 7
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=56229;
 2 LINVLIMA 7
 Mitochondrion
 Ochrotomys.
 SEQUENCE
 SEQUENCE
 021593
 021588
 021588
 RESULT 17
021593
ID 021593
 Matches
 RESULT 16
 021588
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STRAIN=TLS / ATCC 49652 / DSM 12025;

MEDLINE=22103685; PubMed=12093901;

A Eisen J.A., Nealson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

A Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

Vamathevan J.C., Tettelin H., Bryant D.A., Fraser C.M.;

The complete genome sequence of Chlorobium tepidum TLS, a

photosynthetic, anaerobic, green-sulfur bacterium.";

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
 Gaps
 Gaps
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Cetacea, Odontoceti,
Physeteridae, Physeter.
 MEDLINE=20296818; PubMed=10835487;
Arnason U., Gullberg A., Gretarsdottir S., Ursing B., Janke A.;
The mitochondrial genome of the sperm whale and a new molecula,
reference for estimating eutherian divergence dates.";
J. Mol. Evol. 50:569-578 (2000).
EMBL, AJ277029; CAB98278.1;
InterPro; IPR001131; Oxidored 41.
 ö
 74.2%; Score 23; DB 16; Length 95; 66.7%; Pred. No. 7.1e+02; ive 2; Mismatches 0; Indels
 74.2%; Score 23; DB 8; Length 98; 66.7%; Pred. No. 7.3e+02; tive 2; Mismatches 0; Indels
 Physeter catodon (Sperm whale) (Physeter macrocephalus).
 Hypothetical protein; Complete proteome.
SEQUENCE 95 AA; 10702 MW; 529E865CCEB2816F CRC64;
 98 AA; 10767 MW; B2EB09927D25AD1B CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 QBW9B6;
1-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADH dehydrogenase subunit 4L.
 98 AA.
 98 AA
 PRT;
 NADH dehydrogenase subunit 4L. NADH4L.
 Pfam; PF00420; oxidored q2; 1.
ProDom; PD000359; Oxidred4L; 1
 Best Local Similarity 66.7
Matches 4; Conservative
 Best Local Similarity 66. Matches 4; Conservative
 PRELIMINARY;
 PRELIMINARY;
 |||:|:
50 ALNILL 55
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MINVMMA 11
 SEQUENCE FROM N.A.
 1 ALNVLM 6
 2 LINVLIMA 7
 NCBI_TaxID=9755;
 TIGR; CT1389; -
 Mitochondrion.
 Mitochondrion
 SEQUENCE
 Query Match
 Query Match
 O9MES8
 986M80
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RESULT 14 Q9MES8

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Gaps

RESULT 15 Q8W9B6 ID Q8W9B AC Q6W9B DT 01-MAI DT 01-MAI DT 01-MAI

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Gaps

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PRT;
 71.0%;
80.0%;
 Query Match
Best Local Similarity 80.v.
 4; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Query Match
Best Local Similarity
Matches 4; Conserv
 SEQUENCE FROM N.A.
 9 NILMA 13
 NCBI_TaxID=49087;
 3 NVLMA 7
 9 NILMA 13
 3 NVLMA 7
 Q9BM46;
 Q9BM45
 Q9BM46
 RESULT 20
 RESULT 19
Q9BM46
 29BM45
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 Gaps
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 Mitocĥondrion.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
 ADDIANCE STORM N. Taylor J.F., Davis S.K.;

Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;

Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;

Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;

Engel S.R., Hogan K.M., Taylor J.F.,

Molecular systematics and paleobiogeography of the South American sigmodontine rodents.";

Mol. Biol. Evol. 15:35-49(1998).

Engel: Bayll; Abs87158.1;

InterPro; IPR00113; Oxidored 4L.

InterPro; IPR001214; Oxidored 4L.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae; Reithrodontomys.
 MEDLINE-98152303; PubMed-9491603;
Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
"Molecular systematics and paleobiogeography of the South American
 ;
0
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0
 74.2%; Score 23; DB 8; Length 98; 66.7%; Pred. No. 7.3e+02; rative 2; Mismatches 0; Indels
 y Match
Local Similarity 66.7%; Pred. No. 7.3e+02;
hes 4; Conservative 2; Mismatches 0; Indels
 98 AA; 10785 MW; BD00880FEE64CDF4 CRC64;
 98 AA; 10774 MW; 653067658DDB77EC CRC64;
 01-JTN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JAN-1998 (TrEMBLrel. 21, Last annotation update) NADH dehydrogenase subunit 41.
 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 Reithrodontomys fulvescens (Fulvous harvest mouse)
 Bolomys lactens (rufous-bellied bolo mouse).
 98 AA.
 aigmodontine rodents";
Mol. Biol. EVOl. 15:35-49(1998).
EMBL; U83832; AAB87233.1; -.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR00214; Oxidored 4L.
Pfam; PP00420; oxidored q2; 1.
ProDom; PD000359; Oxidored q2; 1.
 PRT;
 Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1.
 NADH dehydrogenase subunit 4L.
 Query Match
Best Local Similarity 66.77
 PRELIMINARY;
 ||:|:|
6 LNILLA 11
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 2 LINVLIMA 7
 NCBI_TaxID=56217;
 Mitochondrion
 SEQUENCE
 SEQUENCE
 Query Match
 Matches
 RESULT 18
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||:|:| LNILLA 11

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2 LINVLMA 7

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 Gaps
 Euperipatoides rowelli.
Eukaryota, Metazoa, Onychophora, Peripatopsidae, Euperipatoides.
 LINE-like reverse transcriptase (Fragment).

Euperipatoides rowelli.

Eukaryota; Metazoa; Onychophora; Peripatopsidae; Euperipatoldes.

NCBI_TaxID=49087;
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 TRANSPOSON-LRT-L3 retrotransposon;
MEDLINE-20570504; PubMed=11121049;
Arkhipova I., Meselson M.;
"Transposable elements in sexual and ancient asexual taxa.";
"Transposable elements in sexual and ancient asexual taxa.";
"Transposable elements in sexual and ancient asexual taxa.";
EMBL; AX013950; AAG59933.1; -.
RNA-directed DNA polymerase.

NON TER 1 1 1
NON TER 25 25
SEQÜENCE 25 AA; 2757 WW; ED30E0AD8052B998 CRC64;
 TEQUENCE FROM N.A.
TRANSPOSONELETT-12 retrotransposon;
MEDLINE-20570504; Pubwed=11121049;
Arkhipova 1., Meselson M.;
Transposable elemente in sexual and ancient asexual taxa.";
Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477 (2000).
ENBL; AV013949; AAG59912.1;
FNA-directed DNA polymerase.
 71.0%; Score 22; DB 5; Length 25; 80.0%; Pred. No. 3.6e+02; tive 1; Mismatches 0; Indels
 Score 22; DB 5; Length 25;
Pred. No. 3.6e+02;
1; Mismatches 0; Indels
 NON TER 1 1
NON TER 25 25
SEQUENCE 25 AA; 2809 MW; 5BBAE0AEE0458F32 CRC64;
 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) LINE-like reverse transcriptase (Fragment).
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 32 AA.
 25 AA.
 Q8GPX7 PRELIMINARY; PRT;
Q8GPX7;
01-MAR-2003 (TrEMBLrel, 23, Created)
 PRT;
 RESULT 21
Q8GPX7
ID Q8GPX
AC Q8GPX
DT 01-MA
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Gaps

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MEDLINE=99412383; PubMed=10482618;
Lucchini S., Desiere F., Brussow H.;
"Comparative genomics of Streptococcus thermophilus phage species
 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Proteus.
 Streptococcus thermophilus bacteriophage SFil8.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 Koronakis V., Hughes C.; "Identification of the promotors directing in vivo expression of hemolysin genes in Proteus vulgaris and Escherichia coli."; Mol. Gen. Genet. 213:99-104 (1988).

EMBL, X12571; CAA31083.1; -...
 Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
 Score 22; DB 2; Length 54;
Pred. No. 7.4e+02;
1; Mismatches 1; Indels
 Length 47;
 1; Indels
 supports a modular evolution theory.";
J. Virol. 73:8647-865(1999).
BEMBL, AB5601; AP63076.1;
SEQUENCE 47 AA; 5650 MW; 0A50F8A33EB231C6 CRC64;
 54 AA; 6205 MW; 7C9E7EF903D954AA CRC64;
 Last sequence update)
Last annotation update)
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Similarity to proline/betaine transporter.
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 Score 22; DB 9; Pred. No. 6.5e+02;
 55 AA.
 54 AA
 1; Mismatches
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
HlyC gene 5' region (Fragment).
 SEQUENCE FROM N.A. MEDLINE-89127151; Pubmed=3065612;
 71.0%;
71.4%;
 h 71.0%;
Similarity 71.4%;
5; Conservative
 Query Match
Best Local Similarity 71.*.
S. Conservative
 PRELIMINARY;
 PRELIMINARY;
 Pfam; PF02794; HlyC; 1.
 |:||| |
28 AVNVLSA 34
 AINVLPA 39
 Rickettsia conorii.
 7
 Best Local Similarity
Matches 5; Conser
 1 ALNVLMA 7
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=74382;
 1 ALNVLMA
 Proteus vulgaris
 NCBI_TaxID=585;
 SEQUENCE
 33
 Query Match
 NON TER
 052616
 Q92G28
 092G28
 RC1297
 RESULT 25
Q92G28
 RESULT 24
 052616
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 STRAIN-SG17M;
MEDLINE-22313472; PubMed=12426355;
MEDLINE-22313472; PubMed=12426355;
Larbig K.D., Christmann A., Johann A., Klockgether J., Hartsch T.,
Merkl R., Wiehlmann L., Fritz H.J., Tummler B.;
"Gene Islands Integrated into tRNA(Gly) Genes Confer Genome Diversity
 Gaps
 Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.; "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks."
 Gaps
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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 71.0%; Score 22; DB 16; Length 42; 83.3%; Pred. No: 5.9e+02; ive 1; Mismatches 0; Indels
 71.0%; Score 22; DB 2; Length 32; 100.0%; Pred. No. 4.5e+02;
 0; Indels
 Strept_coccus pyogenes (serotype M18).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
 Hypothetical protein.
SEQUENCE 32 AA; 3435 MW; 6281AD17052C2682 CRC64;
 Hypothetical protein, Complete proteome.
SEQUENCE 42 AA; 4452 MW; 48CD6FEB4B0CD799 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein.
 01-0CT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein spyM18_1343.
 Last sequence update)
 Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002)
EMBL; AE010055; AAL97944.1; -.
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 100.0%; Pred. ...
 42 AA
 on a Pseudomonas aeruginosa Clone.";
J. Bacteriol. 184:6665-6680(2002).
EMBL; AF440524; AAN62247.1; -.
 Created)
 PRT;
 STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
 Best Local Similarity 100.
Matches 5; Conservative
 Local Similarity 83.3
1es 5; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Pseudomonas aeruginosa.
 ||:|||
ALSVLM 42
 Streptococcus.
NCBI_TaxID=186103;
 SEQUENCE FROM N.A.
 9
 26 ALNVL 30
 SEQUENCE FROM N.A.
 1 ALNVL 5
 ALNVLM
 NCBI_TaxID=287;
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 Query Match
 Query Match
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Q9MCH4;
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RESULT 23 Q9MCH4 ID Q9MCH AC Q9MCH DT 01-OC

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Gaps

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PERCUENCE FROM N.A.

PERCUENCE FROM N.A.

MEDLINE=93096482; PubMed=1281306;

MARCALLE C., Eichmann A.;

"Molecular cloning of a family of protein kinase genes expressed in "Molecular cloning of a family of protein kinase genes expressed in "The avian embryo.";

"Molecular cloning of a family of protein kinase genes expressed in "Molecular cloning of a family of protein kinase."

In the avian embryo.";

"Moncogene 7:2479-2487(1992).

In the repro; IPR00069; Prote kinase.

In the repro; IPR00069; Prote kinase.

Prodom; PR00069; Protein Kinase.

MATP-binding; Transferase.

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SQ SEQÜENCE 57 AA; 6347 MW; 4F96EA9245FEAA86 CRC64;
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 SEQUENCE FROM N.A.
STRAIN=UALS9 / ATCC 700610 / Serotype C;
MEDINE=222595063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
 Score 22; DB 13; Length 57;
Pred. No. 7.8e+02;
1; Mismatches 1; Indel8
 Length 61;
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 1; Indels
 TISSUE-Lung;
Strausberg R.;
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC007928; AAH07928.1; -.
Hypothetical protein.
SEQUENCE 61 AA; 6513 MW; 03E51D2F5484DBAA CRC64;
 Last sequence update)
Last annotation update)
 01-DBC-2001 (TrEMBLrel. 19, Created)
01-DBC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
 Query Match. 71.0%; Score 22; DB 4; I
Best Local Similarity 71.4%; Pred. No. 8.3e+02;
Matches 5; Conservative 1; Mismatches 1;
 64 AA
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
 PRT;
 71.0%;
71.4%;
 PRELIMINARY;
 Conservative
 PRELIMINARY;
 Streptococcus mutans.
 Putative ferredoxin
 29 ALRVLLA 35
 1 ALNVLMA 7
 Best Local Similarity
Matches 5: Conserv
 SEQUENCE FROM N.A.
 1 ALNVLMA 7
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2 ARNVLLA 8
 Streptococcus.
NCBI_TaxID=1309;
 NCBI_TaxID=9606;
 SMU.694C.
 Query Match
 Q8DV25
 Q96HZ7
 RESULT 29
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 Q96HZ7
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 Gallus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae, Arabidopsis.

NCBI_TaxID=3702;
 Gaps
 "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
EMBL; AE008676; AAL03835.1; -
 STRAIN=Malish 7;
BarbinE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 SEQUENCE FROM N.A.
STRAIN=Eil-O; TISSUE=Leaf;
STRAIN=Eil-O; TISSUE=Leaf;
STRAIN=Eil-O; TISSUE=Leaf;
Thuemmler F., Kirchner M., Teuber R., Dittrich P.;
"Differential accumulation of the transcripts of 22 novel protein
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 71.0%; Score 22; DB 10; Length 56; 80.0%; Pred. No. 7.7e+02; tive 1; Mismatches 0; Indels
 Score 22; DB 16; Length 55;
Pred. No. 7.6e+02;
1; Mismatches 1; Indels
 NON TER 1 1 1 SB123279AE5DA111 CRC64; SEQUENCE 56 AA; 5804 MM; 58123279AE5DA111 CRC64;
 Complete proteome.
SEQUENCE 55 AA; 6227 MW; E87478DCDC00174A CRC64;
 Last sequence update)
Last annotation update)
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Protein kinase catalytic domain (Fragment).
 kinase genes in Arabidopsis thaliana."; Plant Mol. Biol. 29:551-565(1995).
EMBL. X86964; CAA60527.1; EINERFO.; IPRO00719; Proc kinase.
Pram; PPO0069; pkinase; 1. Probom; PD000001; Prot kinase; 1. PROSTIP: PSSO011; PROTEIN KINASE DOM; 1. ATP-binding; Kinase; Transferase.
 56 AA
 Created)
 PRT;
 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23,
 71.0%;
71.4%;
 Protein kinase (Fragment).
 4; Conservative
 PRELIMINARY;
 Query Match
Best Local Similarity 71.4
Matches 5; Conservative
 PRELIMINARY;
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ALNVMPA 10
 Query Match
Best Local Similarity
Matches 4; Conserv
 1 ALINVLMA 7
 Gallus.
NCBL_TaxID=9036;
 3 NVLMA 7
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4 NILMA 8
 Raoult D.;
 Q9PSL0
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Q38984

RESULT 26

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Gaps

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RESULT 27 Q9PSL0

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
 MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Kaneko T., Iriguchi M., Ishikwa A., Kawashima K., Kimura T.,
Watanabe A., Iriguchi M., Matsumoto M., Matsumo A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
BMBL; AP003596; BAB76027.1;
"Hypothetical protein: Complete proteome.
SEQUENCE 68 AA; 7648 MW; 8876D5D9FFCC4B14 CRC64;
 SEQUENCE FROM N.A.
TISSUE-Hematopoietic bone marrow;
Koritschoner N., Bartunek P., Knespel S., Zenke M.;
"Assessing the gene expression by domain-directed differential
 Similarity 71.4%; Score 22; DB 13; Length 68; Similarity 71.4%; Pred. No. 9.2e+02; 5; Conservative 1; Mismatches 1; Indels
 71.0%; Score 22; DB 16; Length 68; 71.4%; Pred. No. 9.2e+02; Live 1; Mismatches 1; Indels
 Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
 display.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
 68 AA; 7660 MW; 07C70CFC6EE2DC88 CRC64;
 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein As14328.
01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAX-2003 (TrEMBLrel. 23, Last annotation update)
Tyrosine kinase PDGFR (Fragment).
 68 AA.
 EMBL; AF041797; AAD02125.1; -. HSSP; P11362; 1FGK.
InterPro; IPR000713; Prot_kinase.
Pram; PP00069; Pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Transferase.
 PRT;
 Best Local Similarity 71.4
Matches 5; Conservative
 PRELIMINARY;
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ARNVLLA 13
 || :|||
ALELLMA 51
 Best Local Similarity
Matches 5; Conserv
 1 ALNVILMA 7
 1 ALINVILMA 7
 SEQUENCE FROM N.A.
 NCBI_TaxID=9031;
 SEQUENCE
 Query Match
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 ASL4328
 Q8YP72
 RESULT 32
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 MEDLINE=22137863; PubMed=12142430; Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., "Genome sequence of Yersinia pestis KIM."; Bacteriol. 184:4601-4611(2002).

EMBL, AJ41150; CAC90669:1; -..

EMBL, AB013849; AAM86011.1; -..
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., 'Lin S., Qian Y., Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.; "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
 MEDLINE-21470413; PubMed=11586360;
MEDLINE-21470413; PubMed=11586360;
Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Genome sequence of Yersinia pestis, the causative agent of plague.";
 Gaps
 Gaps
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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0
 Score 22; DB 16; Length 64;
Pred. No. 8.7e+02;
1; Mismatches 0; Indels
 71.0%; Score 22; DB 16; Length 65; 100.0%; Pred. No. 8.8e+02; ive 0; Mismatches 0; Indels
 424FE786CE93B873 CRC64;
 B0796B51977F8EEC CRC64;
 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002)
EMBL; AE014913; AANS8426.1; -.
 68 AA.
 65 AA.
 Putative membrane protein (Hypothetical).
 Hypothetical protein, Complete proteome
SEQUENCE 65 AA, 7315 MW, B0796B5197
 PRT;
 SEQUENCE FROM N.A.
STRAIN-KIMS / Biovar Mediaevalis;
 Enterobacteriaceae, Yersinia.
 71.0%;
80.0%;
 64 AA; 6965 MW;
 Nature 413:523-527(2001).
 Local Similarity 100.
nes 5; Conservative
 Local Similarity 80.0
 PRELIMINARY;
 PRELIMINARY;
 Complete proteome. SEQUENCE 64 AA;
 SEQUENCE FROM N.A.
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48 NILMA 52
 ALMVL 53
 3 NVLMA 7
 1 ALNVL 5
 Yersinia pestis
 NCBI_TaxID=632;
 pathogen.
 Query Match
 Query Match
 Q9Y143
Q9Y143;
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**082F66** RESULT 30 Q8ZF66

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RESULT 31 Q9YI43 ID Q9YI4 AC Q9YI4

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SEQUENCE FROM N.A. MADARED 11021991; MEDINE-20478054; PubMed=11021991; MEDINE-20478054; PubMed=11021991; Sraves M.V., Van Etten J.L.; San L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.; (Characterization of a beta-1,3-glucanase encoded by chlorella virus
 MEDLINE=20013326; PubMed=10544099; Kaieer A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W., Lisec A.D., Nickerson K.W., Van Etten J.L.; "Chlorella virus PBCV-1 encodes a functional homospermidine
 SEQUENCE FROM N.A.
MEDLINE=96400190; PubMed=8806566;
Kutish G.F., Li Y., Lu Z., Furuta M., Rock D.L., Van Etten J.L.;
"Analysis of 76 kb of the chlorella virus PBCV-1 330-kb genome: map positions 182 to 258.";
 Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
NCBI_TaxID=10506;
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Morganella.
NCBI_TaxID=582;
 Hayes F.;
"A family of stability determinants in pathogenic bacteria.";
J. Bacteriol. 180:6415-6418 (1998).
Bacteriol. 180:6415-6418 (1998).
Hypothetical protein; Plasmid.
SEQUENCE 81 AA; 8925 MW; B42EB1330E00AD41 CRC64;
 Length 81;
 SEQUENCE FROM N.A. Graves M.V., Van Etten J.L.; Graves M.V., Van Etten J.L.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 0; Indels
 Van Etten J.L.; Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
 Van Etten J.L.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
 Van Etten J.L.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
 098461;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
A409R protein.
 n
Similarity 66.7%; Pred. No. 1.1e+03;
4; Conservative 2; Mismatches 0;
 82 AA
 SEQUENCE FROM N.A.
MEDLINE=99047595; PubMed=9829958;
 Virology 223:303-317(1996).
 Virology 263:254-262(1999)
 Virology 276:27-36(2000)
 PRELIMINARY;
 SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Best Local Similarity
Matches 4; Conserv
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72 ALNILV 77
 SEQUENCE FROM N.A.
 1 ALNVLM 6
Plasmid R485
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 Van Etten
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 098461
 RESULT 36
Q98461
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 SEQUENCE FROM N.A.

Hirt L., Hirsch-Behnam A., de Villiers E.M.;

Hirt L., Hirsch-Behnam A., de Villiers E.M.;

HNUcleotide sequence of human papillomavirus (HPV) type 41: an unusual

HPV type without a typical E2 binding site consensus sequence.";

Virus Res. 18:179-190(11990).

EMBL, X56147; CAA39620.1; -

EQUENCE 77 AA; 9513 MW; 618D681AACDE9062 CRC64;
 Gaps
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 Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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 SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
STRAIN=cv. Nipponbare;
SSBBARI T., Matsumocto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
 71.0%; Score 22; DB 12; Length 77; 83.3%; Pred. No. 1e+03; 1; Indels :ive 0; Mismatches 1; Indels
 y Match 71.0%; Score 22; DB 10; Length 75; Local Similarity 83.3%; Pred. No. 1e+03; hes 5; Conservative 0; Mismatches 1; Indels
 clone:B1065E10.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
EMBL, AP003561; BAB90373.1; -.
 Human papillomavirus type 41.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
Hypothetical 8-9 kDa protein.
Morganella morganii (Proteus morganii).
 RZP1; -.
75 AA; 8090 MW; 62DE4A3CF83365D6 CRC64;
 Q84212;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 Last sequence update)
Last annotation update)
 81 AA
 77 AA
 75 AA
 Created)
 PRT;
 01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
B1065E10.24 protein.
B1065E10.24.
 (TrEMBLrel. 21,
 Query Match 71.0
Best Local Similarity 83.3
Matches 5; Conservative
 PRELIMINARY;
 PRELIMINARY;
 PRELIMINARY;
 28 LNVAMA 33
 AANVLM 57
 2 LINVLMA 7
 1 ALNVLM 6
 Papillomavirus.
NCBI TaxID=10589;
 NCBI_TaxID=39947;
 Gramene; Q8RZP1;
 ORF X protein.
 01-JUN-2002
 25
 SEQUENCE
 Query Match
 09ZH41
 084212
 QBRZP1
 RESULT 35
 RESULT 33
Q8RZP1
 Matches
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"Medianisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
BMBL, AE008682; AAL03902.1; -.
InterPro; IPR002199; ADH short.
Pfam; PF00106; adh_short; 1.
 SEQUENCE FROM N.A.
STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.;
 Rickettsia conorii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
 86 AA; 9233 MW; 3050E6D15699ABF6 CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similarity to oxidoreductase.
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 NADH dehydrogenase subunit 3.
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 38 ALNVIL 43
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 1 ALNVLM 6
 NCBI_TaxID=10041;
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 SPECIES—Streptococcus thermophilus bacteriophage TP-J34;
SPECIES—STRAIN—TP-J34;
MEDLINE=98122991; PubMed=9454717;
Neve H., Zenz K.I., Desiere F., Koch A., Heller K.J., Brussow H.;
"Comparison of the lysogeny modules from the temperate Streptococcus thermophilus bacteriophages TP-J34 and Sfi21: implications for the modular theory of phage evolution.";
Virology 241:61-72(1998).
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 Lucchini S., Desiere F., Brussow H.;
"Comparative genomics of Streptococcus thermophilus phage species
supports a modular evolution theory.";
J. Virol. 73:8647-8656(1999).
 Streptococcus thermophilus bacteriophage TP-034, and Streptococcus thermophilus bacteriophage Sfill. Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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 Score 22; DB 12; Length 82;
Pred. No. 1.1e+03;
2; Mismatches 0; Indels
 Score 22; DB 9; Length 83;
Pred. No. 1.1e+03;
 1; Indels
[8]
SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 142580; AAC96777.1; -
SEQUENCE 82 AA: 9006 MM; 0B489ED6C3BB6E18 CRC64;
 Desiere F., Lucchini S., Bruessow H.;
Submitted (APR.2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF020798; AAC03451.1;
EMBL; AF158609; AAC03451.1;
SEQUENCE 83 AA; 9876 WW; 5EA33A0DA177EE52 CRC64;
 SEQUENCE FROM N.A. SPECIES-Streptococcus thermophilus bacteriophage Sfill;
 SPECIES-Streptococcus thermophilus bacteriophage Sfill; MEDLINE-99412383; PubMed=10482618;
 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
0RF83 (GP83)
 83 AA.
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 Q92FW3;
01-DEC-2001 (TrEMBLrel. 19, Created)
 71.0%;
66.7%;
 71.0%;
71.4%;
 Query Match
Best Local Similarity 66.7°,
Best A; Conservative
 5; Conservative
 NCBI_TaxID=73422, 78541;
 PRELIMINARY;
 PRELIMINARY;
 Best Local Similarity
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28 AVNVLSA 34
 1 ALINVLMA 7
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38 SINVLM 43
 SEQUENCE FROM N.A.
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 1 ALNVLM 6
 SEQUENCE FROM N.A.
 Query Match
 048385;
 Q92FW3
 048385
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048385
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 Hogan K.M., Davis S.K., Greenbaum I.P.;
"Mitochondrial DNA analysis of the systematic relationships within the Peromycus maniculatus species group.";
Bubmitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U40252; AAB17918.1; -- EMBL/GenBank/DDBJ databases.
InterPro: IRR000440; Oxidored_q4.
Mitochondrion.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
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71.0%; Score 22; DB 16; Length 86; 66.7%; Pred. No. 1.1e+03; ive 2; Mismatches 0; Indels
 71.0%; Score 22; DB 8; Length 89; 66.7%; Pred. No. 1.2e+03; tive 2; Mismatches 0; Indels
 89 AA; 10270 MW; DB35F046BA902D1E CRC64;
 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 90 AA.
 89 AA.
 Peromyscus leucopus (White-footed mouse).
 01-MAR-2003 (TrEMBLrel. 23, Created)
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SEQUENCE FROM N.A.
MEDIATRE-21437601; PubMed=11553538;
MEDIATRE-21437601; PubMed=11553538;
Luck S.N., Turner S.A., Rajakumar K., Sakellaris H., Adler B.;
"Perric Dicitrate Transport System (Fec) of Shigella flexneri 2a
YSH6000 Is Brocaded on a Novel Pathogenicity Island Carrying Multiple
Antibiotic Resistance Genes.";
Infect. Immun. 69:6012-6021(2001).
EMBI. AR326777; AAL08466.1; -.
EMBI. AR326777; AAL08466.1; -.
SEQUENCE 92 AA; 10730 MW; 086451277558E0DD CRC64;
 Gaps
 Gaps
 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
 Xanthomonas axonopodis (pv. citri), and
Xanthomonas campestris (pv. campestris)
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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 SPECIES=X.a.citri, and X.c.campestris;
STRAIN=306 / ATCC 13902 / XV 101, and ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
 Score 22; DB 16; Length 91;
Pred. No. 1.2e+03;
3; Mismatches 0; Indels
 71.0%; Score 22; DB 2; Length 92; 80.0%; Pred. No. 1.2e+03; tive 1; Mismatches 0; Indels
 91 AA; 9838 MW; 531AA81CA1F71F3B CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 10.7 kDa protein.
Shigella flexneri 2a.
 92 AA.
 PRT;
 EMBL; AE011905; AAM37496.1; -. EMBL; AE012412; AAM42249.1; -.
 Enterobacteriaceae; Shigella.
NCBI_TaxID=42897;
 h 71.0%;
Similarity 57.1%;
4; Conservative
 ORF90 OR XAC2649 OR XCC2977.
 Nature 417:459-463(2002).
 Query Match
Best Local Similarity 80.0
Matches 4; Conservative
 PRELIMINARY;
 Query Match
Best Local Similarity
Matches 4; Conserv
 1 ALNVLMA 7
 Complete proteome. SEQUENCE 91 AA;
 SEQUENCE FROM N.A.
 3 NVLMA 7
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 Janka A.; "Sorbitol fermenting Shiga toxin producing Escherichia coli O157:H-"Sorbitol fermenting Shigella resistance locus (SRL) contains homologues of the Shigella resistance locus (SRL) pathogenicity island-sequence of Shigella flexneri 2a."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AJ534392; CAD58981.1;
 Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
Meissenbach J., Boucher C.A.;
Nature 415:497-502(2002).

EMBL; AL646066; CAD15404.1;
 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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 Probable transmembrane protein.
RSC1702 OR RS02891.
Ralstonia golanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Ralstoniaceae; Ralstonia.
 Score 22; DB 16; Length 91;
Pred. No. 1.2e+03;
1; Mismatches 1; Indels
 Score 22; DB 2; Length 90;
Pred. No. 1.2e+03;
1; Mismatches 0; Indels
 Hypothetical protein.
SEQUENCE 90 AA; 10424 MW; 6171FAB668992C32 CRC64;
 91 AA; 9778 MW; 431E829AC56608FA CRC64;
 Created)
Last sequence update)
Last annotation update)
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Last annotation update)
 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein.
 91 AA.
 91 AA
 Created)
 PRT;
 PRT;
 STRAIN=GM11000;
MEDLINE=21681879; PubMed=11823852;
 71.0%;
80.0%;
 71.0%;
 71.48;
 01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
 QBNL30;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
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Best Local Similarity 71.47
5. Conservative
 Query Match
Best Local Similarity 80.0
Local 4; Conservative
 PRELIMINARY;
 PRELIMINARY;
 61 ALNVAVA 67
 1 ALINVLMA 7
 Complete proteome.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A. STRAIN=493/89;
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20 NILMA 24
 3 NVLMA 7
 Escherichia coli
 NCBI_TaxID=305;
 NCBI_TaxID=562;
 SEQUENCE
 QBNL30
 08XY06
 RESULT 42
Q8NL30
ID Q8NL3
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 "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).

EMBL, AE008580; AAL02678.1;.

EMPL, AE008580; ADCOLEIN; Complete proteome.

SEQUENCE 95 AA; 10750 MW; 7253E0673CBA777C CRC64;
 STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.,
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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 Rickettsia conorii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
 71.0%; Score 22; DB 16; Length 92; 80.0%; Pred. No. 1.2e+03; Live 1; Mismatches 0; Indels
 71.0%; Score 22; DB 16; Length 95; 66.7%; Pred. No. 1.3e+03; tive 2; Mismatches 0; Indels
 Last sequence update)
Last annotation update)
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein RC0140.
 95 AA.
 92 AA
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 PRT;
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 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein. C2505.
 Query Match
Best Local Similarity 66.74
 Query Match
Best Local Similarity 80.0
Matches 4; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Escherichia coli 06
 SEQUENCE FROM N.A.
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22 NILMA 26
 SEQUENCE FROM N.A.
 3 NVLMA 7
 NCBI_TaxID=781;
 QBFG80
QBFG80;
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 RESULT 44
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 SEQUENCE FROM N.A.

TISSUE-Venom gland;

MEDLINE-994029813, p. Dand;

Zhu S.-Y., Li W.-X., Zeng X.-C., Jiang D.-H., Mao X., Liu H.;

Zhu S.-Y., Ki M. Annuel Dlocking of two 'short chain' and two 'long chain' K(+) channel blocking peptides from the Chinese scorpion Buthus martensii Karsch.";

FEBS Lett. 457:509-514 (1999).
 Xu Y.Q., Wu J.H., Pei J.M., Shi Y.Y., Ji Y.H., Tong Q.C.;
"Solution structure of BmP02, a new potassium channel blocker from the venom of the Chinese scorpion Buthus martensi Karsch.";
Biochemistry 39:13669-13675(2000).
-!- FUNCTION: Blocks potassium channels.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: BELONGS TO THE SCORPION LEIUROTOXIN FAMILY.
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Neurotoxin BmP02 precursor (Potassium ion channel blocker P02P).
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Bukaryota: Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthidae; Mesobuthus.
 P41307
P92667
P80898 1
P34101
P58566
P13188 P
P00123
P38460
P41908
 Length 56;
 0; Indels
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 Toxin; Neurotoxin; Ionic channel inhibitor;
Potassium channel inhibitor; Signal; 3D-structure.
SIGNAL 1 28
 Score 27; DB 1;
Pred. No. 5.5;
2; Mismatches
 NEUROTOXIN BMP02
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 ALIGNMENTS
 NULM_DIDMA
NULM_MACRO
IPYR_PSEAN
PKI_DICDI
PSAX_ANASP
PSAX_ANASP
COXE_BOVIN
CS55_CHLLT
 ARCFU
 MARPO
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MEDLINE=20530297; PubMed=11076505;
 EMBL; AF132975; AAF31296.1; -.
 6015 MW;
 87.1%;
ilarity 71.4%;
Conservative
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 NCBI_TaxID=34649;
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 escherichia
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 archaeoglob
homo sapien
 octodon deg
 ornithorhyn
 Q9myw0 bos taurus
Q18060 caenorhabdi
O67242 aquifex aeo
 ovis aries
caenorhabdi
 borrelia bu
 synechococc
 balaenopter
 dasypus nov
 methanobact
 proteus vul
 09njp7 mesobuthus
09u8dl mesobuthus
 pyrococcus
 pyrococcus
 pyrococcus
 ureaplasma
 Pebruary 17, 2004, 10:50:13 ; Search time 2.21782 Seconds
(without alignments)
148.428 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 P41301
P82708
P36768
 P39603
P03902
Q9zzy3
P56632
 027734
P22889
P55757
Q8w9m8
Q36457
P23320
 P24976
021333
 09zjz9
P20927
 078754
Q22702
029561
Q15513
 09v0y8
074016
Q8u0p4
 Q9ppy4
P49394
 P00114
P00115
 13973
 5.1.6
Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 127863 segs, 47026705 residues
 GenCore version
Copyright (c) 1993 - 2004
 SUMMARIES
 NULM BOVIN
NULM BOVIN
NULM PIG
NULM SHEEP
YCUS CAREL
Y697_ARCFU
 SPHA_HUMAN
RUXX_PYRAB
RUXX_PYRHO
RUXX_PYRFU
EP1B_METTH
IAPP_OCTUE
 NULM DUGDU
 PSAX_SYNVU
ACPH_UREPA
RS20_BORBU
CYC6_SYNLI
 NULM BALPH
NULM DASNO
 SCP3 MESMA NULM BALMU
 summaries
 HELPJ
 PROVU
 SERMA
 BOVIN
 TIE AQUAE
 CAEEL
 OM protein - protein search, using sw model
 Gapop 10.0 , Gapext 0.5
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
 DB
 US-09-900-147-7
 SwissProt_41:*
 Length
 1 ALNVLMA 7
 length: 0
length: 100
 BLOSUM62
 Query
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Score

Result No.

 $^{3}$ 

sed sed

Minimum DB Maximum DB

Database :

Scoring table:

Searched:

Perfect score:

Run on:

Sequence:

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Gaps

98 A.A.

STANDARD;

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RETS BOVIN
P82708;
NULM BALMU
 Query Match
 RETS_BOVIN
 RESULT 4
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 ö
 SEQUENCE FROM N.A.

TISSUB-Venom gland;
MEDLINE-99402983; PubMed=10471839;
MEDLINE-99402983; PubMed=10471839;
MADLINE-97., Li W.-X., Zeng X.-C., Jiang D.-H., Mao X., Liu H.;
"Nolecular cloning and sequencing of two 'short chain' and two 'long chain' K(+) channel-blocking peptides from the Chinese scorpion Buthus
 TISSUE=Venom gland;
MEDLINE=99313193; PubMed=10386622;
MU J.J., Dai L., Lan Z.D., Chi C.-W.;
MU J.J., Dai L., Lan C.D., Chi C.-W.;
"Genomic organization of three neurotoxins active on small conductance
"Genomic organization of three neurotoxins active on small conductance
Ca2+-activated potassium channels from the scorpion Buthus martensi
 Gaps
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurotoxin BmD03 precursor (Potassium ion Channel blocker P03).
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metacasi Arthropoda; Chelicerata; Arachnida; Scorpiones;
 FEBS Lett. 4577509-514(1999).
 ö
 -i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Expressed by the venom gland.
-i- SIMILARITY: BELONGS TO THE SCORPION LEIUROTOXIN FAMILY.
 Score 27; DB 1; Length 56;
Pred. No. 5.5;
2; Mismatches 0; Indels
 70953032007E8672 CRC64;
 Toxin; Neurotoxin; Ionic channel inhibitor; Potassium channel inhibitor; Signal.
SIGNAL 29 56 NEUROTOXIN BMP03.
DISULRID 31 47 BY SIMILARITY.
DISULRID 34 52 BY SIMILARITY.
DISULRID 38 54 BY SIMILARITY.
 56 AA
 EMBL; AF097408; AAF01253.1; -.
EMBL; AF156170; AAF29463.1; -.
 87.1%;
71.4%;
 FEBS Lett. 452:360-364(1999)
 6001 MW;
 5; Conservative
 STANDARD;
 13 AMNVMMA 19
 HSSP; Q9NJP7; 1DU9.
 martensii Karsch.";
 Query Match
Best Local Similarity
Matches 5; Conserv
 1 ALNVLMA 7
 13 AMNVMMA 19
 56 AA;
 7
 SEQUENCE FROM N.A.
 NCBI_TaxID=34649;
 1 ALNVLMA
 channels.
 MESMA
 DISULFID
DISULFID
DISULFID
SEQUENCE
 Karsch.
 09U8D1;
 SCP3_MESMA
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NULM BALMU

RESULT 3

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 Gape
 SEQUENCE FROM N.A.
MEDLINE=9414932; PubMed=8308901;
MEDLINE=9414932; PubMed=8308901;
Arnason U., Gullberg A.;
"Comparison between the complete mtDNA sequences of the blue and the fin whale, two species that can hybridize in nature.";
J. Nol. Evol. 37:312-322[1993].
J. CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. MCBI_TaxID=9913;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
Balaenopteridae; Balaenoptera.
 SECURIOR, AND FUNCTION.

TISSUB=Kidney;

MEDLINE=21173623; PubMed=11274389;

MEDLINE=21173623; PubMed=11274389;

MEDLINE=21173623; PubMed=11274389;

Stoppini M., Berni R.;

"Identification, retinoid binding and X-ray analysis of a human retinol-binding proceain.";

Proc. Natl. Acad. Sci. U.S.A. 98:3710-3715(2001).

-!- FUNCTION: Intracellular transport of retinol.

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 .
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Retinol-binding protein III, cellular (CRBP-III) (Fragment)
 Score 25; DB 1; Length 98; Pred. No. 31;
 IndelB
 Pfam; PF00420; oxidored_q2; 1.
Probom; PD000359; Oxidored4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10747 MW; 9P770651FE65ED1B CRC64;
 01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
MYDHQL OR NADH
 ..
 42 AA.
 1; Mismatches
 PRT;
 EMBL, X72204; CAA51003.1;
PIR; S41828; S41828.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
01-FEB-1995 (Rel. 31, Created)
 80.6%;
 Best Local Similarity 83.3
Matches 5; Conservative
 STANDARD;
 Bos taurus (Bovine).
 6 MINULMA 11
 2 LINVLMA 7
 NCBI_TaxID=9771;
```

us-09-900-147-7.rsp

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NULM BALPH
P24976;
 SEQUENCE
 Query Match
 EMBL;
EMBL;
 RESULT 6
NULM BALPH
 EMBL;
 EMBL;
 EMBL;
 .
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 A D
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 K.,
Lin D.,
 SPECIES=E.coli; STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhaw G.F., Rose D.J., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
 MEDLINE=56400909; PubMed=807285;
Ryder L., Sharples G.J., Lloyd R.G.;
"Recombination-dependent growth in exonuclease-depleted recBC sbcBC
Btrains of Escherichia coll K-12.";
Genetics 143:1101-1114(1996).
 MEDLINE=97426617; PubMed=9278503; MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Duncan M., Allen B., Araujo R., Aparicio A.M., Chung E., Davie
Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H.,
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
 ö
 Q
 Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
 Score 24; DB 1; Length 42;
Pred. No. 23;
0; Mismatches 1; Indels
-i- TISSUE SPECIFICITY: Kidney.
-i- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY
 YAIE ECOLI STANDARD; PRT; 94 AA.
PSG768; P77343;
01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
YAIE OR B0391 OR C0499 OR Z0487 OR ECS0441 OR SF0327.
Escherichia coli,
 42 AA; 4892 MW; ACB4F1399FDD7F09 CRC64;
 of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
 HSSP; P82980; IGG.
InterPro; IPR000463; Fatty acid BP.
InterPro; IPR000566; Libocin cyFFABP.
PFam; PF00061; Libocalin; 1.
PROSITE; PS00214; FABP; FALSE_NEG.
Vitamin A; Retinol-binding; Transport.
NON_TER.
42
 NCBI_TaxID=562, 217992, 83334, 623;
 Enterobacteriaceae; Escherichia
 Escherichia coli 06,
Escherichia coli 0157:H7, and
 Similarity 85.7%; 6; Conservative
 SPECIES=E.coli; STRAIN=K12;
 22 ALINVNIMA 28
 Best Local Similarity
Matches 6; Conserv
 1 ALINVLMA 7
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 TRANSPORTERS.
 Shigella flexner:
 SPECIES=E.coli;
 SEQUENCE
 Query Match
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 Complete proteome.

4 SEFHLOVABEYSICGRYL -> TVSFICKLPNPPLICAAIC
NSSPSP (IN REF. 1).
N3FPSCOAFD86D661 CRC64;
 SPECIES=E.COli, STRAIN=0157.H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
 "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
 Gaps
 SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Zang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
SEQUENCE FROM N.A.
SPECIESE.coli, STRAIN=0157:H7 / EDL933 / ATCC 700927;
SPECIESE.coli, STRAIN=0157:H7 / EDL933 / ATCC 700927;
BEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Fosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Menome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
 ö
 77.4%; Score 24; DB 1; Length 94; 83.3%; Pred. No. 53;
 Indels
 Ź
 Pred. No. 53;
1; Mismatches
 98
 PRT;
 EMBL; X76979; CAA54286.1; -. EMBL; AE000145; AAC73494.1; -.
 U73857; AAB18115.1; -.
 94 AA; 10234 MW;
 5; Conservative
 STANDARD;
 EcoGene, EG12159; yaiE.
 Hypothetical protein; C
CONFLICT 77 94
 PIR; A90684; A90684.
PIR; E85534; E85534.
PIR; G64767; G64767.
 Best Local Similarity
 |||||:
51 ALNVLL 56
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 1 ALNVLM 6
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Trust T.J.;
 RESULT 8
CS53_HELPJ
ID _CS53_HELPJ
 InterPro
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 ö
 STRAIN=Isolate No. 27 / Anno 1987; TISSUE=Liver;
MEDLINE=92139449; PubMed=1779436;
Arnason U., Gullberg A., Widegren B.;
"The complete nucleotide sequence of the mitochondrial DNA of the fin
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Edentata, Dasypodidae, Dasypus.
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Cetacea, Mysticeti,
Balaenopteridae, Balaenoptera.
 ö
 whale, Balaenoptera physalus.";
J. Mol. Bvol. 33:556-568(1991).
-1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 Score 24; DB 1; Length 98; Pred. No. 55;
 0; Indels
 Prom, PF00420; oxidored q2; 1.
Probom, PD000359; Oxidred4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SROUENCE 98 AA; 10763 WW; 0070D3D6C3AE805F CRC64;
 15-UTL-1998 (Rel. 36, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
15-UTL-1998 (Rel. 36, Last annotation update)
15-UTL-1998 (Rel. 36, Last annotation update)
MADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
MTND4L OR ND4L OR NADH4L.
 МТИD4L ОŘ ND4L ОR NADH4L.
Balaenoptera physalus (Finback whale) (Common rorqual)
 01-WAR-1992 (Rel. 21, Created)
01-WAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
 77.4%; Scor. 66.7%; Pred. No. 55,
 Dasypus novemcinctus (Nine-banded armadillo) Mitochondrion.
 98 AA.
 PRT;
 EMBL, X61145, CAA4347.1; -. PIR; A58851; S24920. InterPro; IPR001133; Oxidored 4L. InterPro; IPR003214; Oxidred4L.
 Query Match
Best Local Similarity 66.7
Matches 4; Conservative
 STANDARD;
 :|:|||
6 MNILMA 11
 2 LINVLMA 7
 SEQUENCE FROM N.A.
 NCBI_TaxID=9361;
 NCBI_TaxID=9770;
 DASNO
 NULM DA
021333
 DASNO
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
 R BEBL; AE001542; AAD06721.1; -.

R HSSP; P04032; 2DVH.

R INGEPPO; IPR003088; Cyt_CI.

R INTERPO; IPR003289; Cyt_CIC.

R INTERPO; IPR000345; CytCohrome_c; 1.

R PRINTS; RR00605; CYTCHROMECIC.

R PRINTS; RR00605; CYTCHROMECIC.

R PRINTS; RR006020; CYTCHROMECIC.

R PRINTS; RR006020; CYTCHROMECIC.

R PRINTS; RS00190; CYTCHROMECIC.

R PRODOM; PS00190; CYTCHROMECIC.

R PRINTS; RS00190; CYTCHROMEC; 1.

R RICCIRCON LYANGER SIGNAL

R SIGNAL

T SIGNAL

T GHAIN
 SEQUENCE FROM N.A.
MEDIJNE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.U., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 -i- FUNCTION: Natural electron acceptor for a formate dehydrogenase.
-i- SUBCELLULAR LOCATION: Periplasmic.
-i- PTM: BINDS ONE HEME GROUP PER MOLECULE.
-i- SIMILARITY: BELONGS TO THE CLASS I CYTOCHROME C FAMILY.
 Gaps
 Helicobacter pylori 199 (Campylobacter pylori 199).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=85963;
 "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
 ö
 Score 24; DB 1; Length 98;
Pred. No. 55;
2; Mismatches 0; Indels
 Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1.
Oxidoreductase, NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10840 MW; D0FF9BC309048774 CRC64;
 092075;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
24-FEB-2003 (Rel. 41, Last annotation update)
JHP1148.
 96 AA
 send an email to license@isb-sib.ch).
 EMBL; Y11832; CAA72524.1; -.
PIR; T11449; T11449.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
 Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
 STANDARD;
 Nature 397:176-180(1999)
 ||::||
LNIIMA 11
 2 LINVLMA 7
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**X Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

**X Kunst F., Ogasawara N.G., Bessieres P., Bolotin A., Borchert S.,

**Ravedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

**Barisa R., Bourscher L., Brans A., Braun M., Brignell S.C., Bron S.,

**Bruschi C., Caldwell B., Capuano V., Carter N.M.,

**Raberolilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

**Raberolilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

**Raberolilet S., Bruschi C., Connerton I.F., Cummings N.J., Daniel R.A.,

**Raberolilet S., Brington J., Fabret C., Ferrari E., Foulger D.,

**Raberolilet S., Borine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

**Raberolilet S., Hosono S., Hullo M.F., Itaya M., Jones L.,

**A Chajashi Y., Koelter P., Koningstein G., Krooph S., Kunano M.,

**A Libert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

**A Norbyashii Y., Koelter P., Koningstein G., Krooph S., Kunano M.,

**A Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

**A Norbyashii Y., Koelter P., Mizuno M., Moestl D., Nakai S., Noback M.,

**Raidina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

**Raidina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

**Raidina N., Rivolta C., Rocha B., Rapoport G., Rey M., Reynolds S.,

**Raider M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y.,

**Raider M., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

**Sarlan B., Sarlous B., Seror S.J., Serror P., Shin B.S., Soldo B.,

**Sorokin A., Tacconi E., Takagi T., Takabashi H., Takemaru K.,

**A Takeuchi M., Tamakoshi A., Tanaka T., Takamaru P., Yanamoto K., Yanamoto E., Wobhikawa H.P., Danchin A.,

**The complete genome sequence of the Gram-positive bacterium Bacillus

**The complete genome sequence of the Gram-positive bacterium Bacillus

**The complete genome sequence of the Gram-positive data f. S.,

**The complete genome sequence of the Capano f.,

**The complete
 MEDLINE=55020537; PubMed=7934828; Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W., Glaser P., Kunst F., Arnaud M., Cubdart M.P., Gonzales W., Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I., Perescan E., Santana M., Schneider E., Schweizer J., Vertes A., Rapoport G., Danchin A.; Rapoport G., Danchin A.; Rapoport G., Danchin A.; Rapoport G., Bastilus subtlike genome project: cloning and sequencing of the 97 Mol. Microbiol. 10:371-384(1993).
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 Hypothetical protein ywcB precursor.
 MEDLINE=98044033; PubMed=9384377;
 EMBL, X73124, CAA51597.1, -. EMBL, Z99123, CAB15839.1, -. PIR, S39696, S39696. Subtilist, BG10587; ywcE.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Bacillus subtilis
 NCBI_TaxID=1423;
 WCE OR IPA-41R.
 STRAIN=168;
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 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Proteus.
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 (HEME AXIAL LIGAND) (BY
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 74.2%; Score 23; DB 1; Length 96; 83.3%; Pred. No. 95;
 0; Indels
 1; Indels
 IRON (HEME AXIAL LIGAND)
SIMILARITY).
3E607AE5D422AD82 CRC64;
 Score 23; DB 1; Length Pred. No. 95;
 96 AA; 10300 MW; EC094F1F37956EE3 CRC64;
 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
FRD operon hypothetical protein C.
 74.2%; Sco...
100.0%; Pred. No. ...
0; Mismatches
 87 AA.
 0; Mismatches
HEME (COVALIE COVALIE INON (HEME ISIMILARITY)
 PRT;
 PRINTS; PRO0445; HUPFHYPC.
ProDom; PD003112; HUPF HYPC; 1.
TIGREAMS; TIGRO0074; hypC hupF; 1.
PROSITE; PS01097; HUPF HYPC; 1.
 PIR; S00119; S00119.
InterPro; IPR001109; HupF HypC.
Pfam; PF01455; HupF HypC; 1.
PIRSF; PIRSF005518; HupF HypC; 1.
 MEDLINE=88004470; PubMed=3308458;
 96 AA; 10354 MW;
 EMBL; X06151; CAA29511.1; -.
 Local Similarity 83.3
nes 5; Conservative
 Local Similarity 100.
 STANDARD;
 STANDARD;
 333
 73
 Hypothetical protein.
 SEQUENCE FROM N.A.
 LINALIMA 74
 2 LINVLMA 7
 NVLMA 19
 Proteus vulgaris.
 3 NVLMA 7
 33
 73
 NCBI_TaxID=585;
 RESULT 10
YWCE BACSU
ID YWCE BACSU
AC P39603;
 YFRC PROVU
P20927;
 69
 SEQUENCE
 Query Match
 SEQUENCE
 Query Match
BINDING
 RESULT 9
YFRC_PROVU
 METAL
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Nature 390:249-256(1997).
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 Transmembrane; Signal; Complete proteome
 POTENTIAL.
HYPOTHETICAL PROTEIN YWCE.
 POTENTIAL. POTENTIAL.
 TRANSMEM
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CC74135F423940CB CRC64;

87 AA; 9959 MW;

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 Ursing B.M., Arnason U.; "The complete mitochondrial DNA sequence of the pig (Sus scrofs)."; J. Mol. Evol. 47:302-306(1998).
 Ursing B.M., Arnason U.;
"Analyses of mitochondrial genomes strongly support a hippopotamus-
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Hippopotamidae; Hippopotamus.
NCBI_TaxID=9833;
 Proc. R. Soc. Lond., B, Biol. Sci. 265:2251-2255(1998).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 71.0%; Score 22; DB 1; Length 98; 50.0%; Pred. No. 1.76+02; tive 3; Mismatches 0; Indel8
 EMBL, AJ010957; CAA09436.1; -.
InterPro; IPR001133; Oxidored 41.
InterPro; IPR0012134; Oxidored 41.
InterPro; Oxidored 42.
Propom; PD000359; Oxidored 42: 1.
Probom; PD000359; Oxidred 41: 1.
Oxidoreducase; NAD: Ubiquinone; Mitochondrion.
Oxidoreducase; NAD: Ubiquinone; Mitochondrion.
SEQUENCE 98 AA: 10776 WW; SF095988CE0652F0 CRC64;
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UUL-1999 (Rel. 38, Last annocation update)
MADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
MIND4L OR ND4L OR NADH4L.
 Q9ZAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annocation update)
MDH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
 98 AA.
 98 AA
 Hippopotamus amphibius (Hippopotamus).
 PRT;
 MEDLINE=98404150; PubMed=9732457;
 SEQUENCE FROM N.A. MEDLINE=99098146; PubMed=9881471;
 SEQUENCE FROM N.A.
STRAIN=Landrace; TISSUE=Heart;
 Query Match
Best Local Similarity 50.0.
 STANDARD;
 STANDARD;
 SEQUENCE FROM N.A.
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6 MNIIMA 11
 2 LINVLMA 7
 Sus scrofa (Pig).
 NCBI_TaxID=9823;
 whale clade.";
 Mitochondrion.
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 NULM HIPAM
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 "Complete sequence of bovine mitochondrial DNA. Conserved features of the mammalian mitochondrial genome."; J. Mol. Biol. 156:683-717(1982).
 Gaps
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 MEDLINE-83010260; PubMed=7120390;
Anderson S., de Bruijn M.H.L., Coulson A.R., Eperon I.C., Sanger F.,
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Boyidae, Bovinae, Bos
 SEQUENCE FROM N.A.
STRAIN=65, 66, D, and F;
Wettstein P.J.;
"Bos taurus mitochondrial protein coding regions.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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 71.0%; Score 22; DB 1; Length 98; 50.0%; Pred. No. 1.7e+02; tive 3; Mismatches 0; Indels
 Score 22; DB 1; Length 87;
Pred. No. 1.5e+02;
3; Mismatches 0; Indels
 Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
VARIANT 65 65 V -> A (IN STRAIN 66).
SEQUENCE 98 AA; 10797 MW; 4DB48B7DA59C1881 CRC64;
 MULM BOOVIN STANDARD; PRT; 98 AA. P01302; QBSTX7; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) NADH-ubiquinnen oxidoreductase chain 4L (EC 1.6.5.3). Marnota (Bovine).
 EMBL, AF493541; AAM12797.1; -. EMBL, AF493542; AAM12810.1; -. EMBL, EMBL, OXBO4L. InterPro; IPR00133; Oxidored 4L. InterPro; IPR003214; Oxidred4L.
 Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1.
 EMBL, V00654; CAA24004.1; -.
EMBL, J01394; AABS9276.1; -.
EMBL, AF490528; AAM0832.1; -.
EMBL, AF490529; AAM08338.1; -.
 71.0%;
57.1%;
 Local Similarity 50.0
nes 3, Conservative
Query Match
Best Local Similarity 57.1.
4; Conservative
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62 AVNVIVA 68
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6 MNIMMA 11
 1 ALINVLMA 7
 SEQUENCE FROM N.A.
 2 LNVLMA 7
 NCBI_TaxID=9913;
 Mitochondrion.
 rissum=Heart;
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 Lin C.S., Sun Y.L., Liu C.Y., Yang P.C., Chang L.C., Cheng I.C.,
Mao S.J.T., Huang M.C.;
"Complete nucleotide sequence of pig (Sus scrofa) mitochondrial genome
and dating evolutionary divergence within artiodactyla.";
Gene 236:107-114(1999).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 SEQUENCE FROM N.A.
STRAIN=Merinolandschaf; TISSUE=Liver;
STRAIN=Merinolandschaf; TISSUE=Liver;
MEDLINE=9844071; bubMed=9767689;
Hiendleder S., Lewalski H., Wassmuth R., Janke A.;
Hiendleder S., Lewalski H., Wassmuth R., Janke A.;
"The complete mitochondrial DNA sequence of the domestic sheep (Ovis arise) and comparison with the other major ovine haplotype.";
arise Svol. 47741-448 (1998).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
MCBI_TaxID=9940,
 ö
 Score 22; DB 1; Length 98;
Pred. No. 1.7e+02;
3; Mismatches 0; Indels
 828C7F511A4E3AFA CRC64;
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
 Pfam; PF00420; oxidored 92; 1.
ProDom; PD000359; Oxidred4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 98 AA.
MEDLINE=99365306; PubMed=10433971;
 EMBL; AJ002189; CAA05240.1; -. EMBL; AF034253; AAD34193.1; -. ITR; T10980; T10980. InterPro; IPR001133; Oxidored 4L. InterPro; IPR003214; Oxidred4L.
 PIR; T11058; T11058.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
 EMBL; AF010406; AAD10103.1; -..
 Pfam; PF00420; oxidored_q2; 1.
 10824 MW;
 71.0%;
50.0%;
 3; Conservative
 STANDARD;
 Ovis aries (Sheep).
Mitochondrion.
 Query Match
Best Local Similarity
 :|::||
MNIIMA 11
 98 AA;
 2 LINVLIMA 7
 MIND4L OR ND4L.
 NULM SHEEP
078754:
 SEQUENCE
 NULM SHEEP
 Matches
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 Gaps
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 Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
 Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE UPP0057 (PMP3) FAMILY.
 ö
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 Length 57;
 71.0%; Score 22; DB 1; Length 98; 50.0%; Pred. No. 1.7e+02; rive 3; Mismatches 0; Indels
 Length 98;
 Indels
 Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Oxidoreductase, NAD, Ubiquinone, Mitochondrion. SEQUENCE 98 AA, 10837 MW, ECOC943C752F8691 CRC64;
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hypothetical 6.3 kDa protein T2372.5 in chromosome X.
 2A2654626D3F0490 CRC64;
 67.7%; Score 21; DB 1; I
50.0%; Pred. No. 1.7e+02;
tive 3; Mismatches 0;
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF0697.
 57 AA.
 61 AA.
 or send an email to license@isb-sib.ch).
 POTENTIAL. POTENTIAL.
 Pfam; PF01679; UPF0057; 1.
PROSITE; PS01309; UPF0057; 1.
Hypothetical protein; Transmembrane.
 PRT;
 PRT;
 WormPep; T23F2.5; CE05000.
InterPro; IPR000612; UPF0057.
 EMBL; U39649; AAA80387.1; -.
 57 AA; 6275 MW;
 Query Match 71.0
Best Local Similarity 50.0
Matches 3; Conservative
 3; Conservative
 STANDARD;
 STANDARD;
 Archaeoglobus fulgidus.
 Caenorhabditis elegans
 PIR; T16930; T16930
 Best Local Similarity
 |:|:|:
33 AINILL 38
 6 MINIMMA 11
 SEQUENCE FROM N.A. STRAIN=Bristol N2;
 2 LINVLIMA 7
 1 ALNVLM 6
 NCBI_TaxID=6239;
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us-09-900-147-7.rsp

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Query Match
Best Local Similarity 66...
At Conservative
 SM00651; Sm; 1.
 Pfam; PF01423; Sm; 1
 Orsay;
 SEQUENCE FROM N.A.
 |||:|
22 ALNIL 26
 2 LINVLMA 7
 PD020287;
 Pyrococcus.
NCBI_TaxID=29292;
 1 ALNVL 5
 PubMed=12622808;
 3D-structure
SEQUENCE 75
 RUXX PYRAB
 Query Match
 ProDom;
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 STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MEDLINE=98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.F., White O., Nelson K.E.,

Klenk H.-P., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNail L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 Sperling K.; "Irreversible repression of DNA synthesis in Fanconi anemia cells is alleviated by the product of a novel cyclin-related gene."; Mol. Cell. Biol. 15:305-314(1995).
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
 ö
 Digweed M., Guenthert U., Schneider R., Seyschab H., Friedl R.,
 Score 21; DB 1; Length 61;
Pred. No. 1.9e+02;
2; Mismatches 0; Indels
 Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 Hypothetical protein; Transmembrane; Complete proteome.
 4 23 POTENTIAL.
61 AA; 7060 MW; 13B07F577570DF60 CRC64;
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein SPHAR (S-phase response protein).
 63 AA
 SEQUENCE FROM N.A.
MEDLINE=95098005; PubMed=7799938;
 Archaeoglobaceae, Archaeoglobus
 EMBL; AE001056; AAB90542.1; -.
 67.78;
 Nature 390:364-370(1997).
 Local Similarity 66.7 les 4; Conservative
 STANDARD;
 PIR; A69337; A69337.
TIGR; AF0697; -.
 Homo sapiens (Human)
 |||:|:
17 ALNLLL 22
 SEQUENCE FROM N.A.
 1 ALNVLM 6
 Venter J.C.;
 SPHA HUMAN
Q15513;
 SEQUENCE
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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 Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi.";
Mol. Microbiol. 47:1495-1512(2003).
-!- SIMILARITY: Belongs to the snRNP Sm proteins family.
 Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 Gaps
 Gape
 .
0
 .;
0
 Hypothetical protein; Ribonucleoprotein; Complete proteome;
 Score 21, DB 1; Length 63;
Pred. No. 1.9e+02;
1; Mismatches 0; Indels
 Score 21, DB 1, Length 75;
Pred. No. 2.3e+02;
2; Mismatches 0; Indels
 EMBL; AL117350; CAC17573.1; -.
PIR; 138244; 138244.
GO: 00006260; P:DNa replication; TAS.
GO: GO: 000074; P:regulation of cell cycle; TAS.
SEQUENCE 63 AA; 7515 MW; 81CAB20A4E39C4AF CRC64;
 75 AA; 8489 MW; CB08295C82D03F1E CRC64;
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
PARABO6500 OR PAB8160.
 75 AA.
 or send an email to_license@isb-sib.ch).
 EMBL; AJ248285; CAB49563.1; -. PIR; B75106; B75106. PDB; 1M8V; 11-FEB-03.
 EMBL; X82554; CAA57901.1; -..
 67.7%;
80.0%;
 67.7%;
66.7%;
 HAMAP; MF 00257; -; 1.
InterPro; IPR006649; BRRNP.
InterPro; IPR001163; BRRNP
 snRNP; 1.
 Best Local Similarity 80.0 Matches 4; Conservative
 STANDARD;
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4; Conservative
 STANDARD;
 Similarity
 38 LNVVLA 43
 NCBI_TaxID=187420;
 SEQUENCE FROM N.A.
 2 LNVLMA 7
 STRUCTURE BY NMR.
 EF1B OR MTH1699.
 STRAIN=Delta H;
 EF1B METTH O27734;
 Query Match
Best Local
 BF1B_METTH
 Matches
 RESULT 21
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 ö
 Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosuqi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
 Archaea, Buryarchaeota, Thermococci, Thermococcales, Thermococcaceae, Pyrococcus.
NCBI_TaxID=2261;
 Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 Gaps
 ö
 SMART; SM00651; Sm; 1. Hypothetical protein; Complete.proteome. SRQUENCE 75 AA; 8447 MW; CB082950C4CF3FIB CRC64;
 Score 21; DB 1; Length 75;
Pred. No. 2.3e+02;
2; Mismatches 0; Indels
 DNA Res. 5:55-76(1998).
-!- SIMILARITY: Belongs to the snRNP Sm proteins family.
 15-JUL 1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
PH1518.2 OR PHS042.
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative snRNP Sm-like protein.
 75 AA
 76 AA
 PRT;
 MEDLINE=98344137; PubMed=9679194;
 HAMAP; MF_00257; -; 1.
InterPro; IPR006649; snRNP.
InterPro; IPR001163; snRNP_Sm.
 EMBL; AP000006; BAA30628.1; -. PIR; D71028; D71028.
 67.7%;
66.7%;
 ProDom; PD020287; snRNP; 1.
 Conservative
 STANDARD;
 STANDARD;
 Pyrococcus horikoshii.
 Pfam; PF01423; Sm; 1
 Pyrococcus furiosus.
|||::|
LNVVLA 43
 Local Similarity
 |||::|
LNVVLA 43
 SEQUENCE FROM N.A.
 LINVLMA 7
 NCBI_TaxID=53953;
 4;
 RUXX PYRFU
Q8U0P4;
 RUXX PYRHO 074016;
 STRAIN=OT3;
 38
 38
 Query Match
 PF1542.
 RUXX PYRHO
 RUXX PYRFU
 Matches
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 Gaps
 elongation factor lbeta from Methanobacterium thermoautotrophicum."; J. Biomol. NMR 17:187-194 (2000).
-!- FUNCTION: PROMOTES THE BXCHANGE OF GDP FOR GTP IN EF-1-ALPHA/GDP, THUS ALLOWING THE REGERERATION OF EF-1-ALPHA/GTP THAT COULD THEN BE USED TO FORM THE TERNARY COMPLEX EF-1-ALPHA/GTP/AATRNA.
 Dubois J.,
 MEDLINE=20414184; PubMed=10959626; Kozlov G., Ekiel I., Beglova N., Yee A., Dharamsi A., Engel A., Siddiqui N., Nong A., Gehring K., Siddiqui N., Nong A., Gehring K., "Rapid fold and structure determination of the archaeal translation
 Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothher B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M., "Complete genome sequence of Methanobacterium thermoautotrophicum deltah: functional analysis and comparative genomics.";
 ;
 Methanobacterium thermoautotrophicum.
Archaea, Buryarchaeota, Methanobacteria, Methanobacteriales,
Methanobacteriaceae, Methanothermobacter.
STRAIN=VCI / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the BMBL/GenBank/DDBJ databases.
-! SIMILARITY: Belongs to the snRNP Sm proteins family.
 Length 76;
 0; Indels
 HAMAP; MF 00257; -; 1.
InterPro; IPR006649; snRNP.
InterPro; IPR001163; snRNP.Sm.
ProDom; PD020287; snRNP; 1.
SMART; SM00651; Sn. 1.
Hypothetical, protein; Ribonucleoprotein; Complete pro SEQUENCE 76 AA; 8443 MW; 532A3PF95C434BEI CRC64;
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Blongation factor 1-beta (EF-1-beta) (aBF-1beta)
 Score 21; DB 1; I
Pred. No. 2.4e+02;
 89 AA.
 2; Mismatches
 MEDLINE=98037514; PubMed=9371463;
 EMBL; AE010255; AAL81666.1; -.
 67.7%;
66.7%;
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modified and this statement is not removed.
 Serratia marcescens.
 16 ALNTLKA 22
 Query Match
Best Local Similarity
Matches 5; Conserv
 1 ALNVLMA 7
 Query Match
Best Local Similarity
Matches 5; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=615;
 IDENTIFICATION.
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P55757;
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 ö
 Endocrinol. 4:1192-1198(1990).
FUNCTION: SELECTIVELY INHIBITS INSULIN-STIMULATED GLUCOSE UTILIZATION AND GLYCOGEN DEPOSITION IN MUSCLE, WHILE NOT AFFECTING
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Octodontidae; Octodon.
NCBI_TaxID=10160;
 MEDINE=91155952; PubMed=2293024;
Mishi M., Steiner D.F.;
"Cloning of complementary DNAs encoding islet amyloid polypeptide, insulin, and glucagon precursors from a New World rodent, the degu,
 ö
 SIMILARITY: BELONGS TO THE EP-1-BETA/EP-1-DELTA FAMILY.
 PIR; B69094; B69094.
PDB; 1GH8; 13-DEC-00.
HAMAP, WF 00043; -; 1.
InterPro; IPR001326; EF1_BD.
InferPro; IPR001326; EF1_BD.
INFRAMB; TIGRPAMB; TIGRO4099; BEF-1 beta; 1.
Elongation factor; Protein biosynthesis; Calcium-binding;
 Score 21; DB 1; Length 89;
Pred. No. 2.8e+02;
2; Mismatches 0; Indels
 17CC49327D3B773D CRC64;
 SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Islet amyloid polypeptide precursor (Amylin).
 91 AA
 ADIPOCYTE GLUCOSE METABOLISM SUBCELLULAR LOCATION: Secret
MISCELLANEOUS: BINDS CALCIUM
 Complete proteome
 EMBL; AE000927; AAB86171.1; -.
 67.7%;
66.7%;
 9532 MW;
 Query Match
Best Local Similarity 66....
4; Conservative
 STANDARD;
 Octodon degus (Degu)
 |||||:
ALNVMV 55
 41
62
66
72
78
 SEQUENCE FROM N.A.
 1 ALNVLM 6
 Octodon degus.";
Mol. Endocrinol.
 3D-structure;
 OCTDE
 SEQUENCE
 IAPP OC
P22889;
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or send an email to license@isb-sib.ch).
 Gaps
 Gaps
 Akatsuka H., Kawai E., Komatsubara S., Tosa T.;
to the EMBL/GenBank/DDBJ databases.
 AMIDATION (G-74 PROVIDE AMIDE GROUP) 42AB31AE1CE9EA99 CRC64;
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 PIR; A36118; A36118.
InterPro; IPR001643; Amylin.
InterPro; IPR00163; Calcitonin-like.
InterPro; IPR002163; Calcitonin B.
Emi, PR00214; Calc CGRP IAAPP; I.
PRINTS; PR00817; CalcITONINB.
PRINTS; PR00818; ISLETAMYLOID.
SMRAT; SM0013; CALCITONIN', 1.
PROSTIE; PS00258; CALCITONIN', 1.
Hormone; Cleavage on pair of basic residues; Amidation; Amyloid;
 ö
 ö
 67.7%; Score 21; DB 1; Length 91; 71.4%; Pred. No. 2.8e+02; ive 1; Mismatches 1; Indels
 Score 21; DB 1; Length 91;
Pred. No. 2.8e+02;
0; Mismatches 2; Indels
 ISLET AMYLOID POLYPEPTIDE
 91 AA; 10102 MW; 4E442754797D69F7 CRC64;
 01-NOV-1997 (Rel. 35, Created)
101-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 10.1 kDa protein in bioA 5'region.
 91 AA.
 BY SIMILARITY.
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or send an email to license@isb-sib.ch)
 POTENTIAL
 Rudd K.E.;
Unpublished observations (MAR-1996).
-!- SIMILARITY: TO E.COLI YAIN.
 EMBL, D17468; -; NOT ANNOTATED_CDS.
InterPro; IPR003735; DUF156.
Pfam; PF02583; DUF156; 1.
Hypochetical procein.
SEQUENCE 91 AA; 10102 MW; 4E442
 Enterobacteriaceae; Serratia.
 22
34
73
91
43
73
 EMBL; M57669; AAA40589.1; -.
 67.78;
71.48;
 Conservative
 Conservative
 STANDARD;
 STRAIN=Sr41;
Sakurai N., Imai Y.,
Submitted (AUG-1993)
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Janke A., Gemmell N., Feldmaier-Fuchs G., von Haeseler A.,
 2 LINVLIMA 7
 01-NOV-1991 (
01-NOV-1991 (
28-FEB-2003 (
 Q9PP<u>Y</u>4;
28-FEB-2003
28-FEB-2003
15-SEP-2003
 PSAX SYNVU
P23320;
 ACPH UREPA
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 Query Match
 RESULT 27
ACPH UREPA
 PSAX_SYNVU
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 MEDLINE=22056029; PubMed=12034869;
Arnason U., Adegoke J.A., Bodin K., Born E.W., Esa Y.B., Gullberg A.,
Nilsson M., Short R.V., Xu X., Janke A.;
"Mammalian mitogenomic relationships and the root of the eutherian
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Monotremata, Ornithorhynchidae, Ornithorhynchus.
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Sirenia; Dugongidae; Dugong
 -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol
 67.7%; Score 21; DB 1; Length 98; 50.0%; Pred. No. 3.18+02; ive 3; Mismatches 0; Indels
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
MADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
MTND4L OR ND4L OR NADH4L.
Dugong dugon (Dugong).
 D; Ubiquinone; Mitochondrion.
10921 MW; CCE86F1849FC007C CRC64;
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
MTND4L OR ND4L.
Ornithorhynchus anatinus (Duckbill platypus).
 Proc. Natl. Acad. Sci. U.S.A. 99:8151-8156(2002).
 98 A.A.
 98 A.A.
 PRT;
 InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
Pfam; PF00420; oxidored q2; 1.
ProDom; PD000359; Oxidred4L; 1.
 SEQUENCE FROM N.A.
TISSUE=Heart, and Liver;
MEDLINE=97077300; PubMed=8919867;
 EMBL; AJ421723; CAD18916.1; -.
 Best Local Similarity 50.0
Matches 3; Conservative
 STANDARD;
 STANDARD;
 NAD;
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AVNGLMA 54
 :|:|:|
INILLA 11
 SEQUENCE FROM N.A.
 98 AA;
 2 LINVLMA 7
 NCBI_TaxID=29137;
 1 ALNVLMA
 NCBI TaxID=9258;
 Oxidoreductase;
 Mitochondrion.
 Mitochondrion
 NULM ORNAN
Q36457;
 NULM DUGDU
 SEQUENCE
 Query Match
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 Gaps
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 MEDILINE-89338747; PubMed=2503399;
Koike H., Ikeuchi M., Hiyama T., Inoue Y.;
Klentification of photosystem I components from the cyanobacterium,
Synechococcus vulcanus by N-terminal sequencing.";
FEBS Lett. 253:257-263(1989).
-!- SIMILARITY: BELONGS TO THE PSAX FAMILY.
Photosynthesis; Photosystem I.
NON_TER. 29 29
 (Ornithorhynchus anatinus).";
J. Mol. Evol. 42:153-159(1996).
-1- CATALYIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 ö
 ;
0
 Synechococcus vulcanus (Thermosynechococcus vulcanus).
Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
NCBI_TaxID=32053;
 64.5%; Score 20; DB 1; Length 29; 57.1%; Pred. No. 1.5e+02;
 67.7%; Score 21; DB 1; Length 98; 66.7%; Pred. No. 3.18+02; ive 2; Mismatches 0; Indels
Pabo S.;
The mitochondrial genome of a monotreme -- the platypus
 1; Indels
 EMBL; X83427; CAA58463.1; -.
PIR, A58889; A58889
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
Pfam; PF0420; oxidored q2; 1.
Prodon; PD000359; Oxidored q2; 1.
Prodon; PD000359; Oxidored d2; 1.
SEQUENCE 98 AA; 10852 NW; 30F80723A3D36090 CRC64;
 29 AA; 3172 MW; DCF1BBF6418042FF CRC64;
 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FBR-2003 (Rel. 41, Last annotation update)
Photosystem I 4.8 kDa protein (Fragment).
 (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
 29 AA.
 77 AA.
 2; Mismatches
 PRT;
 Best Local Similarity 57.1
Matches 4; Conservative
 4; Conservative
 STANDARD;
 STANDARD;
 21 AINFLVA 27
 Best Local Similarity
Matches 4; Conserv
 1 ALINVLIMA 7
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6 LNLLLA 11
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 C -1 - SUBUNIT: Monomer (By similarity).

C -1 - SUBCELLULAR LOCATION: Cytoplasmic (Potential).

-1 - STM: Binds one heme group per molecule.

-1 - PTM: Binds one heme group per molecule.

R PIR, A00106; CCYCGL.

R HAMAP: MF 00594; -1.

R InterPro; IPR00345; Cyt_CI.

R InterPro; IPR00345; Cyt_CI.

R InterPro; IPR00345; Cyt_CI.

R InterPro; IPR00345; Cyt_CI.

R PERMYES; PR00655; CYTCHROMECI.

R PRINTS; PR00655; CYTCHROMECI.

R PRINTS; PR00619; CYTCHROMEC; 1.

R PRINTS; PR00199; CYTCHROMEC; 1.

R PRINTS; PR00655; CYTCHROMEC; 1.

R PRINTS; PR00199; CYTCHROMEC; 1.

R PRINTING 14 HEWE (COVALENT).

T BINDING 17 HEWE (COVALENT).
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome C6 (Soluble cytochrome f) (Cytochrome c-
 Borden D., Margoliash E.;
Submitted (DEC-1979) to the PIR data bank.
-!- FUNCTION: Functions as an electron carrier between membrane-bound
 cytochrome b6f and photosystem I in oxygenic photosynthesis (By
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.
 Nature 390:580-586(1997).
-!- FUNCTION: Binds directly to 16S ribosomal RNA (By similarity)
-!- SIMILARITY: BELONGS TO THE S20P FAMILY OF RIBOSOMAL PROTEINS.
 ö
 "Genomic sequence of a Lyme disease spirochaete, Borrelia
 h Similarity 80.0%; Pred. No. 4.7e+02; 4; Conservative 1; Mismatches 0; Indels
 Synechococcus lividus.
Bacteria; Cyanobacteria; Chroococcales; Synechococcus
NCBL_TaxID=33070;
 ing; Complete proteome.
EBAC874CD12397FA CRC64;
 87 AA.
 Tick; DECALO.;

HAMAP, BOSOO;

InterPro; IPR002583; Ribosomal S20p.
Pfam; PF014643; Ribosomal S20p; 1.

ProDom; PD004231; Ribosomal S20p; 1.

Ribosomal protein; rRNA-binding; Com
srATENCE 85 AA; 9947 MW; EBAC874
 AE001133; AAC66616.1; ALT_INIT
 EMBL; U35673; AAB41459.1;
 STANDARD;
 Query Match
Best Local Similarity
 LINVLL 83
 2 LINVLM 6
 SYNLI
 79
 SEQUENCE.
 CYCG SYNLI
ID CYCG SYN
AC P00114;
 EMBL;
 Best Loc
Matches
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 RESULT 29
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 ö
 SEQUENCE FROM N.A.
STRAIN-ATC 35210 / B31;
STRAIN-B-98065943; Pubmed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 Nature 407:757-762 (2000).

Nature 407:757-762 (2000).

Nature 407:757-762 (2000).

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Nature 407:757-762 (2000).

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Nature 407:757-762 (2000).

Na
 Gaps
 InterPro; IPR006163; Pp_bind.
InterPro; IPR006162; Ppantne_attach.
InterPro; IPR005162; Ppantne_attach.
InterPro; IPR00550; pp-binding; 1.
PROSITE; PSS0075; ACDOMAIN; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
Hypothetical protein; Fatty acid biosynthesis; Phosphopantetheine;
 Borrelia burgdorferi (Lyme disease spirochete).
Bacteria, Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 PHOSPHOPANTETHEINE (BY SIMILARITY). 3CDB655FBFA968C6 CRC64;
 Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen B.Y., Cassell G.H.; The complete sequence of the mucosal pathogen Ureaplasma
 Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Pirmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
 ö
 Score 20; DB 1; Length 77; Pred. No. 4.2e+02; 3; Mismatches 0; Indels
 Tilly K.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RPST OR BE0233.
 85 AA.
carrier protein homolog (ACP).
 STRAIN=Serovar 3;
MEDLINE=20500219; PubMed=11048724;
 64.5%;
 77 AA; 8750 MW;
 EMBL; AE002149; AAF30918.1;
 Local Similarity 50.0
1es 3; Conservative
 STANDARD;
 36
 Complete proteome.
 AMNLIM 44
 SEQUENCE FROM N.A.
 1 ALNVLM 6
 SEQUENCE FROM N.A
 NCBI_TaxID=139;
 urealyticum.";
 RS20 BORBU
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 ILG1 CAI
Q18060;
 ILG1_CAEEL
 Matches
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 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Cytochrome C6 (Soluble cytochrome f) (Cytochrome c553) (Cytochrome c-552).
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0
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 Score 20; DB 1; Length 87;
Pred. No. 4.8e+02;
1; Mismatches 0; Indels
IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).
37713EC6405EBEEE CRC64;
 Synechococcus sp. (strain PCC 6312 / ATCC 27167).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=195253;
 [6-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 41, Last annotation update)
Transient receptor potential channel 6 (Fragment).
TRPC6 OF TRP6.
 MEDLINE=80068924; PubMed=228936;
18
58
9129 MW;
 64.5%;
80.0%;
 4; Conservative
 STANDARD;
 STANDARD;
 Bos taurus (Bovine).
 Local Similarity
18
58
87 AA;
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NVVMA 27
 3 NVLMA 7
 3 NVLMA 7
 RESULT 31
TRP6 BOVIN
ID TRP6 BOVIN
AC Q9MYW0;
DT 16-OCT-2001
DT 28-FEB-2003
DE Transient rec
GN TRPC6 OF TRP
CS BOS taurus (f)
 CYC6 SYNP3
P00115;
 Aitken A.;
METAL
METAL
SEQUENCE
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 Query Match
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MEDLINE=20179038; PubMed=10816590;

MEDLINE=20179038; PubMed=10816590;

A Schroth G., Kretz O., Nastainczyk W., Cavalie A., Hoth M.,

R Flockerzi V.;

TRP4 (CCEI) protein is part of native calcium release-activated Ca2+-

TRP5 (CCEI) protein is part of native calcium release-activated Ca2+-

TRP5 (CCEI) protein is part of native calcium release-activated Ca2+-

TRP6 (CCEI) protein is part of native calcium release-activated Ca2+-

TRP7 (CCEI) protein is part of native calcium release-activated Ca2+-

TRP9 (CCEI) protein is part of native calcium release-activated Ca2+-

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 Gaps
 Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
18-SPRB-2003 (Rel. 41, Last annotation update)
Probable insulin-like peptide gamma-type 1 precursor (Ceinsulin-3).
INS-11 OR C17C3.4
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
 SIMILARLIYY).
-- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
--- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
 .
0
 EMBL; AJ271069; CACO1677.1; -.
Interpro; IPR002111; Cat channel TrpL.
Ionic channel; Transmembrane; Ion transport; Calcium channel
NON TER 1
 Kawano T.;
"mRNA for a putative insulin-like peptide of Caenorhabditis
 Length 89;
 64.5%; Score 20; DB 1; Length 89; llarity 66.7%; Pred. No. 4.9e+02; Conservative 2; Mismatches 0; Indels
 Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 8E1D54F051F1E7ED CRC64;
 91 AA.
 POTENTIAL.
 POTENTIAL
 89
10315 MW;
 STANDARD;
 Caenorhabditis elegans.
 21
 Local Similarity
nes 4; Conserv
 89 AA;
 ||:|:|
81 LNMLIA 86
 SEQUENCE FROM N.A.
 2 LINVLIMA 7
 SEQUENCE FROM N.A.
 NCBI_TaxID=9913;
 SUBFAMILY.
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NCBI_TaxID=562;
 IDENTIFICATION
 YGBF_ECOLI
ID YGBF_ECOLI
AC P45956;
 4.
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 Matches
 RESULT 34
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 ö
 This SWISS-PROT entry is copyright. It is produced through a collaboration
 POTENTIAL.
PROBABLE INSULIN-LIKE PEPTIDE GAMMA-TYPE
 Gaps
 MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gassterland T., Young W.G., Lenox A.L., Grahan D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
 MEDLINE=98217375; PubMed=9548970;
Duret L., Guex N., Peitsch M.C., Bairoch A.;
Duret L., Guex N., Peitsch M.C., Bairoch A.;
New insulin-like proteins with atypical disulfide bond pattern characterized in Caenorhaboditis elegans by comparative sequence analysis and homology modeling.";
Genome Res. 8:348-353(1998).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SUBCELLULAR LOCATION: Secreted (POTENTIAL).
 ö
 (POTENTIAL)
 Score 20; DB 1; Length 91;
Pred. No. 5e+02;
1; Mismatches 0; Indels
 Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
 Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
 22BF958BF759F254 CRC64;
 B-CHAIN-LIKE PEPTIDE
A-CHAIN-LIKE PEPTIDE
 Flagellar hook basal body complex protein file.
FLIE OR AQ 1182.1 OR AQ 1182A.
Aquifex aeolicus.
 067242;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
 93 AA
 Nature 392:353-358(1998).
-!- SIMILARITY: BELONGS TO THE FLIE FAMILY.
 POTENTIAL.
 POTENTIAL.
 WormPep; C17C3.4; CE04024.
InterPro; IPR0040425; Ins/IGF/relax.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Signal.
 PRT;
 EMBL; AB032258; BAA84470.1; -.
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 EMBL; U41279; AAK31418.1; -. PIR; T37327; T37327.
 64.5%;
 80.08;
 Local Similarity 80.0
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 SIMILARITY TO INSULIN.
 34
61
37
49
65
91 AA;
 SEQUENCE FROM N.A.
STRAIN-Bristol N2;
 ALNVM 48
 1 ALNVL 5
 FLIE_AQUAE
 STRAIN=VF5
 DISULFID
 DISULFID
 SEQUENCE
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 PEPTIDE
 PLIE AQUAE

TO FLIE AQUAE

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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 Danchin A.;
"Detection of new genes in a bacterial genome using Markov models for three gene classes.";
Nucleic Acids Res. 23:3554-3562(1995).
 Gарв
 125
STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=978., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 Bacherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 MEDLINE=96032851; PubMed=7567469;
Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,
 ö
 Nakata A., Amemura M., Makino K.; "Unusual nucleocitde arrangement with repeated sequences in the "Escherichia coli K-12 chromosome."; J. Bacteriol. 171:353-3556(1989).
 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
 Length 93;
 Indele
 Flagella; Complete proteome.
SEQUENCE 93 AA; 10764 MW; 6180AEA1C8FB9C39 CRC64;
 Score 20; DB 1; Le.
Pred. No. 5.1e+02;
2; Mismatches 0;
 01-NOV-1995 (Rel. 32, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
YGBF OR B2754.
 94 AA
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 MEDLINE=89255132; PubMed=2656660;
 Enterobacteriaceae, Escherichia
 EMBL; AE000727; AAC07208.1; -
 PRINTS; PR01006; FLGHOOKFLIE.
TIGREAMS; TIGR00205; flie; 1.
 64.5%;
66.7%;
 PIR, G70401, G70401.
InterPro, IPR001624; FliE.
Pfam; PF02049; FliE; 1.
 Conservative
 STANDARD;
 1 ALNVLM 6
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70 ALNLLI 75
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
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98 AA.

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PRT;
 EMBL; 229573; CAA82685.1; -. PIR; S47878; S47878. InterPro; IPR001133; Oxidored 4L. InterPro; IPR003214; Oxidred4L.
 Best Local Similarity 50.0 Matches 3; Conservative
 STANDARD;
 STANDARD;
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6 LNIIVA 11
 SEQUENCE FROM N.A.
 2 LINVLMA 7
 SEQUENCE FROM N.A.
 NCBI_TaxID=9267;
 NCBI_TaxID=9319;
 WIND4L OR ND4L.
 Mitochondrion.
 NULM MACRO
 mammals."
 Query Match
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 STRAIN-VC-16 DSW 4304 / ATCC 49558;
MEDLINE-98049343; PubMed=9389475;
MEDLINE-98049343; PubMed=9389475;
MEDLINE-98049343; PubMed=9389475;
MEDLINE-98049343; PubMed=9389475;
MEDLINE-98049343; PubMed=9389475;
METCHARCHORN R.J., Town M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Fulii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 Gaps
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 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
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 64.5%; Score 20; DB 1; Length 94; 80.0%; Pred. No. 5.2e+02; tive 1; Mismatches 0; Indels
 64.5%; Score 20; DB 1; Length 95; 66.7%; Pred. No. 5.3e+02; ive 1; Mismatches 1; Indels
 Archaea; Buryarchãeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBL_TaxID=2234;
 PIR; E69422; E69422.
TIGR; AF18182; Hypochetical protein; Complete proteome.
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 Hypothetical protein; Complete proteome.
SEQUENCE 94 AA; 10518 MW; DIC159D924B477B4 CRC64;
 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF1382.
 95 AA
 EMBL; AE000359; AAC75796.1; ALT_INIT. EcoGene; EG12845; YGDF.
EMBL; M27059; -; NOT ANNOTATED CDS. EMBL; U29579; AAA69264.1; -
 EMBL; AE001009; AAB89883.1; -.
 Nature 390:364-370(1997).
 Local Similarity 80.0
les 4; Conservative
 4; Conservative
 STANDARD;
 Archaeoglobus fulgidus.
 Best Local Similarity
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14 ALBILM 19
 1 ALNVLM 6
 SEQUENCE FROM N.A.
 55 NVVMA 59
 NVLMA 7
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 This SWISS-PROT entry is copyright. It is produced through a collaboration
 Gaps
 MEDLINE=94333786; PubMed=8056314;
Janke A., Feldmaier-Fuchs G., Thomas K., von Haeseler A., Paabo S.;
"The marsupial mitochondrial genome and the evolution of placental
 Mitochondrion.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis.
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 Generics 137:243-256(1994).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 MEDIANE=97188458; PubMed=9037043;
Janke A., Xu X., Arnason U.;
Janke A., Xu X., Arnason U.;
"The complete mitochondrial genome of the wallaroo (Macropus robustus) and the phylogenetic relationship among Monotremata, Marsupialia, and Butheria.';
Proc. Natl. Acad. Sci. U.S.A. 94:1276-1281(1997).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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0
 Didelphis marsupialis virginiana (North American opossum).
 64.5%; Score 20; DB 1; Length 98; 50.0%; Pred. No. 5.4e+02; tive 3; Mismatches 0; Indels
 Length 98;
 Pram; PF00420; oxidored q2; 1.
ProDom; PD000359; Oxidred4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10815 WW; F988F6026B0A4C59 CRC64;
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
MATND4L OR ND4L OR NADH4L.
MACTOPUS robustus (Wallaroo) (Euro).
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NODH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
 98 AA.
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
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 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phosphohydrolase) (Fragment).
 / Match 64.5%; Score 20; DB 1; Length 98; Local Similarity 57.1%; Pred. No. 5.4e+02; nes 4; Conservative 2; Mismatches 1; Indels
 Score 19; DB 1; Length 25;
Pred. No. 2.3e+02;
1; Mismatches 0; Indels
 Pseudanabaena sp. (strain PCC 6901).
Bacteria; Cyanobacteria; Oscillatoriales; Pseudanabaena
NCBI_TaxID=47918;
 Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 98 AA; 10717 MW; DC9AlD06DBAC81B7 CRC64;
 25 AA; 2630 MW; FB6138F3AED4D43E CRC64;
 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
PKGA.
 33 AA
 25 AA.
 EMBL, Y10524; CAA71544.1; -.
PIR, T11436; T11436.
InterPro; IPR001133; Oxidored 4L.
InterPro; IPR003214; Oxidred4L.
 Pfam; PF00420; oxidored q2; 1.
ProDom; PD000359; Oxidred4L; 1.
 61.3%;
80.0%;
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Best Local Similarity 80.0
اتا 4; Conservative
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 2 LINVLM 6
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AC P3410
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GN PKGA.
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 MEDLINE=91142122; PubMed=1996312;
Haribabu B., Dottin R.P.;
"Identification of a protein kinase multigene family of Dictyostelium discoideum: molecular cloning and expression of a cDNA encoding a developmentally regulated protein kinase.";
Proc. Natl. Acad. Sci. U. 83. 48:1115-1119(1991).
- SIMILARITY: BELONGS TO THE SER/THR PAMILY OF PROTEIN KINASES.
 Gaps
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
 MEDLINE=2195285; PubMed=11759840; Karitz T., Sabamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sabamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawabhima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Yasuda M., Yasuda M., Yamada M., Yasuda
 ö
 Transferase; Serine/threonine-protein kinase; ATP-binding;
 Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
 Score 19; DB 1; Length 33;
Pred. No. 3.1e+02;
2; Mismatches 0; Indels
 D4CBB6AF12FA18DE CRC64;
 Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
NCBI_TaxID=44689;
 DictyDb; DD05046; pkgA.
InterPro; IRR00219; Brot kinase.
InterPro; IPR002290; Ser thr pkinase.
Pfam; PF00069; pkinase; I.
PROSITE; PS00107; PROTEIN KINASE ATP; PARTIAL.
PROSITE; PS00108; PROTEIN KINASE ST; PARTIAL.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Photosystem I 4.8 kDa protein.
 PROTEIN KINASE.
 43 AA
 or send an email to license@isb-sib.ch).
Dictyostelium discoideum (Slime mold)
 PRT;
 EMBL; M59745; AAA33187.1; -.
 3682 MW;
 61.3%;
60.0%;
 Conservative
 STANDARD;
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31
 SEQUENCE FROM N.A.
 <1
31
33
33 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 Phosphorylation.
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1 NILLA 5
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 PSAX ANASP
P58566;
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the Buropean Bioinformatics Institute. There are no restrictions on its way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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 SEQUENCE FROM N.A.

STRAIR=ATCC 15692 / PAO1;

MEDLINB=2043737; Pubmed=10984043;

Stover C.K., Pham X.-Q.T. Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 Gaps
 opportunistic pathogen.";
Nature 406:959-964(2000).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE UPP0057 (PMP3) FAMILY.
 ö
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
 ö
 Score 19; DB 1; Length 43;
Pred. No. 4.1e+02;
2; Mismatches 1; Indels
 Score 19; DB 1; Length 52;
Pred. No. 5e+02;
2; Mismatches 0; Indels
 EMBL; AE004493; AAG03956.1; -.
PIR; H83573; H83573.
InterPro; IPR006612; UPP0657.
Pfam; PF0409; UPF0057; 1.
PROSITE; PS01309; UPF0057; 1.
Hypothetical protein; Transmembrane; Complete proteome.
 PIR; AH1966; AH1966.
Photosystem I; Photosynthesis; Complete proteome.
INIT MET 0 0 BY SIMILARITY
SEQUENCE 43 AA; 4737 MW; 086732FB67A59FEC CRC64;
 CF552458732A04CC CRC64;
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein PA0567.
 or send an email to license@isb-sib.ch).
 POTENTIAL. POTENTIAL.
 EMBL; AP003585; BAB73240.1; -.
 61.3%;
 61.3%;
 Similarity 57.1%;
4; Conservative
 52 AA; 5717 MW;
 Query Match
Best Local Similarity 60.0
...haq 3; Conservative
 STANDARD;
 Pseudomonas aeruginosa,
 |:| |:|
29 AVNFLVA 35
 1 ALNVLMA 7
 Best Local Similarity
 NCBI_TaxID=287;
 PSEAE
 Query Match
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 0915W9;
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 ö
 -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 Gaps
 Biochemistry 27:4909-4914(1988)
-:- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
 Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
 Ewart G.D., Zhang Y.-Z., Capaldi.R.A.;
Switching of bovine cytochrome c oxidase subunit VIa isoforms in
skeletal muscle during development.";
FEBS Lett. 292:79-84(1991).
 Yanamura W., Zhang Y.-Z., Takamiya S., Capaldi R.A.; "Tissue-specific differences between heart and liver cytochrome
 -i- SUBCELLUTAR LOCATION: Mitochondrial inner membrane.
 .
 01-JAN-1990 (Rel. 13, Created)
01-GAN-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cytochrome c oxidase polypeptide VIa-liver (EC 1.9.3.1) (SSG).
 Length 85;
 Score 19; DB 1; Length 85;
Pred. No. 8.3e+02;
0; Mismatches 1; Indels
 L -> Y (IN REF. 2).
V -> L (IN REF. 2).
M -> T (IN REF. 2).
9F493F6979E2E74B CRC64;
 EMBL; M38520; AAA30437.1; -.
PIR; S18314; S18314.
InterPro; IPR001349; COX6A.
PFam; PF02046; COX6A; 1.
PROSITE; PS01329; COX6A; 1.
PROSITE; PS01329; COX6A; 1.
COXIGOTED STATE TO STATE
85 AA.
 PRT;
 MEDLINE=92070527; PubMed=1720401;
 TISSUE=Liver;
MEDLINE=89000697; PubMed=2844245;
 61.3%;
80.0%;
 85 AA; 9507 MW
 4; Conservative
 STANDARD;
 Bos taurus (Bovine)
 Similarity
 SEQUENCE FROM N.A.
 31 LNVFM 35
 SEQUENCE OF 1-32.
 2 LINVLM 6
 NCBI_TaxID=9913;
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0;
 Mitochondrion.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
Marchantiopsida; Marchantiidae; Marchantiales; Marchantiacee;
Marchantiacee; Marchantia.
 Gaps
 Korszun Z.R., Salemme F.R.;
"Structure of cytochrome c555 of Chlorobium thiosulfatophilum:
"primitive low-potential cytochrome c.";
"Proc. Natl. Acad. Sci. U.S.A. 74:5244-5247 (1977).
-I- FUNCTION: This basic c-type monoheme cytochrome has been found exclusively in the green photosynthetic bacteria, although its role in bacterial photosynthesis is not established. It has an unusually low redox potential compared with mitochondrial cytochrome c. It is reactive with cytochrome c oxidases but not
 Shaw E.K.;
"The amino acid sequences of the cytochromes c-555 from two green sulphur bacteria of the genus Chlorobium.";
Biochem. J. 159:757-774(1976).
 SEQUENCE FROM N.A.
MEDIJNE-92114051; PubMed=1731062;
MEDIJNE-92114051; PubMed=1731062;
MAGBHI K., Kanegae T., Ogura Y., Kohchi T., Ohyama K.;
 ö
 van Beeumen J., Ambler R.P., Meyer T.E., Kamen M.D., Olson J.M.
 01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 10.2 kba protein in RPS1-NAD4L intergenic region (ORF 86A).
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cytochrome c-555 (C555).
Chlorobium limicola f.sp. thiosulfatophilum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
 Score 19; DB 1; Length 86;
Pred. No. 8.4e+02;
3; Mismatches 0; Indels
 HEME (COVALENT).
HEME (COVALENT).
IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).
0882D21350DB9D4E CRC64;
 86 AA
 86 AA.
 Electron transport; Photosynthesis; Heme
 X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
MEDLINE-78094383; Pubmed=202947;
 Interpro; IPR003088; Cyt CI.
Interpro; IPR003088; Cyt Ci.
Pfam: PF00034; Cytcchrome C; Ppfam: PF00034; Cytcchrome C; I.
PROSITE; PS00190; CYTCCHROME C; I.
 PRT;
 Marchantia polymorpha (Liverwort).
 MEDLINE=77087088; PubMed=188412;
 8780 MW;
 61.3%;
 50.08;
 Local Similarity 50.0
hes 3; Conservative
 STANDARD;
 STANDARD;
 with reductases.
 HSSP; P11732; 1CC5.
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42 MNVMVA 47
 18
60
86 AA;
 NCBI_TaxID=115852;
 2 LNVLMA 7
 NCBI_TaxID=3197;
 RESULT 44
YM17 MARPO
AC P38460;
DT 01-0CT-1994
DT 01-0CT-1994
DT 16-0CT-2001
DB (ORF 86A).
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 ô
 diphosphate + L-asparaginyl-tRNA(Asn).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
 přam; pr00152; tRNA-synt Z; ĭ.
PRLINTS; PRO1042; TRNASYNTHABD.
PROSITE; PS50862; AA TRNA LIGASE II; PARTIAL.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 Gaps
Marchantia polymorpha mitochondrial DNA. A primitive form of plant mitochondrial genome.";
 MEDLINE=94287708; PubMed=8017101;
Adjiri A., Chanet R., Mezard C., Fabre F.;
"Sequence comparison of the ARG4 chromosomal regions from the two
related yeasts, Saccharomyces cerevisiae and Saccharomyces
 Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=46617;
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative asparaginyl-tRNA synthetase, cytoplasmic (EC 6.1.1.22)
(Asparagine--tRNA ligase) (AsnRS) (Fragment).
 ö
 -!- CATALYTIC ACTIVITY: ATP + L-asparagine + tRNA (Asn) = AMP
 Score 19; DB 1; Length 86; Pred. No. 8.4e+02; i Mismatches 0; Indels
 809246B7664A5F17 CRC64;
 87 AA; 9934 MW; 98174AB082C64E78 CRC64;
 87 AA.
 Interpro; IPRO04364; tRNA-synt_2.
Interpro; IPRO02312; tRNA-synt_asp.
Interpro; IPRO06195; tRNA_ligase_II.
Pfam: PF00152; tRNA-synt_2; 1.
 Mitochondrion; Hypothetical protein.
SEQUENCE 86 AA; 10237 MW; 809246
 PRT;
 Saccharomyces douglasii (Yeast).
 61.3%;
60.0%;
 EMBL; X73886; CAA52090.1; -.
 mitochondrial genome.";
J. Mol. Biol. 223:1-7(1992).
 EMBL; M68929; AAC09428.1; -. PIR; S25987; S25987.
 3; Conservative
 STANDARD;
 Keast 10:309-317(1994)
 Local Similarity
 SEQUENCE FROM N.A.
 36 LNILL 40
 2 LINVLM 6
 P04802
 SYNC_SACDO
P41908;
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0; Gaps 0;
Query Match 61.3%; Score 19; DB 1; Length 87; Best Local Similarity 66.7%; Pred. No. 8.5e+02; Matches 4; Conservative 1; Mismatches 1; Indels
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2 LNVLMA 7 :| ||| 21 MNELMA 26

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Search completed: February 17, 2004, 10:57:05 Job time : 3.21782 secs

(OT92U) XWAJB 39A9 21HT